NCBI GI	g1628583
BLAST score	354
E value	1.0e-33
Match length	88
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143936
Seq. ID	LIB3168-034-P1-K1-E10
Method	BLASTX
NCBI GI	g112682
BLAST score	675
E value	3.0e-71
Match length	137
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143937
Seq. ID	LIB3168-034-P1-K1-E11
Method	BLASTX
NCBI GI	g112682
BLAST score	576
E value	1.0e-59
Match length	120
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143938
Seq. ID	LIB3168-034-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	252
E value	1.0e-21
Match length	51
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143939
Seq. ID	LIB3168-034-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	585
E value	1.0e-60

Match length	111
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143940
Seq. ID	LIB3168-034-P1-K1-E3
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	2.0e-60
Match length	136
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143941
Seq. ID	LIB3168-034-P1-K1-E5
Method	BLASTX
NCBI GI	g4204298
BLAST score	538
E value	4.0e-55
Match length	131
% identity	80
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	143942
Seq. ID	LIB3168-034-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	708
E value	4.0e-75
Match length	136
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143943
Seq. ID	LIB3168-034-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	722
E value	9.0e-77
Match length	137
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143944
Seq. ID	LIB3168-034-P1-K1-E8

Method	BLASTN
NCBI GI	g3046853
BLAST score	367
E value	0.0e+00
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	143945
Seq. ID	LIB3168-034-P1-K1-E9
Method	BLASTN
NCBI GI	g4220635
BLAST score	52
E value	2.0e-20
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	143946
Seq. ID	LIB3168-034-P1-K1-F1
Method	BLASTN
NCBI GI	g3282170
BLAST score	301
E value	1.0e-169
Match length	430
% identity	66
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	143947
Seq. ID	LIB3168-034-P1-K1-F10
Method	BLASTX
NCBI GI	g1703723
BLAST score	466
E value	9.0e-47
Match length	106
% identity	86
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_733448 (U23082) CF1 ATP synthase beta subunit [Spinacia oleracea]

Seq. No.	143948
Seq. ID	LIB3168-034-P1-K1-F12
Method	BLASTN
NCBI GI	g3522932
BLAST score	161
E value	2.0e-85
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	143949
Seq. ID	LIB3168-034-P1-K1-F3
Method	BLASTX
NCBI GI	g2809258

BLAST score 124
E value 3.0e-42
Match length 89
% identity 100
NCBI Description (AC002560) F21B7.27 [Arabidopsis thaliana]

Seq. No. 143950
Seq. ID LIB3168-034-P1-K1-F4
Method BLASTX
NCBI GI g1172873
BLAST score 634
E value 2.0e-66
Match length 125
% identity 100
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No. 143951
Seq. ID LIB3168-034-P1-K1-F5
Method BLASTX
NCBI GI g1174850
BLAST score 517
E value 1.0e-52
Match length 112
% identity 88
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No. 143952
Seq. ID LIB3168-034-P1-K1-F7
Method BLASTX
NCBI GI g861366
BLAST score 349
E value 5.0e-33
Match length 123
% identity 54
NCBI Description (U28991) coded for by C. elegans cDNA cm21c7 [Caenorhabditis elegans]

Seq. No. 143953
Seq. ID LIB3168-034-P1-K1-F8
Method BLASTX
NCBI GI g2924262
BLAST score 595
E value 6.0e-62
Match length 126
% identity 90
NCBI Description (Z00044) PSII 44kd protein [Nicotiana tabacum]

Seq. No. 143954
Seq. ID LIB3168-034-P1-K1-F9
Method BLASTN
NCBI GI g4662628
BLAST score 261
E value 1.0e-145

Match length	417
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	143955
Seq. ID	LIB3168-034-P1-K1-G1
Method	BLASTX
NCBI GI	g112737
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	143956
Seq. ID	LIB3168-034-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	548
E value	2.0e-56
Match length	138
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143957
Seq. ID	LIB3168-034-P1-K1-G11
Method	BLASTX
NCBI GI	g1170034
BLAST score	218
E value	2.0e-21
Match length	66
% identity	79
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	143958
Seq. ID	LIB3168-034-P1-K1-G3
Method	BLASTN
NCBI GI	g3449331
BLAST score	360
E value	0.0e+00
Match length	408
% identity	24
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	143959
Seq. ID	LIB3168-034-P1-K1-G5
Method	BLASTX
NCBI GI	g2829918
BLAST score	609
E value	2.0e-63
Match length	126
% identity	95
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	143960
Seq. ID	LIB3168-034-P1-K1-G7
Method	BLASTX
NCBI GI	g266693
BLAST score	382
E value	4.0e-41
Match length	130
% identity	72
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	143961
Seq. ID	LIB3168-034-P1-K1-G9
Method	BLASTN
NCBI GI	g4490717
BLAST score	201
E value	1.0e-109
Match length	366
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	143962
Seq. ID	LIB3168-034-P1-K1-H2
Method	BLASTN
NCBI GI	g3046853
BLAST score	152
E value	6.0e-80
Match length	318
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	143963
Seq. ID	LIB3168-034-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143964
Seq. ID	LIB3168-034-P1-K1-H5
Method	BLASTX
NCBI GI	g1169598
BLAST score	400
E value	5.0e-39
Match length	90
% identity	82
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	143965
Seq. ID	LIB3168-034-P1-K1-H7
Method	BLASTX
NCBI GI	g112682
BLAST score	557
E value	2.0e-57
Match length	132
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143966
Seq. ID	LIB3168-034-P1-K1-H8
Method	BLASTX
NCBI GI	g464775
BLAST score	393
E value	4.0e-38
Match length	98
% identity	73
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	143967
Seq. ID	LIB3168-034-P1-K1-H9
Method	BLASTN
NCBI GI	g2924257
BLAST score	55
E value	2.0e-22
Match length	87
% identity	91
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	143968
Seq. ID	LIB3168-035-P1-K1-A1
Method	BLASTX
NCBI GI	g231683
BLAST score	542
E value	1.0e-55

Match length	124
% identity	81
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	143969
Seq. ID	LIB3168-035-P1-K1-A10
Method	BLASTX
NCBI GI	g112681
BLAST score	610
E value	1.0e-63
Match length	122
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143970
Seq. ID	LIB3168-035-P1-K1-A11
Method	BLASTX
NCBI GI	g112743
BLAST score	547
E value	3.0e-56
Match length	119
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	143971
Seq. ID	LIB3168-035-P1-K1-A12
Method	BLASTN
NCBI GI	g3461810
BLAST score	174
E value	4.0e-93
Match length	304
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	143972
Seq. ID	LIB3168-035-P1-K1-A2
Method	BLASTX
NCBI GI	g4522003
BLAST score	468
E value	1.0e-50
Match length	125
% identity	78
NCBI Description	(AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No.	143973
Seq. ID	LIB3168-035-P1-K1-A5
Method	BLASTX
NCBI GI	g112737
BLAST score	566
E value	2.0e-58
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	143974
Seq. ID	LIB3168-035-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	610
E value	1.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143975
Seq. ID	LIB3168-035-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	479
E value	3.0e-48
Match length	136
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143976
Seq. ID	LIB3168-035-P1-K1-A8
Method	BLASTX
NCBI GI	g112682
BLAST score	441
E value	4.0e-44
Match length	91
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143977
Seq. ID	LIB3168-035-P1-K1-B1
Method	BLASTX
NCBI GI	g3153205
BLAST score	365
E value	7.0e-35
Match length	71
% identity	100
NCBI Description	(U80922) serine/threonine protein phosphatase type one [Arabidopsis thaliana]

Seq. No.	143978
Seq. ID	LIB3168-035-P1-K1-B10
Method	BLASTN
NCBI GI	g2760168
BLAST score	426
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	143979
Seq. ID	LIB3168-035-P1-K1-B12
Method	BLASTX
NCBI GI	g4262250
BLAST score	416
E value	7.0e-41
Match length	83
% identity	100
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	143980
Seq. ID	LIB3168-035-P1-K1-B2
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	8.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143981
Seq. ID	LIB3168-035-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	3.0e-56
Match length	116
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143982
Seq. ID	LIB3168-035-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	651
E value	2.0e-68
Match length	126
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143983
Seq. ID	LIB3168-035-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	574
E value	2.0e-59
Match length	116
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143984
Seq. ID	LIB3168-035-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	521
E value	3.0e-53
Match length	133
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143985
Seq. ID	LIB3168-035-P1-K1-B9
Method	BLASTN
NCBI GI	g2924505
BLAST score	389
E value	0.0e+00
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	143986
Seq. ID	LIB3168-035-P1-K1-C10
Method	BLASTX
NCBI GI	g112737
BLAST score	454
E value	3.0e-45
Match length	134
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	143987
Seq. ID	LIB3168-035-P1-K1-C11
Method	BLASTN
NCBI GI	g2842474
BLAST score	266
E value	1.0e-148
Match length	266
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	143988
Seq. ID	LIB3168-035-P1-K1-C12
Method	BLASTX
NCBI GI	g112682
BLAST score	523
E value	2.0e-53
Match length	112
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143989
Seq. ID	LIB3168-035-P1-K1-C2
Method	BLASTX
NCBI GI	g112682
BLAST score	586
E value	9.0e-61
Match length	138
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143990
Seq. ID	LIB3168-035-P1-K1-C4
Method	BLASTN
NCBI GI	g3047074
BLAST score	242
E value	1.0e-133
Match length	394
% identity	92
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	143991

Seq. ID	LIB3168-035-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	589
E value	3.0e-61
Match length	119
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143992
Seq. ID	LIB3168-035-P1-K1-C7
Method	BLASTX
NCBI GI	g4539293
BLAST score	615
E value	3.0e-64
Match length	140
% identity	86
NCBI Description	(AL049480) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	143993
Seq. ID	LIB3168-035-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	592
E value	1.0e-61
Match length	116
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143994
Seq. ID	LIB3168-035-P1-K1-C9
Method	BLASTX
NCBI GI	g4512675
BLAST score	451
E value	6.0e-45
Match length	121
% identity	76
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	143995
Seq. ID	LIB3168-035-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	143996

Seq. ID	LIB3168-035-P1-K1-D10
Method	BLASTX
NCBI GI	g4678261
BLAST score	535
E value	3.0e-56
Match length	120
% identity	100
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	143997
Seq. ID	LIB3168-035-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	342
E value	1.0e-32
Match length	79
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	143998
Seq. ID	LIB3168-035-P1-K1-D12
Method	BLASTN
NCBI GI	g2244788
BLAST score	197
E value	1.0e-107
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	143999
Seq. ID	LIB3168-035-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	616
E value	2.0e-64
Match length	126
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144000
Seq. ID	LIB3168-035-P1-K1-D3
Method	BLASTN
NCBI GI	g4580386
BLAST score	227
E value	1.0e-124
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	144001
Seq. ID	LIB3168-035-P1-K1-D4
Method	BLASTN
NCBI GI	g3264774
BLAST score	141
E value	2.0e-73
Match length	338
% identity	97
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	144002
Seq. ID	LIB3168-035-P1-K1-D5
Method	BLASTN
NCBI GI	g166609
BLAST score	107
E value	1.0e-53
Match length	107
% identity	100
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	144003
Seq. ID	LIB3168-035-P1-K1-D6
Method	BLASTX
NCBI GI	g112682
BLAST score	367
E value	2.0e-35
Match length	87
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144004
Seq. ID	LIB3168-035-P1-K1-D7
Method	BLASTX
NCBI GI	g112681
BLAST score	229
E value	3.0e-19
Match length	79
% identity	61
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144005
Seq. ID	LIB3168-035-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	369
E value	1.0e-36

Match length	96
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144006
Seq. ID	LIB3168-035-P1-K1-E1
Method	BLASTX
NCBI GI	g112681
BLAST score	474
E value	9.0e-48
Match length	115
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144007
Seq. ID	LIB3168-035-P1-K1-E10
Method	BLASTN
NCBI GI	g2842474
BLAST score	287
E value	1.0e-160
Match length	343
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144008
Seq. ID	LIB3168-035-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	657
E value	4.0e-69
Match length	127
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144009
Seq. ID	LIB3168-035-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	656
E value	5.0e-69
Match length	131
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144010
Seq. ID	LIB3168-035-P1-K1-E2

Method	BLASTX
NCBI GI	g3170525
BLAST score	413
E value	2.0e-40
Match length	101
% identity	79
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	144011
Seq. ID	LIB3168-035-P1-K1-E3
Method	BLASTX
NCBI GI	g2129657
BLAST score	340
E value	6.0e-32
Match length	98
% identity	74
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144012
Seq. ID	LIB3168-035-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	332
E value	2.0e-31
Match length	82
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144013
Seq. ID	LIB3168-035-P1-K1-E6
Method	BLASTN
NCBI GI	g166569
BLAST score	102
E value	1.0e-50
Match length	142
% identity	93
NCBI Description	Arabidopsis thaliana glycine rich protein (RAB18) gene, complete cds

Seq. No.	144014
Seq. ID	LIB3168-035-P1-K1-E7
Method	BLASTX
NCBI GI	g4678285
BLAST score	166
E value	8.0e-12
Match length	49
% identity	59
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	144015
Seq. ID	LIB3168-035-P1-K1-E8
Method	BLASTX

NCBI GI	g1628583
BLAST score	565
E value	2.0e-58
Match length	127
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144016
Seq. ID	LIB3168-035-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	486
E value	2.0e-49
Match length	97
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144017
Seq. ID	LIB3168-035-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	564
E value	3.0e-58
Match length	119
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144018
Seq. ID	LIB3168-035-P1-K1-F12
Method	BLASTN
NCBI GI	g16236
BLAST score	86
E value	8.0e-41
Match length	173
% identity	87
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	144019
Seq. ID	LIB3168-035-P1-K1-F5
Method	BLASTX
NCBI GI	g2605714
BLAST score	43
E value	1.0e-12
Match length	54
% identity	81
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	144020
Seq. ID	LIB3168-035-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	560
E value	9.0e-58
Match length	131
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144021
Seq. ID	LIB3168-035-P1-K1-G10
Method	BLASTX
NCBI GI	g112681
BLAST score	541
E value	1.0e-55
Match length	110
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144022
Seq. ID	LIB3168-035-P1-K1-G11
Method	BLASTX
NCBI GI	g112741
BLAST score	51
E value	3.0e-67
Match length	129
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144023
Seq. ID	LIB3168-035-P1-K1-G2
Method	BLASTX
NCBI GI	g3695023
BLAST score	599
E value	2.0e-62
Match length	115
% identity	100
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	144024
Seq. ID	LIB3168-035-P1-K1-G3

Method	BLASTX
NCBI GI	g4056489
BLAST score	443
E value	5.0e-44
Match length	111
% identity	72
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	144025
Seq. ID	LIB3168-035-P1-K1-G4
Method	BLASTX
NCBI GI	g112681
BLAST score	538
E value	4.0e-55
Match length	144
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144026
Seq. ID	LIB3168-035-P1-K1-G5
Method	BLASTN
NCBI GI	g3510339
BLAST score	226
E value	1.0e-124
Match length	258
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	144027
Seq. ID	LIB3168-035-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	542
E value	1.0e-55
Match length	116
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144028
Seq. ID	LIB3168-035-P1-K1-G7
Method	BLASTX
NCBI GI	g112681
BLAST score	323
E value	3.0e-30
Match length	90
% identity	70
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	144029
Seq. ID	LIB3168-035-P1-K1-G8
Method	BLASTN
NCBI GI	g2924257
BLAST score	51
E value	8.0e-20
Match length	219
% identity	85
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	144030
Seq. ID	LIB3168-035-P1-K1-H1
Method	BLASTX
NCBI GI	g3913418
BLAST score	738
E value	1.0e-78
Match length	141
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	144031
Seq. ID	LIB3168-035-P1-K1-H10
Method	BLASTN
NCBI GI	g4199934
BLAST score	225
E value	1.0e-123
Match length	241
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	144032
Seq. ID	LIB3168-035-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	638
E value	6.0e-67
Match length	125
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144033
Seq. ID	LIB3168-035-P1-K1-H12
Method	BLASTX
NCBI GI	g112737
BLAST score	299
E value	4.0e-27
Match length	129
% identity	52
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144034
Seq. ID	LIB3168-035-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	661
E value	1.0e-69
Match length	133
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144035
Seq. ID	LIB3168-035-P1-K1-H3
Method	BLASTN
NCBI GI	g4376087
BLAST score	241
E value	1.0e-133
Match length	352
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	144036
Seq. ID	LIB3168-035-P1-K1-H6
Method	BLASTN
NCBI GI	g4159703
BLAST score	31
E value	1.0e-08
Match length	58
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	144037
Seq. ID	LIB3168-035-P1-K1-H7
Method	BLASTX
NCBI GI	g112741
BLAST score	482
E value	2.0e-50
Match length	111
% identity	93
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144038

Seq. ID	LIB3168-036-P1-K1-A10
Method	BLASTX
NCBI GI	g112739
BLAST score	568
E value	1.0e-58
Match length	150
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144039
Seq. ID	LIB3168-036-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	734
E value	4.0e-78
Match length	154
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144040
Seq. ID	LIB3168-036-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	878
E value	7.0e-95
Match length	179
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144041
Seq. ID	LIB3168-036-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144042
Seq. ID	LIB3168-036-P1-K1-A5
Method	BLASTX
NCBI GI	g2924779
BLAST score	711
E value	2.0e-75

Match length	141
% identity	99
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	144043
Seq. ID	LIB3168-036-P1-K1-A8
Method	BLASTX
NCBI GI	g112682
BLAST score	257
E value	8.0e-23
Match length	69
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144044
Seq. ID	LIB3168-036-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64
Match length	131
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144045
Seq. ID	LIB3168-036-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	579
E value	7.0e-60
Match length	117
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144046
Seq. ID	LIB3168-036-P1-K1-B10
Method	BLASTN
NCBI GI	g4646215
BLAST score	102
E value	6.0e-50
Match length	487
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No.	144047
Seq. ID	LIB3168-036-P1-K1-B12
Method	BLASTX
NCBI GI	g112682
BLAST score	717
E value	5.0e-76
Match length	159
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144048
Seq. ID	LIB3168-036-P1-K1-B2
Method	BLASTX
NCBI GI	g166410
BLAST score	306
E value	4.0e-30
Match length	123
% identity	59
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	144049
Seq. ID	LIB3168-036-P1-K1-B4
Method	BLASTN
NCBI GI	g3047060
BLAST score	238
E value	1.0e-131
Match length	274
% identity	97
NCBI Description	Arabidopsis thaliana BAC F7N22

Seq. No.	144050
Seq. ID	LIB3168-036-P1-K1-B5
Method	BLASTX
NCBI GI	g1076442
BLAST score	595
E value	1.0e-61
Match length	133
% identity	74
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	144051
Seq. ID	LIB3168-036-P1-K1-B6
Method	BLASTX
NCBI GI	g112681
BLAST score	367
E value	9.0e-52
Match length	151
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144052
Seq. ID	LIB3168-036-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	727
E value	4.0e-77
Match length	179
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144053
Seq. ID	LIB3168-036-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	9.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144054
Seq. ID	LIB3168-036-P1-K1-C1
Method	BLASTN
NCBI GI	g3461810
BLAST score	44
E value	3.0e-16
Match length	52
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144055
Seq. ID	LIB3168-036-P1-K1-C10
Method	BLASTX
NCBI GI	g3341679
BLAST score	672
E value	9.0e-71
Match length	160
% identity	79
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	144056
Seq. ID	LIB3168-036-P1-K1-C11
Method	BLASTX
NCBI GI	g1402904
BLAST score	664
E value	6.0e-70

Match length	127
% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	144057
Seq. ID	LIB3168-036-P1-K1-C12
Method	BLASTX
NCBI GI	g3738288
BLAST score	711
E value	2.0e-75
Match length	145
% identity	97
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	144058
Seq. ID	LIB3168-036-P1-K1-C2
Method	BLASTX
NCBI GI	g114532
BLAST score	403
E value	4.0e-39
Match length	92
% identity	86
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No.	144059
Seq. ID	LIB3168-036-P1-K1-C4
Method	BLASTX
NCBI GI	g1946355
BLAST score	250
E value	3.0e-21
Match length	104
% identity	48
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	144060
Seq. ID	LIB3168-036-P1-K1-C5
Method	BLASTX
NCBI GI	g2708747
BLAST score	459
E value	4.0e-46
Match length	95
% identity	95
NCBI Description	(AC003952) putative glycine-rich, zinc-finger DNA-binding protein [Arabidopsis thaliana]

Seq. No.	144061
Seq. ID	LIB3168-036-P1-K1-C6
Method	BLASTX

NCBI GI	g1628583
BLAST score	686
E value	2.0e-72
Match length	135
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144062
Seq. ID	LIB3168-036-P1-K1-C8
Method	BLASTX
NCBI GI	g1169598
BLAST score	869
E value	8.0e-94
Match length	170
% identity	92
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	144063
Seq. ID	LIB3168-036-P1-K1-C9
Method	BLASTN
NCBI GI	g4572664
BLAST score	93
E value	4.0e-45
Match length	137
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	144064
Seq. ID	LIB3168-036-P1-K1-D1
Method	BLASTX
NCBI GI	g1694711
BLAST score	358
E value	2.0e-34
Match length	83
% identity	88
NCBI Description	(Y09581) FRO1 [Arabidopsis thaliana]

Seq. No.	144065
Seq. ID	LIB3168-036-P1-K1-D11
Method	BLASTX
NCBI GI	g1063415
BLAST score	607
E value	3.0e-63
Match length	116
% identity	99
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	144066
Seq. ID	LIB3168-036-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	585

E value	8.0e-61
Match length	116
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144067
Seq. ID	LIB3168-036-P1-K1-D2
Method	BLASTN
NCBI GI	g633027
BLAST score	390
E value	0.0e+00
Match length	446
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for protein phosphatase 2C

Seq. No.	144068
Seq. ID	LIB3168-036-P1-K1-D4
Method	BLASTX
NCBI GI	g3377797
BLAST score	405
E value	1.0e-39
Match length	92
% identity	87
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	144069
Seq. ID	LIB3168-036-P1-K1-D7
Method	BLASTX
NCBI GI	g112682
BLAST score	710
E value	3.0e-75
Match length	160
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144070
Seq. ID	LIB3168-036-P1-K1-D8
Method	BLASTX
NCBI GI	g4432860
BLAST score	860
E value	9.0e-93
Match length	180
% identity	36
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	144071
Seq. ID	LIB3168-036-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	228
E value	1.0e-18
Match length	97
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144072
Seq. ID	LIB3168-036-P1-K1-E1
Method	BLASTN
NCBI GI	g4159712
BLAST score	391
E value	0.0e+00
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	144073
Seq. ID	LIB3168-036-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144074
Seq. ID	LIB3168-036-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	257
E value	4.0e-22
Match length	157
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144075
Seq. ID	LIB3168-036-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	578
E value	7.0e-60
Match length	142
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144076
Seq. ID	LIB3168-036-P1-K1-E4
Method	BLASTX
NCBI GI	g4337025
BLAST score	516
E value	9.0e-53
Match length	105
% identity	98
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	144077
Seq. ID	LIB3168-036-P1-K1-E5
Method	BLASTX
NCBI GI	g112682
BLAST score	548
E value	2.0e-56
Match length	118
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144078
Seq. ID	LIB3168-036-P1-K1-E6
Method	BLASTX
NCBI GI	g1169598
BLAST score	333
E value	3.0e-31
Match length	79
% identity	80
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	144079
Seq. ID	LIB3168-036-P1-K1-E7
Method	BLASTN
NCBI GI	g3510339
BLAST score	462
E value	0.0e+00
Match length	494
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	144080
Seq. ID	LIB3168-036-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	666
E value	3.0e-70
Match length	131

% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144081
Seq. ID	LIB3168-036-P1-K1-F10
Method	BLASTX
NCBI GI	g4204298
BLAST score	600
E value	2.0e-62
Match length	149
% identity	79
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144082
Seq. ID	LIB3168-036-P1-K1-F11
Method	BLASTX
NCBI GI	g3914541
BLAST score	490
E value	2.0e-49
Match length	113
% identity	84
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_1928872 (U91966) ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Arabidopsis thaliana]

Seq. No.	144083
Seq. ID	LIB3168-036-P1-K1-F2
Method	BLASTX
NCBI GI	g112682
BLAST score	816
E value	1.0e-87
Match length	161
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144084
Seq. ID	LIB3168-036-P1-K1-F4
Method	BLASTX
NCBI GI	g112682
BLAST score	579
E value	5.0e-60
Match length	124
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144085
Seq. ID	LIB3168-036-P1-K1-F5
Method	BLASTX
NCBI GI	g2583125
BLAST score	633
E value	7.0e-69
Match length	132
% identity	99
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	144086
Seq. ID	LIB3168-036-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	49
E value	5.0e-61
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144087
Seq. ID	LIB3168-036-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144088
Seq. ID	LIB3168-036-P1-K1-F8
Method	BLASTX
NCBI GI	g112739
BLAST score	510
E value	2.0e-54
Match length	151
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144089
Seq. ID	LIB3168-036-P1-K1-G1
Method	BLASTN
NCBI GI	g4079614
BLAST score	111
E value	6.0e-56

Match length	143
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144090
Seq. ID	LIB3168-036-P1-K1-G10
Method	BLASTX
NCBI GI	g2129657
BLAST score	458
E value	9.0e-46
Match length	121
% identity	79
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144091
Seq. ID	LIB3168-036-P1-K1-G11
Method	BLASTN
NCBI GI	g4732166
BLAST score	340
E value	0.0e+00
Match length	488
% identity	29
NCBI Description	Arabidopsis thaliana BAC F21I2

Seq. No.	144092
Seq. ID	LIB3168-036-P1-K1-G12
Method	BLASTX
NCBI GI	g1352463
BLAST score	601
E value	1.0e-62
Match length	121
% identity	96
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	144093
Seq. ID	LIB3168-036-P1-K1-G2
Method	BLASTX
NCBI GI	g112682
BLAST score	558
E value	2.0e-57
Match length	126
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144094
Seq. ID	LIB3168-036-P1-K1-G3
Method	BLASTN

NCBI GI	g3746057
BLAST score	294
E value	1.0e-164
Match length	359
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144095
Seq. ID	LIB3168-036-P1-K1-G4
Method	BLASTX
NCBI GI	g2583125
BLAST score	758
E value	6.0e-81
Match length	148
% identity	91
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	144096
Seq. ID	LIB3168-036-P1-K1-G5
Method	BLASTX
NCBI GI	g112682
BLAST score	717
E value	5.0e-76
Match length	159
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144097
Seq. ID	LIB3168-036-P1-K1-G6
Method	BLASTX
NCBI GI	g112682
BLAST score	259
E value	9.0e-77
Match length	164
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144098
Seq. ID	LIB3168-036-P1-K1-G7
Method	BLASTN
NCBI GI	g395203
BLAST score	111
E value	4.0e-56
Match length	111
% identity	53
NCBI Description	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

Seq. No.	144099
Seq. ID	LIB3168-036-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144100
Seq. ID	LIB3168-036-P1-K1-H1
Method	BLASTX
NCBI GI	g112681
BLAST score	622
E value	6.0e-65
Match length	126
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144101
Seq. ID	LIB3168-036-P1-K1-H11
Method	BLASTN
NCBI GI	g4159706
BLAST score	107
E value	3.0e-53
Match length	111
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	144102
Seq. ID	LIB3168-036-P1-K1-H12
Method	BLASTX
NCBI GI	g2961390
BLAST score	584
E value	1.0e-60
Match length	117
% identity	93
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	144103
Seq. ID	LIB3168-036-P1-K1-H2
Method	BLASTN
NCBI GI	g3128136
BLAST score	393
E value	0.0e+00
Match length	507
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	144104
Seq. ID	LIB3168-036-P1-K1-H3
Method	BLASTX
NCBI GI	g3757514
BLAST score	563
E value	5.0e-60
Match length	121
% identity	98
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana] >gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	144105
Seq. ID	LIB3168-036-P1-K1-H4
Method	BLASTX
NCBI GI	g112681
BLAST score	654
E value	8.0e-69
Match length	129
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144106
Seq. ID	LIB3168-036-P1-K1-H5
Method	BLASTX
NCBI GI	g1628583
BLAST score	371
E value	6.0e-36
Match length	86
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144107
Seq. ID	LIB3168-036-P1-K1-H6
Method	BLASTN
NCBI GI	g4159706
BLAST score	284
E value	1.0e-158
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	144108
Seq. ID	LIB3168-036-P1-K1-H7
Method	BLASTN
NCBI GI	g4741184
BLAST score	183

E value	2.0e-98
Match length	465
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	144109
Seq. ID	LIB3168-036-P1-K1-H8
Method	BLASTX
NCBI GI	g2129659
BLAST score	200
E value	9.0e-16
Match length	93
% identity	51
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	144110
Seq. ID	LIB3168-036-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	479
E value	2.0e-48
Match length	103
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144111
Seq. ID	LIB3168-037-P1-K1-A11
Method	BLASTX
NCBI GI	g3540190
BLAST score	204
E value	7.0e-16
Match length	139
% identity	39
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	144112
Seq. ID	LIB3168-037-P1-K1-A12
Method	BLASTN
NCBI GI	g4325365
BLAST score	60
E value	5.0e-25
Match length	136
% identity	46
NCBI Description	Arabidopsis thaliana BAC T3H13

Seq. No.	144113
Seq. ID	LIB3168-037-P1-K1-A3
Method	BLASTN
NCBI GI	g511598
BLAST score	261
E value	1.0e-145
Match length	322
% identity	35

NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	144114
Seq. ID	LIB3168-037-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	330
E value	2.0e-31
Match length	70
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144115
Seq. ID	LIB3168-037-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	610
E value	2.0e-63
Match length	155
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144116
Seq. ID	LIB3168-037-P1-K1-A6
Method	BLASTN
NCBI GI	g3510347
BLAST score	179
E value	6.0e-96
Match length	427
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	144117
Seq. ID	LIB3168-037-P1-K1-A7
Method	BLASTN
NCBI GI	g3075383
BLAST score	276
E value	1.0e-154
Match length	406
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144118
Seq. ID	LIB3168-037-P1-K1-A8
Method	BLASTN
NCBI GI	g1483217
BLAST score	424
E value	0.0e+00
Match length	492
% identity	98

NCBI Description A.thaliana gene induced upon wounding stress

Seq. No. 144119
Seq. ID LIB3168-037-P1-K1-A9
Method BLASTX
NCBI GI g3169059
BLAST score 208
E value 1.0e-16
Match length 81
% identity 49
NCBI Description (AL023704) weak similarity to B.subtilis spore outgrowth f actor B [Schizosaccharomyces pombe]

Seq. No. 144120
Seq. ID LIB3168-037-P1-K1-B1
Method BLASTX
NCBI GI g4204299
BLAST score 174
E value 4.0e-13
Match length 43
% identity 81
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 144121
Seq. ID LIB3168-037-P1-K1-B10
Method BLASTX
NCBI GI g112681
BLAST score 590
E value 3.0e-61
Match length 155
% identity 79
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144122
Seq. ID LIB3168-037-P1-K1-B2
Method BLASTX
NCBI GI g112739
BLAST score 378
E value 3.0e-36
Match length 150
% identity 54
NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 144123
Seq. ID LIB3168-037-P1-K1-B3
Method BLASTX

NCBI GI	g1628583
BLAST score	418
E value	2.0e-41
Match length	95
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144124
Seq. ID	LIB3168-037-P1-K1-B4
Method	BLASTX
NCBI GI	g2194125
BLAST score	230
E value	6.0e-19
Match length	59
% identity	80
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	144125
Seq. ID	LIB3168-037-P1-K1-B6
Method	BLASTN
NCBI GI	g4185120
BLAST score	254
E value	1.0e-140
Match length	437
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144126
Seq. ID	LIB3168-037-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	631
E value	5.0e-66
Match length	144
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144127
Seq. ID	LIB3168-037-P1-K1-B8
Method	BLASTX
NCBI GI	g112682
BLAST score	510
E value	5.0e-52
Match length	113
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	144128
Seq. ID	LIB3168-037-P1-K1-C1
Method	BLASTX
NCBI GI	g4263704
BLAST score	211
E value	7.0e-17
Match length	74
% identity	49
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	144129
Seq. ID	LIB3168-037-P1-K1-C10
Method	BLASTX
NCBI GI	g4234941
BLAST score	268
E value	5.0e-24
Match length	68
% identity	82
NCBI Description	(AF097938) cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]

Seq. No.	144130
Seq. ID	LIB3168-037-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	543
E value	8.0e-56
Match length	126
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144131
Seq. ID	LIB3168-037-P1-K1-C12
Method	BLASTX
NCBI GI	g4204299
BLAST score	603
E value	1.0e-62
Match length	120
% identity	98
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144132
Seq. ID	LIB3168-037-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	59
E value	4.0e-27
Match length	76
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144133
Seq. ID	LIB3168-037-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	229
E value	4.0e-19
Match length	89
% identity	57
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144134
Seq. ID	LIB3168-037-P1-K1-C4
Method	BLASTN
NCBI GI	g4581103
BLAST score	223
E value	1.0e-122
Match length	440
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	144135
Seq. ID	LIB3168-037-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	485
E value	4.0e-49
Match length	101
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144136
Seq. ID	LIB3168-037-P1-K1-C6
Method	BLASTX
NCBI GI	g1107501
BLAST score	477
E value	5.0e-48
Match length	124
% identity	79
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	144137
Seq. ID	LIB3168-037-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	573
E value	4.0e-59
Match length	123

% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144138
Seq. ID	LIB3168-037-P1-K1-C8
Method	BLASTX
NCBI GI	g4263704
BLAST score	218
E value	2.0e-17
Match length	75
% identity	49
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	144139
Seq. ID	LIB3168-037-P1-K1-C9
Method	BLASTX
NCBI GI	g3023848
BLAST score	614
E value	5.0e-64
Match length	131
% identity	49
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	144140
Seq. ID	LIB3168-037-P1-K1-D1
Method	BLASTN
NCBI GI	g3059018
BLAST score	107
E value	2.0e-53
Match length	179
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	144141
Seq. ID	LIB3168-037-P1-K1-D10
Method	BLASTX
NCBI GI	g112682
BLAST score	733
E value	7.0e-78
Match length	165
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144142
Seq. ID	LIB3168-037-P1-K1-D11
Method	BLASTX

NCBI GI	g1628583
BLAST score	561
E value	6.0e-58
Match length	117
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144143
Seq. ID	LIB3168-037-P1-K1-D2
Method	BLASTX
NCBI GI	g2642441
BLAST score	397
E value	5.0e-39
Match length	80
% identity	97
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	144144
Seq. ID	LIB3168-037-P1-K1-D3
Method	BLASTN
NCBI GI	g2842474
BLAST score	40
E value	6.0e-14
Match length	72
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	144145
Seq. ID	LIB3168-037-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	97
E value	2.0e-44
Match length	107
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144146
Seq. ID	LIB3168-037-P1-K1-D5
Method	BLASTN
NCBI GI	g3228389
BLAST score	269
E value	1.0e-150
Match length	313
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	144147
Seq. ID	LIB3168-037-P1-K1-D6

Method	BLASTX
NCBI GI	g4006858
BLAST score	106
E value	5.0e-32
Match length	91
% identity	91
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	144148
Seq. ID	LIB3168-037-P1-K1-D7
Method	BLASTN
NCBI GI	g4519193
BLAST score	450
E value	0.0e+00
Match length	458
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	144149
Seq. ID	LIB3168-037-P1-K1-D8
Method	BLASTN
NCBI GI	g3395421
BLAST score	409
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144150
Seq. ID	LIB3168-037-P1-K1-D9
Method	BLASTX
NCBI GI	g112739
BLAST score	518
E value	1.0e-52
Match length	151
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144151
Seq. ID	LIB3168-037-P1-K1-E1
Method	BLASTX
NCBI GI	g112682
BLAST score	354
E value	6.0e-34
Match length	89
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144152
Seq. ID	LIB3168-037-P1-K1-E11
Method	BLASTX
NCBI GI	g3928086
BLAST score	79
E value	2.0e-77
Match length	156
% identity	96
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	144153
Seq. ID	LIB3168-037-P1-K1-E12
Method	BLASTX
NCBI GI	g4204299
BLAST score	816
E value	1.0e-87
Match length	178
% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144154
Seq. ID	LIB3168-037-P1-K1-E3
Method	BLASTX
NCBI GI	g4006897
BLAST score	539
E value	3.0e-55
Match length	138
% identity	76
NCBI Description	(Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.	144155
Seq. ID	LIB3168-037-P1-K1-E4
Method	BLASTX
NCBI GI	g112682
BLAST score	676
E value	3.0e-71
Match length	159
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144156
Seq. ID	LIB3168-037-P1-K1-E5
Method	BLASTX
NCBI GI	g3915847
BLAST score	273
E value	3.0e-24
Match length	63
% identity	86

NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	144157
Seq. ID	LIB3168-037-P1-K1-E6
Method	BLASTN
NCBI GI	g4490324
BLAST score	306
E value	1.0e-172
Match length	390
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	144158
Seq. ID	LIB3168-037-P1-K1-E7
Method	BLASTN
NCBI GI	g560770
BLAST score	500
E value	0.0e+00
Match length	532
% identity	98
NCBI Description	Arabidopsis thaliana rd22 gene, complete cds

Seq. No.	144159
Seq. ID	LIB3168-037-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	1.0e-56
Match length	120
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144160
Seq. ID	LIB3168-037-P1-K1-E9
Method	BLASTX
NCBI GI	g4538963
BLAST score	70
E value	4.0e-52
Match length	138
% identity	75
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	144161
Seq. ID	LIB3168-037-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	722
E value	1.0e-76
Match length	145
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144162
Seq. ID	LIB3168-037-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144163
Seq. ID	LIB3168-037-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144164
Seq. ID	LIB3168-037-P1-K1-F2
Method	BLASTX
NCBI GI	g1669601
BLAST score	211
E value	4.0e-33
Match length	117
% identity	68
NCBI Description	(D88747) AR401 [Arabidopsis thaliana]

Seq. No.	144165
Seq. ID	LIB3168-037-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	543
E value	7.0e-56
Match length	108
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144166
Seq. ID	LIB3168-037-P1-K1-F4
Method	BLASTX
NCBI GI	g267073
BLAST score	281
E value	2.0e-25

Match length	52
% identity	98
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	144167
Seq. ID	LIB3168-037-P1-K1-F7
Method	BLASTX
NCBI GI	g2894574
BLAST score	480
E value	3.0e-48
Match length	123
% identity	78
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	144168
Seq. ID	LIB3168-037-P1-K1-F8
Method	BLASTX
NCBI GI	g1161171
BLAST score	133
E value	1.0e-07
Match length	124
% identity	18
NCBI Description	(L42465) late embryogenesis abundant protein [Picea glauca]

Seq. No.	144169
Seq. ID	LIB3168-037-P1-K1-F9
Method	BLASTN
NCBI GI	g3659491
BLAST score	292
E value	1.0e-163
Match length	476
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	144170
Seq. ID	LIB3168-037-P1-K1-G1
Method	BLASTX
NCBI GI	g112737
BLAST score	169
E value	2.0e-12
Match length	35
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144171

Seq. ID	LIB3168-037-P1-K1-G10
Method	BLASTX
NCBI GI	g3850063
BLAST score	196
E value	5.0e-15
Match length	116
% identity	36
NCBI Description	(AJ223830) ARE1 [Rattus norvegicus]

Seq. No.	144172
Seq. ID	LIB3168-037-P1-K1-G11
Method	BLASTX
NCBI GI	g1628583
BLAST score	555
E value	3.0e-57
Match length	116
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144173
Seq. ID	LIB3168-037-P1-K1-G12
Method	BLASTX
NCBI GI	g461841
BLAST score	333
E value	2.0e-31
Match length	78
% identity	81
NCBI Description	CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN)

Seq. No.	144174
Seq. ID	LIB3168-037-P1-K1-G2
Method	BLASTX
NCBI GI	g112743
BLAST score	418
E value	3.0e-41
Match length	115
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144175
Seq. ID	LIB3168-037-P1-K1-G3
Method	BLASTN
NCBI GI	g4159712
BLAST score	250
E value	1.0e-138
Match length	281
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No.	144176
Seq. ID	LIB3168-037-P1-K1-G4
Method	BLASTX
NCBI GI	g544424
BLAST score	450
E value	5.0e-45
Match length	87
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	144177
Seq. ID	LIB3168-037-P1-K1-G5
Method	BLASTX
NCBI GI	g112682
BLAST score	630
E value	6.0e-66
Match length	136
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144178
Seq. ID	LIB3168-037-P1-K1-G6
Method	BLASTX
NCBI GI	g2244759
BLAST score	413
E value	1.0e-40
Match length	116
% identity	74
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	144179
Seq. ID	LIB3168-037-P1-K1-G7
Method	BLASTX
NCBI GI	g112682
BLAST score	821
E value	3.0e-88
Match length	155
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144180

Seq. ID	LIB3168-037-P1-K1-G8
Method	BLASTX
NCBI GI	g421826
BLAST score	448
E value	1.0e-44
Match length	117
% identity	74
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	144181
Seq. ID	LIB3168-037-P1-K1-G9
Method	BLASTX
NCBI GI	g4006848
BLAST score	74
E value	1.3e+00
Match length	114
% identity	63
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	144182
Seq. ID	LIB3168-037-P1-K1-H1
Method	BLASTX
NCBI GI	g112682
BLAST score	167
E value	3.0e-12
Match length	47
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144183
Seq. ID	LIB3168-037-P1-K1-H10
Method	BLASTX
NCBI GI	g112682
BLAST score	559
E value	1.0e-57
Match length	106
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144184
Seq. ID	LIB3168-037-P1-K1-H11
Method	BLASTN
NCBI GI	g2842474
BLAST score	216
E value	1.0e-118
Match length	240

% identity	63
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144185
Seq. ID	LIB3168-037-P1-K1-H12
Method	BLASTX
NCBI GI	g112682
BLAST score	324
E value	1.0e-30
Match length	66
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144186
Seq. ID	LIB3168-037-P1-K1-H2
Method	BLASTX
NCBI GI	g112741
BLAST score	334
E value	2.0e-34
Match length	77
% identity	96
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144187
Seq. ID	LIB3168-037-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	697
E value	6.0e-77
Match length	154
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144188
Seq. ID	LIB3168-037-P1-K1-H4
Method	BLASTX
NCBI GI	g3860165
BLAST score	597
E value	6.0e-62
Match length	155
% identity	43
NCBI Description	(AF098963) disease resistance protein RPP1-WsB [Arabidopsis thaliana]

Seq. No.	144189
Seq. ID	LIB3168-037-P1-K1-H5
Method	BLASTX
NCBI GI	g112682
BLAST score	755
E value	1.0e-80
Match length	144
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144190
Seq. ID	LIB3168-037-P1-K1-H6
Method	BLASTX
NCBI GI	g4204298
BLAST score	387
E value	8.0e-38
Match length	79
% identity	94
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144191
Seq. ID	LIB3168-037-P1-K1-H7
Method	BLASTX
NCBI GI	g112682
BLAST score	705
E value	1.0e-74
Match length	157
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144192
Seq. ID	LIB3168-037-P1-K1-H8
Method	BLASTX
NCBI GI	g4204298
BLAST score	596
E value	7.0e-62
Match length	150
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144193
Seq. ID	LIB3168-037-P1-K1-H9
Method	BLASTX
NCBI GI	g112741
BLAST score	109
E value	1.0e-38
Match length	102

% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144194
Seq. ID	LIB3168-040-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144195
Seq. ID	LIB3168-040-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144196
Seq. ID	LIB3168-040-P1-K1-A2
Method	BLASTX
NCBI GI	g4056488
BLAST score	381
E value	8.0e-37
Match length	70
% identity	96
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	144197
Seq. ID	LIB3168-040-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	604
E value	7.0e-63
Match length	147
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144198
Seq. ID	LIB3168-040-P1-K1-A4

Method	BLASTX
NCBI GI	g112681
BLAST score	441
E value	2.0e-54
Match length	154
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144199
Seq. ID	LIB3168-040-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	46
E value	8.0e-72
Match length	148
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144200
Seq. ID	LIB3168-040-P1-K1-A9
Method	BLASTX
NCBI GI	g2689720
BLAST score	747
E value	1.0e-79
Match length	149
% identity	99
NCBI Description	(AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No.	144201
Seq. ID	LIB3168-040-P1-K1-B10
Method	BLASTN
NCBI GI	g2494106
BLAST score	380
E value	0.0e+00
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144202
Seq. ID	LIB3168-040-P1-K1-B11
Method	BLASTN
NCBI GI	g4490701
BLAST score	94
E value	3.0e-45
Match length	262
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	144203

Seq. ID	LIB3168-040-P1-K1-B2
Method	BLASTX
NCBI GI	g4204299
BLAST score	675
E value	4.0e-71
Match length	131
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144204
Seq. ID	LIB3168-040-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	201
E value	7.0e-16
Match length	45
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144205
Seq. ID	LIB3168-040-P1-K1-B6
Method	BLASTX
NCBI GI	g2511725
BLAST score	535
E value	7.0e-55
Match length	115
% identity	91
NCBI Description	(AF021937) catalase 1 [Arabidopsis thaliana]

Seq. No.	144206
Seq. ID	LIB3168-040-P1-K1-B7
Method	BLASTN
NCBI GI	g1935913
BLAST score	49
E value	1.0e-18
Match length	113
% identity	86
NCBI Description	Arabidopsis thaliana lethal leaf-spot 1 homolog (Lls1) mRNA, partial cds

Seq. No.	144207
Seq. ID	LIB3168-040-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	609
E value	2.0e-63
Match length	151
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144208
Seq. ID	LIB3168-040-P1-K1-C1

Method	BLASTX
NCBI GI	g1628583
BLAST score	626
E value	2.0e-65
Match length	153
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144209
Seq. ID	LIB3168-040-P1-K1-C12
Method	BLASTN
NCBI GI	g4662609
BLAST score	212
E value	1.0e-116
Match length	233
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	144210
Seq. ID	LIB3168-040-P1-K1-C2
Method	BLASTX
NCBI GI	g3172023
BLAST score	587
E value	6.0e-61
Match length	124
% identity	94
NCBI Description	(AB005804) aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	144211
Seq. ID	LIB3168-040-P1-K1-C3
Method	BLASTX
NCBI GI	g3869088
BLAST score	689
E value	8.0e-73
Match length	136
% identity	98
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	144212
Seq. ID	LIB3168-040-P1-K1-C4
Method	BLASTN
NCBI GI	g4159705
BLAST score	125
E value	6.0e-64
Match length	294
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	144213
Seq. ID	LIB3168-040-P1-K1-C5
Method	BLASTN
NCBI GI	g1628582
BLAST score	41

E value	6.0e-14
Match length	55
% identity	96
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	144214
Seq. ID	LIB3168-040-P1-K1-C6
Method	BLASTX
NCBI GI	g1695717
BLAST score	511
E value	2.0e-64
Match length	137
% identity	90
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	144215
Seq. ID	LIB3168-040-P1-K1-C7
Method	BLASTX
NCBI GI	g3935145
BLAST score	216
E value	2.0e-17
Match length	86
% identity	50
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	144216
Seq. ID	LIB3168-040-P1-K1-D10
Method	BLASTX
NCBI GI	g4519671
BLAST score	269
E value	1.0e-23
Match length	95
% identity	59
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	144217
Seq. ID	LIB3168-040-P1-K1-D11
Method	BLASTN
NCBI GI	g3355463
BLAST score	444
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144218
Seq. ID	LIB3168-040-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144219
Seq. ID	LIB3168-040-P1-K1-D4
Method	BLASTX
NCBI GI	g2129659
BLAST score	302
E value	1.0e-27
Match length	93
% identity	65
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	144220
Seq. ID	LIB3168-040-P1-K1-D5
Method	BLASTN
NCBI GI	g987013
BLAST score	104
E value	8.0e-52
Match length	128
% identity	95
NCBI Description	A.thaliana mRNA for oleosin (isoform; 841 bp) >gi_987015_emb_Z54165_ATOLEOSN3 A.thaliana mRNA for oleosin (isoform; 841 bp)

Seq. No.	144221
Seq. ID	LIB3168-040-P1-K1-D7
Method	BLASTX
NCBI GI	g2924262
BLAST score	283
E value	7.0e-26
Match length	62
% identity	87
NCBI Description	(Z00044) PSII 44kd protein [Nicotiana tabacum]

Seq. No.	144222
Seq. ID	LIB3168-040-P1-K1-E10
Method	BLASTN
NCBI GI	g4510392
BLAST score	63
E value	7.0e-27
Match length	233
% identity	70
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No.	144223
Seq. ID	LIB3168-040-P1-K1-E11
Method	BLASTX
NCBI GI	g2062164
BLAST score	94
E value	5.0e-03
Match length	135
% identity	11
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	144224
Seq. ID	LIB3168-040-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	649
E value	4.0e-68
Match length	127
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144225
Seq. ID	LIB3168-040-P1-K1-E2
Method	BLASTX
NCBI GI	g2160151
BLAST score	82
E value	2.0e-48
Match length	117
% identity	91
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	144226
Seq. ID	LIB3168-040-P1-K1-E4
Method	BLASTX
NCBI GI	g166765
BLAST score	472
E value	2.0e-47
Match length	98
% identity	94
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	144227
Seq. ID	LIB3168-040-P1-K1-E7
Method	BLASTN
NCBI GI	g4678266
BLAST score	220
E value	1.0e-120
Match length	244
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	144228
Seq. ID	LIB3168-040-P1-K1-E8
Method	BLASTN
NCBI GI	g2853071
BLAST score	404
E value	0.0e+00
Match length	439
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	144229
Seq. ID	LIB3168-040-P1-K1-E9
Method	BLASTX
NCBI GI	g112739
BLAST score	609
E value	2.0e-63
Match length	142
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144230
Seq. ID	LIB3168-040-P1-K1-F10
Method	BLASTX
NCBI GI	g112741
BLAST score	781
E value	1.0e-83
Match length	146
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144231
Seq. ID	LIB3168-040-P1-K1-F12
Method	BLASTX
NCBI GI	g112737
BLAST score	460
E value	4.0e-46
Match length	115
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144232
Seq. ID	LIB3168-040-P1-K1-F2
Method	BLASTX
NCBI GI	g1628583
BLAST score	394
E value	5.0e-61
Match length	139
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144233
Seq. ID	LIB3168-040-P1-K1-F3
Method	BLASTX
NCBI GI	g2832674
BLAST score	161
E value	3.0e-11
Match length	40
% identity	80
NCBI Description	(AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]

Seq. No.	144234
Seq. ID	LIB3168-040-P1-K1-F4
Method	BLASTX
NCBI GI	g1592670
BLAST score	455
E value	2.0e-45
Match length	123
% identity	70
NCBI Description	(X91920) dehydrin [Arabidopsis thaliana] >gi_4567280_gb_AAD23693.1_AC006841_21 (AC006841) putative dehydrin [Arabidopsis thaliana]

Seq. No.	144235
Seq. ID	LIB3168-040-P1-K1-F5
Method	BLASTN
NCBI GI	g1931636
BLAST score	446
E value	0.0e+00
Match length	470
% identity	99
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	144236
Seq. ID	LIB3168-040-P1-K1-F6
Method	BLASTX
NCBI GI	g2129642
BLAST score	60
E value	3.0e-78
Match length	146
% identity	95
NCBI Description	major latex protein type 3 - Arabidopsis thaliana >gi_1107495_emb_CAA63027_ (X91961) major latex protein type3 [Arabidopsis thaliana]

Seq. No.	144237
Seq. ID	LIB3168-040-P1-K1-F7
Method	BLASTN
NCBI GI	g4582444
BLAST score	102
E value	2.0e-50
Match length	130
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic

sequence, complete sequence

Seq. No.	144238
Seq. ID	LIB3168-040-P1-K1-F8
Method	BLASTN
NCBI GI	g4220630
BLAST score	219
E value	1.0e-120
Match length	404
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2K18, complete sequence [Arabidopsis thaliana]

Seq. No.	144239
Seq. ID	LIB3168-040-P1-K1-G1
Method	BLASTX
NCBI GI	g4704766
BLAST score	562
E value	6.0e-58
Match length	152
% identity	62
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	144240
Seq. ID	LIB3168-040-P1-K1-G10
Method	BLASTX
NCBI GI	g1169476
BLAST score	634
E value	2.0e-66
Match length	127
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	144241
Seq. ID	LIB3168-040-P1-K1-G11
Method	BLASTX
NCBI GI	g4204298
BLAST score	621
E value	8.0e-65
Match length	153
% identity	80
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144242
Seq. ID	LIB3168-040-P1-K1-G12
Method	BLASTN
NCBI GI	g2618603
BLAST score	407
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	144243
Seq. ID	LIB3168-040-P1-K1-G3
Method	BLASTX
NCBI GI	g3915961
BLAST score	295
E value	1.0e-26
Match length	143
% identity	53
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	144244
Seq. ID	LIB3168-040-P1-K1-G4
Method	BLASTX
NCBI GI	g2959781
BLAST score	709
E value	3.0e-75
Match length	137
% identity	96
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	144245
Seq. ID	LIB3168-040-P1-K1-G6
Method	BLASTX
NCBI GI	g4630748
BLAST score	428
E value	3.0e-42
Match length	82
% identity	100
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	144246
Seq. ID	LIB3168-040-P1-K1-G7
Method	BLASTN
NCBI GI	g3335170
BLAST score	115
E value	6.0e-58
Match length	262
% identity	96
NCBI Description	Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No.	144247
Seq. ID	LIB3168-040-P1-K1-G8
Method	BLASTN
NCBI GI	g3402745
BLAST score	216
E value	1.0e-118
Match length	441
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	144248
Seq. ID	LIB3168-040-P1-K1-G9
Method	BLASTN
NCBI GI	g2351064
BLAST score	47
E value	3.0e-17
Match length	456
% identity	49
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	144249
Seq. ID	LIB3168-040-P1-K1-H1
Method	BLASTX
NCBI GI	g112682
BLAST score	620
E value	1.0e-64
Match length	146
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144250
Seq. ID	LIB3168-040-P1-K1-H10
Method	BLASTX
NCBI GI	g3335169
BLAST score	615
E value	4.0e-64
Match length	134
% identity	82
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	144251
Seq. ID	LIB3168-040-P1-K1-H12
Method	BLASTX
NCBI GI	g2650133
BLAST score	265
E value	4.0e-23
Match length	113
% identity	50
NCBI Description	(AE001070) ribonuclease PH (rph) [Archaeoglobus fulgidus]

Seq. No.	144252
Seq. ID	LIB3168-040-P1-K1-H2
Method	BLASTN
NCBI GI	g336917
BLAST score	48
E value	8.0e-18
Match length	120
% identity	90
NCBI Description	Epifagus virginiana chloroplast complete genome

Seq. No.	144253
Seq. ID	LIB3168-040-P1-K1-H4
Method	BLASTX
NCBI GI	g1706749
BLAST score	463
E value	2.0e-46
Match length	99
% identity	95
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]

Seq. No.	144254
Seq. ID	LIB3168-040-P1-K1-H5
Method	BLASTN
NCBI GI	g3885325
BLAST score	149
E value	4.0e-78
Match length	217
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144255
Seq. ID	LIB3168-040-P1-K1-H6
Method	BLASTN
NCBI GI	g3367500
BLAST score	124
E value	2.0e-63
Match length	196
% identity	91
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	144256
Seq. ID	LIB3168-040-P1-K1-H8
Method	BLASTX
NCBI GI	g4063751
BLAST score	198
E value	9.0e-16
Match length	79
% identity	48
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	144257
Seq. ID	LIB3168-040-P1-K1-H9
Method	BLASTN
NCBI GI	g4733991
BLAST score	80
E value	6.0e-37
Match length	238
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T4D8 genomic sequence, complete sequence

Seq. No.	144258
Seq. ID	LIB3168-041-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	175
E value	7.0e-13
Match length	80
% identity	47
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144259
Seq. ID	LIB3168-041-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	606
E value	5.0e-63
Match length	147
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144260
Seq. ID	LIB3168-041-P1-K1-A12
Method	BLASTX
NCBI GI	g112682
BLAST score	630
E value	6.0e-66
Match length	137
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144261
Seq. ID	LIB3168-041-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	237
E value	5.0e-20
Match length	112
% identity	41
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144262
Seq. ID	LIB3168-041-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	564
E value	3.0e-58

Match length	136
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144263
Seq. ID	LIB3168-041-P1-K1-A4
Method	BLASTN
NCBI GI	g4097693
BLAST score	39
E value	2.0e-13
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	144264
Seq. ID	LIB3168-041-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	432
E value	1.0e-42
Match length	120
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144265
Seq. ID	LIB3168-041-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	378
E value	9.0e-49
Match length	110
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144266
Seq. ID	LIB3168-041-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	254
E value	4.0e-22
Match length	84
% identity	61
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144267
Seq. ID	LIB3168-041-P1-K1-B1
Method	BLASTX
NCBI GI	g2129659

BLAST score	277
E value	1.0e-24
Match length	127
% identity	38
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	144268
Seq. ID	LIB3168-041-P1-K1-B10
Method	BLASTX
NCBI GI	g112681
BLAST score	823
E value	2.0e-88
Match length	156
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144269
Seq. ID	LIB3168-041-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144270
Seq. ID	LIB3168-041-P1-K1-B12
Method	BLASTN
NCBI GI	g2264306
BLAST score	208
E value	1.0e-113
Match length	216
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	144271
Seq. ID	LIB3168-041-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	81
E value	2.0e-59
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144272

Seq. ID	LIB3168-041-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	495
E value	3.0e-50
Match length	113
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144273
Seq. ID	LIB3168-041-P1-K1-B4
Method	BLASTX
NCBI GI	g112737
BLAST score	612
E value	9.0e-64
Match length	132
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144274
Seq. ID	LIB3168-041-P1-K1-B5
Method	BLASTN
NCBI GI	g166612
BLAST score	129
E value	1.0e-66
Match length	145
% identity	97
NCBI Description	A.thaliana at2S4 gene encoding albumin 2S subunit 4, complete cds

Seq. No.	144275
Seq. ID	LIB3168-041-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	223
E value	8.0e-19
Match length	48
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144276
Seq. ID	LIB3168-041-P1-K1-B9
Method	BLASTX
NCBI GI	g112741
BLAST score	52
E value	6.0e-13
Match length	43

% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144277
Seq. ID	LIB3168-041-P1-K1-C10
Method	BLASTX
NCBI GI	g2244994
BLAST score	582
E value	3.0e-60
Match length	155
% identity	79
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	144278
Seq. ID	LIB3168-041-P1-K1-C11
Method	BLASTX
NCBI GI	g112741
BLAST score	196
E value	5.0e-21
Match length	117
% identity	55
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144279
Seq. ID	LIB3168-041-P1-K1-C12
Method	BLASTX
NCBI GI	g4185505
BLAST score	419
E value	4.0e-41
Match length	112
% identity	73
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	144280
Seq. ID	LIB3168-041-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	366
E value	4.0e-35
Match length	84
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144281
Seq. ID	LIB3168-041-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	503
E value	5.0e-51
Match length	102
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144282
Seq. ID	LIB3168-041-P1-K1-C6
Method	BLASTX
NCBI GI	g112739
BLAST score	533
E value	2.0e-54
Match length	149
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144283
Seq. ID	LIB3168-041-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	435
E value	2.0e-43
Match length	95
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144284
Seq. ID	LIB3168-041-P1-K1-C8
Method	BLASTX
NCBI GI	g226120
BLAST score	54
E value	2.0e-18
Match length	154
% identity	38
NCBI Description	vicilin gene B [Saguinus oedipus]

Seq. No.	144285
Seq. ID	LIB3168-041-P1-K1-C9
Method	BLASTN
NCBI GI	g4469002
BLAST score	240

E value	1.0e-132
Match length	304
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	144286
Seq. ID	LIB3168-041-P1-K1-D10
Method	BLASTX
NCBI GI	g112737
BLAST score	675
E value	4.0e-71
Match length	156
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144287
Seq. ID	LIB3168-041-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	649
E value	4.0e-68
Match length	145
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144288
Seq. ID	LIB3168-041-P1-K1-D12
Method	BLASTX
NCBI GI	g1001311
BLAST score	155
E value	4.0e-10
Match length	81
% identity	48
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	144289
Seq. ID	LIB3168-041-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	88
E value	4.0e-77
Match length	151
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144290
Seq. ID	LIB3168-041-P1-K1-D3
Method	BLASTX
NCBI GI	g112737
BLAST score	641
E value	4.0e-67
Match length	135
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144291
Seq. ID	LIB3168-041-P1-K1-D5
Method	BLASTN
NCBI GI	g2760165
BLAST score	175
E value	1.0e-93
Match length	463
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	144292
Seq. ID	LIB3168-041-P1-K1-D6
Method	BLASTN
NCBI GI	g3449313
BLAST score	56
E value	2.0e-23
Match length	77
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	144293
Seq. ID	LIB3168-041-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	440
E value	1.0e-43
Match length	118
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144294
Seq. ID	LIB3168-041-P1-K1-D9
Method	BLASTX
NCBI GI	g3157930
BLAST score	641
E value	4.0e-67

Match length	120
% identity	99
NCBI Description	(AC002131) Strong similarity to amino-cyclopropane-carboxylic acid oxidase gb_L27664 from Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from this gene. [Arabidopsis thaliana]

Seq. No.	144295
Seq. ID	LIB3168-041-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	807
E value	1.0e-86
Match length	157
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144296
Seq. ID	LIB3168-041-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	7.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144297
Seq. ID	LIB3168-041-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	648
E value	5.0e-68
Match length	150
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144298
Seq. ID	LIB3168-041-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	185
E value	2.0e-14
Match length	41
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144299
Seq. ID	LIB3168-041-P1-K1-E4
Method	BLASTN
NCBI GI	g2288979
BLAST score	93
E value	3.0e-45
Match length	153
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144300
Seq. ID	LIB3168-041-P1-K1-E5
Method	BLASTX
NCBI GI	g1931647
BLAST score	576
E value	1.0e-59
Match length	127
% identity	84
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	144301
Seq. ID	LIB3168-041-P1-K1-E6
Method	BLASTX
NCBI GI	g3877252
BLAST score	255
E value	5.0e-22
Match length	119
% identity	45
NCBI Description	(Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No.	144302
Seq. ID	LIB3168-041-P1-K1-E7
Method	BLASTX
NCBI GI	g112681
BLAST score	638
E value	8.0e-67
Match length	147
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144303
Seq. ID	LIB3168-041-P1-K1-E8
Method	BLASTX
NCBI GI	g112739
BLAST score	434
E value	5.0e-43
Match length	119
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit

2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144304
Seq. ID	LIB3168-041-P1-K1-E9
Method	BLASTN
NCBI GI	g886433
BLAST score	96
E value	2.0e-46
Match length	193
% identity	98
NCBI Description	A.thaliana mRNA for ARP protein

Seq. No.	144305
Seq. ID	LIB3168-041-P1-K1-F1
Method	BLASTX
NCBI GI	g112682
BLAST score	232
E value	2.0e-19
Match length	84
% identity	61
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144306
Seq. ID	LIB3168-041-P1-K1-F10
Method	BLASTN
NCBI GI	g4432829
BLAST score	438
E value	0.0e+00
Match length	470
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144307
Seq. ID	LIB3168-041-P1-K1-F11
Method	BLASTN
NCBI GI	g3176695
BLAST score	295
E value	1.0e-165
Match length	355
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	144308
Seq. ID	LIB3168-041-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	85

E value	5.0e-51
Match length	120
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144309
Seq. ID	LIB3168-041-P1-K1-F2
Method	BLASTN
NCBI GI	g4220635
BLAST score	215
E value	1.0e-117
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	144310
Seq. ID	LIB3168-041-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	79
E value	2.8e-01
Match length	119
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144311
Seq. ID	LIB3168-041-P1-K1-F5
Method	BLASTX
NCBI GI	g4160573
BLAST score	152
E value	1.0e-10
Match length	82
% identity	45
NCBI Description	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

Seq. No.	144312
Seq. ID	LIB3168-041-P1-K1-F6
Method	BLASTX
NCBI GI	g112739
BLAST score	509
E value	1.0e-51
Match length	144
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144313
Seq. ID	LIB3168-041-P1-K1-F7
Method	BLASTX
NCBI GI	g464775
BLAST score	499
E value	1.0e-50
Match length	130
% identity	74
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	144314
Seq. ID	LIB3168-041-P1-K1-F8
Method	BLASTX
NCBI GI	g4567278
BLAST score	673
E value	6.0e-71
Match length	149
% identity	91
NCBI Description	(AC006841) putative anthracycline associated resistance ARX protein [Arabidopsis thaliana]

Seq. No.	144315
Seq. ID	LIB3168-041-P1-K1-F9
Method	BLASTX
NCBI GI	g2384671
BLAST score	789
E value	2.0e-84
Match length	155
% identity	95
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	144316
Seq. ID	LIB3168-041-P1-K1-G1
Method	BLASTN
NCBI GI	g3335170
BLAST score	110
E value	6.0e-55
Match length	332
% identity	95
NCBI Description	Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No.	144317
Seq. ID	LIB3168-041-P1-K1-G10
Method	BLASTN
NCBI GI	g1244740
BLAST score	452
E value	0.0e+00
Match length	464
% identity	99
NCBI Description	Arabidopsis thaliana nuclear ribosomal ITS-1, 5.8S ribosomal RNA, and ITS-2

Seq. No.	144318

Seq. ID	LIB3168-041-P1-K1-G11
Method	BLASTN
NCBI GI	g4519183
BLAST score	175
E value	1.0e-93
Match length	268
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	144319
Seq. ID	LIB3168-041-P1-K1-G2
Method	BLASTN
NCBI GI	g4314374
BLAST score	256
E value	1.0e-142
Match length	446
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144320
Seq. ID	LIB3168-041-P1-K1-G3
Method	BLASTX
NCBI GI	g3021336
BLAST score	194
E value	9.0e-15
Match length	58
% identity	72
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	144321
Seq. ID	LIB3168-041-P1-K1-G4
Method	BLASTX
NCBI GI	g2654868
BLAST score	219
E value	8.0e-23
Match length	63
% identity	92
NCBI Description	(AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No.	144322
Seq. ID	LIB3168-041-P1-K1-G5
Method	BLASTX
NCBI GI	g119143
BLAST score	689
E value	8.0e-73
Match length	137
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana]

>gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]
>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	144323
Seq. ID	LIB3168-041-P1-K1-G6
Method	BLASTN
NCBI GI	g4220643
BLAST score	158
E value	6.0e-84
Match length	178
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	144324
Seq. ID	LIB3168-041-P1-K1-G7
Method	BLASTX
NCBI GI	g4056500
BLAST score	217
E value	2.0e-17
Match length	48
% identity	94
NCBI Description	(AC005896) putative acetyltransferase [Arabidopsis thaliana]

Seq. No.	144325
Seq. ID	LIB3168-041-P1-K1-G8
Method	BLASTN
NCBI GI	g4006885
BLAST score	311
E value	1.0e-175
Match length	469
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	144326
Seq. ID	LIB3168-041-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	634
E value	2.0e-66
Match length	152
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144327
Seq. ID	LIB3168-041-P1-K1-H1
Method	BLASTN
NCBI GI	g4079614
BLAST score	90
E value	1.0e-43
Match length	106

% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144328
Seq. ID	LIB3168-041-P1-K1-H10
Method	BLASTX
NCBI GI	g3132475
BLAST score	655
E value	8.0e-69
Match length	158
% identity	81
NCBI Description	(AC003096) similar to proline-rich protein [Arabidopsis thaliana]

Seq. No.	144329
Seq. ID	LIB3168-041-P1-K1-H11
Method	BLASTX
NCBI GI	g112682
BLAST score	709
E value	4.0e-75
Match length	159
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144330
Seq. ID	LIB3168-041-P1-K1-H2
Method	BLASTX
NCBI GI	g112741
BLAST score	672
E value	2.0e-73
Match length	144
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144331
Seq. ID	LIB3168-041-P1-K1-H4
Method	BLASTX
NCBI GI	g112682
BLAST score	607
E value	2.0e-77
Match length	157
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	144332
Seq. ID	LIB3168-041-P1-K1-H5
Method	BLASTN
NCBI GI	g3869067
BLAST score	250
E value	1.0e-138
Match length	401
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	144333
Seq. ID	LIB3168-041-P1-K1-H7
Method	BLASTX
NCBI GI	g112681
BLAST score	621
E value	8.0e-65
Match length	156
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144334
Seq. ID	LIB3168-041-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	518
E value	9.0e-53
Match length	120
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144335
Seq. ID	LIB3168-043-P1-K1-A1
Method	BLASTX
NCBI GI	g112681
BLAST score	332
E value	4.0e-31
Match length	66
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144336
Seq. ID	LIB3168-043-P1-K1-A10
Method	BLASTX
NCBI GI	g112682

BLAST score	588
E value	4.0e-61
Match length	124
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144337
Seq. ID	LIB3168-043-P1-K1-A11
Method	BLASTX
NCBI GI	g343210
BLAST score	513
E value	3.0e-52
Match length	108
% identity	91
NCBI Description	(M35995) apocytochrome b6 (alt.) [Oryza sativa] >gi_226762_prf__1604469A cytochrome b6 [Oryza sativa]

Seq. No.	144338
Seq. ID	LIB3168-043-P1-K1-A12
Method	BLASTN
NCBI GI	g4587582
BLAST score	47
E value	3.0e-17
Match length	121
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	144339
Seq. ID	LIB3168-043-P1-K1-A2
Method	BLASTN
NCBI GI	g2494110
BLAST score	342
E value	0.0e+00
Match length	354
% identity	99
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	144340
Seq. ID	LIB3168-043-P1-K1-A3
Method	BLASTN
NCBI GI	g3985958
BLAST score	318
E value	1.0e-179
Match length	338
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	144341
Seq. ID	LIB3168-043-P1-K1-A4
Method	BLASTX

NCBI GI	g2129657
BLAST score	243
E value	1.0e-20
Match length	77
% identity	68
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144342
Seq. ID	LIB3168-043-P1-K1-A5
Method	BLASTX
NCBI GI	g3335171
BLAST score	553
E value	5.0e-57
Match length	119
% identity	89
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	144343
Seq. ID	LIB3168-043-P1-K1-A6
Method	BLASTN
NCBI GI	g4567300
BLAST score	50
E value	4.0e-19
Match length	198
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	144344
Seq. ID	LIB3168-043-P1-K1-A7
Method	BLASTX
NCBI GI	g112741
BLAST score	520
E value	4.0e-53
Match length	111
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144345
Seq. ID	LIB3168-043-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	374
E value	5.0e-36
Match length	70
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144346
Seq. ID	LIB3168-043-P1-K1-B1
Method	BLASTX
NCBI GI	g3176874
BLAST score	501
E value	6.0e-51
Match length	96
% identity	99
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	144347
Seq. ID	LIB3168-043-P1-K1-B10
Method	BLASTX
NCBI GI	g4678299
BLAST score	604
E value	6.0e-63
Match length	118
% identity	100
NCBI Description	(AL049655) cysteine proteinase precursor-like protein [Arabidopsis thaliana]

Seq. No.	144348
Seq. ID	LIB3168-043-P1-K1-B11
Method	BLASTN
NCBI GI	g4199934
BLAST score	313
E value	1.0e-176
Match length	317
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	144349
Seq. ID	LIB3168-043-P1-K1-B2
Method	BLASTX
NCBI GI	g112737
BLAST score	363
E value	1.0e-34
Match length	130
% identity	60
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144350
Seq. ID	LIB3168-043-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	550
E value	1.0e-56

Match length	138
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144351
Seq. ID	LIB3168-043-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	375
E value	5.0e-36
Match length	148
% identity	57
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144352
Seq. ID	LIB3168-043-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	659
E value	2.0e-69
Match length	127
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144353
Seq. ID	LIB3168-043-P1-K1-B8
Method	BLASTN
NCBI GI	g1490552
BLAST score	264
E value	1.0e-147
Match length	268
% identity	100
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	144354
Seq. ID	LIB3168-043-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	573
E value	2.0e-70
Match length	138
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144355
Seq. ID	LIB3168-043-P1-K1-C11
Method	BLASTX
NCBI GI	g4335745

BLAST score	226
E value	8.0e-19
Match length	92
% identity	53
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No.	144356
Seq. ID	LIB3168-043-P1-K1-C12
Method	BLASTX
NCBI GI	g112739
BLAST score	338
E value	8.0e-32
Match length	105
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144357
Seq. ID	LIB3168-043-P1-K1-C2
Method	BLASTX
NCBI GI	g112681
BLAST score	603
E value	9.0e-63
Match length	122
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144358
Seq. ID	LIB3168-043-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	543
E value	9.0e-56
Match length	105
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144359
Seq. ID	LIB3168-043-P1-K1-C6
Method	BLASTN
NCBI GI	g3298610
BLAST score	151
E value	2.0e-79
Match length	275

% identity	96
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	144360
Seq. ID	LIB3168-043-P1-K1-D1
Method	BLASTX
NCBI GI	g1076414
BLAST score	650
E value	3.0e-68
Match length	141
% identity	90
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	144361
Seq. ID	LIB3168-043-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	389
E value	1.0e-62
Match length	126
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144362
Seq. ID	LIB3168-043-P1-K1-D2
Method	BLASTX
NCBI GI	g112739
BLAST score	347
E value	6.0e-33
Match length	99
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144363
Seq. ID	LIB3168-043-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	602
E value	1.0e-62
Match length	119
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144364
Seq. ID	LIB3168-043-P1-K1-D4

Method	BLASTN
NCBI GI	g4185120
BLAST score	78
E value	6.0e-36
Match length	202
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144365
Seq. ID	LIB3168-043-P1-K1-D5
Method	BLASTX
NCBI GI	g112682
BLAST score	322
E value	3.0e-30
Match length	79
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144366
Seq. ID	LIB3168-043-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	630
E value	5.0e-66
Match length	124
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144367
Seq. ID	LIB3168-043-P1-K1-D9
Method	BLASTX
NCBI GI	g2129657
BLAST score	346
E value	9.0e-33
Match length	100
% identity	74
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144368
Seq. ID	LIB3168-043-P1-K1-E1
Method	BLASTX
NCBI GI	g2129744
BLAST score	282
E value	4.0e-47
Match length	120
% identity	81
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone

APS3) - Arabidopsis thaliana >gi_459144 (U06275) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	144369
Seq. ID	LIB3168-043-P1-K1-E10
Method	BLASTX
NCBI GI	g112681
BLAST score	44
E value	2.0e-54
Match length	123
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144370
Seq. ID	LIB3168-043-P1-K1-E11
Method	BLASTX
NCBI GI	g112741
BLAST score	46
E value	9.0e-55
Match length	128
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144371
Seq. ID	LIB3168-043-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144372
Seq. ID	LIB3168-043-P1-K1-E3
Method	BLASTX
NCBI GI	g3850816
BLAST score	326
E value	2.0e-30
Match length	78
% identity	74
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No. 144373

Seq. ID	LIB3168-043-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	350
E value	1.0e-50
Match length	140
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144374
Seq. ID	LIB3168-043-P1-K1-E6
Method	BLASTX
NCBI GI	g112737
BLAST score	455
E value	1.0e-45
Match length	114
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144375
Seq. ID	LIB3168-043-P1-K1-E7
Method	BLASTX
NCBI GI	g2244750
BLAST score	56
E value	2.0e-28
Match length	72
% identity	94
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	144376
Seq. ID	LIB3168-043-P1-K1-E8
Method	BLASTX
NCBI GI	g1408471
BLAST score	417
E value	5.0e-41
Match length	93
% identity	85
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	144377
Seq. ID	LIB3168-043-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	455
E value	2.0e-45

Match length	114
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144378
Seq. ID	LIB3168-043-P1-K1-F1
Method	BLASTX
NCBI GI	g1350680
BLAST score	636
E value	1.0e-66
Match length	121
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	144379
Seq. ID	LIB3168-043-P1-K1-F10
Method	BLASTN
NCBI GI	g166610
BLAST score	149
E value	3.0e-78
Match length	286
% identity	91
NCBI Description	A.thaliana at2S2 gene encoding albumin 2S subunit 2, complete cds

Seq. No.	144380
Seq. ID	LIB3168-043-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	8.0e-64
Match length	123
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144381
Seq. ID	LIB3168-043-P1-K1-F12
Method	BLASTX
NCBI GI	g2129657
BLAST score	377
E value	3.0e-36
Match length	105
% identity	76
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144382

Seq. ID	LIB3168-043-P1-K1-F2
Method	BLASTX
NCBI GI	g1628583
BLAST score	469
E value	1.0e-56
Match length	119
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144383
Seq. ID	LIB3168-043-P1-K1-F3
Method	BLASTX
NCBI GI	g2262112
BLAST score	686
E value	2.0e-72
Match length	130
% identity	99
NCBI Description	(AC002343) trehalase precusor isolog [Arabidopsis thaliana]

Seq. No.	144384
Seq. ID	LIB3168-043-P1-K1-F4
Method	BLASTX
NCBI GI	g544425
BLAST score	463
E value	1.0e-46
Match length	90
% identity	99
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	144385
Seq. ID	LIB3168-043-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	512
E value	3.0e-52
Match length	125
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144386
Seq. ID	LIB3168-043-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	586
E value	3.0e-61
Match length	125
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144387
Seq. ID	LIB3168-043-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	569
E value	7.0e-59
Match length	111
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144388
Seq. ID	LIB3168-043-P1-K1-F9
Method	BLASTN
NCBI GI	g4454585
BLAST score	35
E value	2.0e-10
Match length	78
% identity	89
NCBI Description	Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	144389
Seq. ID	LIB3168-043-P1-K1-G11
Method	BLASTX
NCBI GI	g4204298
BLAST score	652
E value	1.0e-68
Match length	123
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144390
Seq. ID	LIB3168-043-P1-K1-G12
Method	BLASTX
NCBI GI	g112682
BLAST score	579
E value	5.0e-60
Match length	129
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144391
Seq. ID	LIB3168-043-P1-K1-G2
Method	BLASTX
NCBI GI	g112737
BLAST score	448
E value	1.0e-44

Match length	96
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144392
Seq. ID	LIB3168-043-P1-K1-G4
Method	BLASTX
NCBI GI	g1334372
BLAST score	172
E value	8.0e-13
Match length	47
% identity	79
NCBI Description	(X13366) pot. alt. CP-a2 protein (AA 1 - 461) [Secale cereale]

Seq. No.	144393
Seq. ID	LIB3168-043-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	390
E value	5.0e-39
Match length	89
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144394
Seq. ID	LIB3168-043-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	402
E value	2.0e-39
Match length	100
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144395
Seq. ID	LIB3168-043-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	374
E value	9.0e-37
Match length	88
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144396
Seq. ID	LIB3168-043-P1-K1-H10
Method	BLASTX
NCBI GI	g1592670
BLAST score	440
E value	1.0e-43
Match length	120
% identity	69
NCBI Description	(X91920) dehydrin [Arabidopsis thaliana] >gi_4567280_gb_AAD23693.1_AC006841_21 (AC006841) putative dehydrin [Arabidopsis thaliana]

Seq. No.	144397
Seq. ID	LIB3168-043-P1-K1-H11
Method	BLASTX
NCBI GI	g112743
BLAST score	485
E value	5.0e-49
Match length	114
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144398
Seq. ID	LIB3168-043-P1-K1-H12
Method	BLASTN
NCBI GI	g4589432
BLAST score	67
E value	3.0e-29
Match length	331
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMJ24, complete sequence

Seq. No.	144399
Seq. ID	LIB3168-043-P1-K1-H4
Method	BLASTX
NCBI GI	g112743
BLAST score	330
E value	4.0e-31
Match length	77
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144400
Seq. ID	LIB3168-043-P1-K1-H5

Method	BLASTX
NCBI GI	g1703115
BLAST score	530
E value	3.0e-54
Match length	97
% identity	100
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	144401
Seq. ID	LIB3168-043-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	551
E value	7.0e-57
Match length	106
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144402
Seq. ID	LIB3168-043-P1-K1-H9
Method	BLASTX
NCBI GI	g131336
BLAST score	334
E value	2.0e-31
Match length	73
% identity	92
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	144403
Seq. ID	LIB3168-044-P1-K1-A1
Method	BLASTX
NCBI GI	g2160151
BLAST score	500
E value	5.0e-51
Match length	95
% identity	99
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	144404
Seq. ID	LIB3168-044-P1-K1-A11
Method	BLASTX
NCBI GI	g112743
BLAST score	558
E value	2.0e-57
Match length	102
% identity	100

NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144405
Seq. ID	LIB3168-044-P1-K1-A12
Method	BLASTN
NCBI GI	g4757411
BLAST score	277
E value	1.0e-154
Match length	389
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	144406
Seq. ID	LIB3168-044-P1-K1-A2
Method	BLASTX
NCBI GI	g4559371
BLAST score	631
E value	4.0e-66
Match length	137
% identity	91
NCBI Description	(AC006585) putative peroxidase [Arabidopsis thaliana]

Seq. No.	144407
Seq. ID	LIB3168-044-P1-K1-A3
Method	BLASTX
NCBI GI	g2894574
BLAST score	632
E value	3.0e-66
Match length	120
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	144408
Seq. ID	LIB3168-044-P1-K1-A5
Method	BLASTX
NCBI GI	g112682
BLAST score	550
E value	1.0e-56
Match length	132
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144409
Seq. ID	LIB3168-044-P1-K1-A6

Method	BLASTN
NCBI GI	g4589428
BLAST score	416
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	144410
Seq. ID	LIB3168-044-P1-K1-A7
Method	BLASTX
NCBI GI	g1345973
BLAST score	487
E value	3.0e-49
Match length	108
% identity	82
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	144411
Seq. ID	LIB3168-044-P1-K1-A8
Method	BLASTX
NCBI GI	g4314379
BLAST score	166
E value	1.0e-11
Match length	70
% identity	46
NCBI Description	(AC006232) unknown protein [Arabidopsis thaliana]

Seq. No.	144412
Seq. ID	LIB3168-044-P1-K1-A9
Method	BLASTX
NCBI GI	g1053093
BLAST score	403
E value	2.0e-39
Match length	98
% identity	83
NCBI Description	(U38550) zeta-carotene desaturase precursor [Arabidopsis thaliana]

Seq. No.	144413
Seq. ID	LIB3168-044-P1-K1-B1
Method	BLASTX
NCBI GI	g112682
BLAST score	444
E value	4.0e-44
Match length	99
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144414
Seq. ID	LIB3168-044-P1-K1-B10
Method	BLASTX
NCBI GI	g112741
BLAST score	679
E value	1.0e-71
Match length	129
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144415
Seq. ID	LIB3168-044-P1-K1-B11
Method	BLASTX
NCBI GI	g112681
BLAST score	517
E value	1.0e-52
Match length	104
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144416
Seq. ID	LIB3168-044-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	670
E value	1.0e-70
Match length	136
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144417
Seq. ID	LIB3168-044-P1-K1-B3
Method	BLASTX
NCBI GI	g99688
BLAST score	511
E value	7.0e-52
Match length	116
% identity	93
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)

elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	144418
Seq. ID	LIB3168-044-P1-K1-B4
Method	BLASTX
NCBI GI	g118926
BLAST score	239
E value	4.0e-20
Match length	100
% identity	50
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	144419
Seq. ID	LIB3168-044-P1-K1-B5
Method	BLASTX
NCBI GI	g112737
BLAST score	191
E value	1.0e-14
Match length	93
% identity	45
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144420
Seq. ID	LIB3168-044-P1-K1-B6
Method	BLASTX
NCBI GI	g2129773
BLAST score	585
E value	1.0e-60
Match length	109
% identity	100
NCBI Description	xyloglucan endotransglycosylase-related protein XTR3 - Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	144421
Seq. ID	LIB3168-044-P1-K1-B7
Method	BLASTN
NCBI GI	g511598
BLAST score	398
E value	0.0e+00
Match length	402
% identity	26
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	144422
Seq. ID	LIB3168-044-P1-K1-B8
Method	BLASTN
NCBI GI	g2842474
BLAST score	262
E value	1.0e-145
Match length	282
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144423
Seq. ID	LIB3168-044-P1-K1-B9
Method	BLASTN
NCBI GI	g166609
BLAST score	75
E value	5.0e-34
Match length	119
% identity	92
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	144424
Seq. ID	LIB3168-044-P1-K1-C1
Method	BLASTX
NCBI GI	g4587680
BLAST score	276
E value	4.0e-27
Match length	104
% identity	67
NCBI Description	(AC007197) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	144425
Seq. ID	LIB3168-044-P1-K1-C10
Method	BLASTX
NCBI GI	g2791834
BLAST score	582
E value	7.0e-64
Match length	130
% identity	94
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	144426
Seq. ID	LIB3168-044-P1-K1-C2
Method	BLASTX
NCBI GI	g3319370
BLAST score	569
E value	8.0e-59
Match length	112
% identity	100
NCBI Description	(AF077409) contains similarity to C3HC4-type zinc fingers (Pfam: zf-C3HC4.hmm, score: 32.94) [Arabidopsis thaliana]

Seq. No.	144427
Seq. ID	LIB3168-044-P1-K1-C3
Method	BLASTX
NCBI GI	g3043415

BLAST score	608
E value	2.0e-63
Match length	116
% identity	100
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	144428
Seq. ID	LIB3168-044-P1-K1-C4
Method	BLASTX
NCBI GI	g112681
BLAST score	607
E value	3.0e-63
Match length	121
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144429
Seq. ID	LIB3168-044-P1-K1-C6
Method	BLASTX
NCBI GI	g1495251
BLAST score	687
E value	1.0e-72
Match length	138
% identity	96
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	144430
Seq. ID	LIB3168-044-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	388
E value	2.0e-37
Match length	135
% identity	69
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144431
Seq. ID	LIB3168-044-P1-K1-C8
Method	BLASTN
NCBI GI	g2842474
BLAST score	253
E value	1.0e-140
Match length	253
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144432
Seq. ID	LIB3168-044-P1-K1-C9
Method	BLASTN
NCBI GI	g1628582

BLAST score	45
E value	2.0e-16
Match length	145
% identity	83
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	144433
Seq. ID	LIB3168-044-P1-K1-D1
Method	BLASTX
NCBI GI	g4455206
BLAST score	403
E value	2.0e-39
Match length	128
% identity	66
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	144434
Seq. ID	LIB3168-044-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	94
E value	1.0e-49
Match length	137
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144435
Seq. ID	LIB3168-044-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	517
E value	1.0e-52
Match length	136
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144436
Seq. ID	LIB3168-044-P1-K1-D2
Method	BLASTX
NCBI GI	g112741
BLAST score	680
E value	8.0e-72
Match length	129
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144437
Seq. ID	LIB3168-044-P1-K1-D3
Method	BLASTX
NCBI GI	g1335862
BLAST score	317
E value	3.0e-29
Match length	81
% identity	80
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	144438
Seq. ID	LIB3168-044-P1-K1-D4
Method	BLASTX
NCBI GI	g1628583
BLAST score	615
E value	3.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144439
Seq. ID	LIB3168-044-P1-K1-D5
Method	BLASTX
NCBI GI	g4204299
BLAST score	608
E value	2.0e-63
Match length	137
% identity	86
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144440
Seq. ID	LIB3168-044-P1-K1-D6
Method	BLASTN
NCBI GI	g4582444
BLAST score	391
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	144441
Seq. ID	LIB3168-044-P1-K1-D7
Method	BLASTN
NCBI GI	g4589414
BLAST score	151
E value	2.0e-79
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	144442
Seq. ID	LIB3168-044-P1-K1-D9
Method	BLASTX
NCBI GI	g1592686
BLAST score	142
E value	9.0e-09
Match length	42
% identity	69
NCBI Description	(X91918) oleosin type4 [Arabidopsis thaliana]

Seq. No.	144443
Seq. ID	LIB3168-044-P1-K1-E1
Method	BLASTN
NCBI GI	g17825
BLAST score	115
E value	7.0e-58
Match length	127
% identity	98
NCBI Description	B.nigra gene (II) for 5S rRNA

Seq. No.	144444
Seq. ID	LIB3168-044-P1-K1-E11
Method	BLASTX
NCBI GI	g4325282
BLAST score	446
E value	2.0e-44
Match length	98
% identity	87
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	144445
Seq. ID	LIB3168-044-P1-K1-E12
Method	BLASTX
NCBI GI	g140508
BLAST score	649
E value	3.0e-68
Match length	138
% identity	92
NCBI Description	PROBABLE INTRON MATURASE >gi_99852_pir__S07168 probable maturase, 63K - white mustard chloroplast >gi_12220_emb_CAA28509_ (X04826) ycf14 (AA1-324) [Sinapis alba]

Seq. No.	144446
Seq. ID	LIB3168-044-P1-K1-E2
Method	BLASTN
NCBI GI	g4454447
BLAST score	37
E value	3.0e-11
Match length	85
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144447
Seq. ID	LIB3168-044-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	542
E value	1.0e-55
Match length	139
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144448
Seq. ID	LIB3168-044-P1-K1-E6
Method	BLASTX
NCBI GI	g166570
BLAST score	198
E value	2.0e-15
Match length	97
% identity	44
NCBI Description	(L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No.	144449
Seq. ID	LIB3168-044-P1-K1-F1
Method	BLASTN
NCBI GI	g16726
BLAST score	108
E value	6.0e-54
Match length	142
% identity	94
NCBI Description	ATTS0156 Gif-SeedA+B Arabidopsis thaliana cDNA clone YAP007T, mRNA sequence [Arabidopsis thaliana] >gi_1107498_emb_X91953_ATORF007 A.thaliana mRNA for unknown protein (clone YAP007)

Seq. No.	144450
Seq. ID	LIB3168-044-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	568
E value	1.0e-58
Match length	133
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144451
Seq. ID	LIB3168-044-P1-K1-F12
Method	BLASTN
NCBI GI	g4199934
BLAST score	225
E value	1.0e-123
Match length	229
% identity	100

NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	144452
Seq. ID	LIB3168-044-P1-K1-F3
Method	BLASTX
NCBI GI	g1351272
BLAST score	448
E value	1.0e-44
Match length	106
% identity	84
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	144453
Seq. ID	LIB3168-044-P1-K1-F4
Method	BLASTX
NCBI GI	g112739
BLAST score	360
E value	3.0e-34
Match length	126
% identity	61
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144454
Seq. ID	LIB3168-044-P1-K1-F5
Method	BLASTX
NCBI GI	g543632
BLAST score	470
E value	3.0e-47
Match length	134
% identity	65
NCBI Description	aldehyde reductase (EC 1.1.1.21), NADPH-dependent - bromegrass >gi_167113 (L12042) aldose reductase-related protein [Bromus inermis]

Seq. No.	144455
Seq. ID	LIB3168-044-P1-K1-F6
Method	BLASTX
NCBI GI	g112737
BLAST score	610
E value	1.0e-63
Match length	134
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144456
Seq. ID	LIB3168-044-P1-K1-F7
Method	BLASTX
NCBI GI	g418908
BLAST score	178
E value	6.0e-13
Match length	73
% identity	44
NCBI Description	vicilin precursor - cacao

Seq. No.	144457
Seq. ID	LIB3168-044-P1-K1-F9
Method	BLASTX
NCBI GI	g2894574
BLAST score	625
E value	2.0e-65
Match length	121
% identity	99
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	144458
Seq. ID	LIB3168-044-P1-K1-G1
Method	BLASTX
NCBI GI	g3776023
BLAST score	575
E value	2.0e-59
Match length	116
% identity	99
NCBI Description	(AJ010473) RNA helicase [Arabidopsis thaliana]

Seq. No.	144459
Seq. ID	LIB3168-044-P1-K1-G11
Method	BLASTX
NCBI GI	g1628583
BLAST score	485
E value	6.0e-49
Match length	126
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144460
Seq. ID	LIB3168-044-P1-K1-G2
Method	BLASTN
NCBI GI	g4580454
BLAST score	367
E value	0.0e+00
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	144461
Seq. ID	LIB3168-044-P1-K1-G3
Method	BLASTN
NCBI GI	g3335170
BLAST score	166
E value	2.0e-88
Match length	265
% identity	91
NCBI Description	Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No.	144462
Seq. ID	LIB3168-044-P1-K1-G4
Method	BLASTN
NCBI GI	g3449320
BLAST score	199
E value	1.0e-108
Match length	421
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	144463
Seq. ID	LIB3168-044-P1-K1-G5
Method	BLASTX
NCBI GI	g112737
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144464
Seq. ID	LIB3168-044-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144465
Seq. ID	LIB3168-044-P1-K1-G8
Method	BLASTX
NCBI GI	g112682
BLAST score	578
E value	7.0e-60

Match length	135
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144466
Seq. ID	LIB3168-044-P1-K1-G9
Method	BLASTX
NCBI GI	g3850579
BLAST score	637
E value	9.0e-67
Match length	136
% identity	88
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	144467
Seq. ID	LIB3168-044-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	240
E value	8.0e-21
Match length	50
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144468
Seq. ID	LIB3168-044-P1-K1-H10
Method	BLASTX
NCBI GI	g1176671
BLAST score	277
E value	1.0e-24
Match length	88
% identity	55
NCBI Description	PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 >gi_3874174_emb_CAA86666_ (Z46676) C08B11.8 [Caenorhabditis elegans]

Seq. No.	144469
Seq. ID	LIB3168-044-P1-K1-H11
Method	BLASTX
NCBI GI	g3860260
BLAST score	292
E value	2.0e-26
Match length	62
% identity	100
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	144470
Seq. ID	LIB3168-044-P1-K1-H12
Method	BLASTX
NCBI GI	g3395432
BLAST score	270
E value	9.0e-24
Match length	91
% identity	56
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	144471
Seq. ID	LIB3168-044-P1-K1-H2
Method	BLASTN
NCBI GI	g3449311
BLAST score	195
E value	1.0e-105
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15I22, complete sequence [Arabidopsis thaliana]

Seq. No.	144472
Seq. ID	LIB3168-044-P1-K1-H3
Method	BLASTX
NCBI GI	g112681
BLAST score	598
E value	3.0e-62
Match length	137
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144473
Seq. ID	LIB3168-044-P1-K1-H4
Method	BLASTX
NCBI GI	g3023848
BLAST score	518
E value	7.0e-53
Match length	108
% identity	36
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	144474
Seq. ID	LIB3168-044-P1-K1-H8
Method	BLASTX
NCBI GI	g633890
BLAST score	307
E value	4.0e-28
Match length	106
% identity	59
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum

vulgare]

Seq. No.	144475
Seq. ID	LIB3168-044-P1-K1-H9
Method	BLASTX
NCBI GI	g2980784
BLAST score	701
E value	3.0e-74
Match length	137
% identity	21
NCBI Description	(AL022198) puative protein [Arabidopsis thaliana]

Seq. No.	144476
Seq. ID	LIB3168-045-P1-K1-A1
Method	BLASTN
NCBI GI	g4589437
BLAST score	171
E value	1.0e-91
Match length	187
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	144477
Seq. ID	LIB3168-045-P1-K1-A10
Method	BLASTN
NCBI GI	g987013
BLAST score	95
E value	3.0e-46
Match length	119
% identity	95
NCBI Description	A.thaliana mRNA for oleosin (isoform; 841 bp) >gi_987015_emb_Z54165_ATOLEOSN3 A.thaliana mRNA for oleosin (isoform; 841 bp)

Seq. No.	144478
Seq. ID	LIB3168-045-P1-K1-A12
Method	BLASTX
NCBI GI	g112739
BLAST score	421
E value	2.0e-41
Match length	120
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144479
Seq. ID	LIB3168-045-P1-K1-A2
Method	BLASTN
NCBI GI	g16335
BLAST score	40
E value	2.0e-13

Match length	109
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for 3-hydroxy-3-methylglutaryl CoA reductase (EC 1.1.1.34)

Seq. No.	144480
Seq. ID	LIB3168-045-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	591
E value	2.0e-61
Match length	128
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144481
Seq. ID	LIB3168-045-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	283
E value	3.0e-25
Match length	130
% identity	39
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144482
Seq. ID	LIB3168-045-P1-K1-A6
Method	BLASTX
NCBI GI	g112739
BLAST score	542
E value	1.0e-55
Match length	144
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144483
Seq. ID	LIB3168-045-P1-K1-A7
Method	BLASTX
NCBI GI	g123340
BLAST score	536
E value	4.0e-55
Match length	106
% identity	98
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA REDUCTASE 1) (HMGR1) >gi_99714_pir__A32107

	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - Arabidopsis thaliana >gi_16336_emb_CAA33139_ (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592) [Arabidopsis thaliana] >gi_166750 (J04537) 3-hydroxy-3-methylglutaryl CoA reductase [Arabidopsis thaliana] >gi_388556 (L19261) hydroxymethylglutaryl CoA reductase [Arabidopsis thaliana]
Seq. No.	144484
Seq. ID	LIB3168-045-P1-K1-A9
Method	BLASTX
NCBI GI	g112741
BLAST score	599
E value	2.0e-62
Match length	112
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	144485
Seq. ID	LIB3168-045-P1-K1-B1
Method	BLASTX
NCBI GI	g112682
BLAST score	491
E value	8.0e-50
Match length	112
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144486
Seq. ID	LIB3168-045-P1-K1-B10
Method	BLASTX
NCBI GI	g112681
BLAST score	490
E value	1.0e-49
Match length	133
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144487
Seq. ID	LIB3168-045-P1-K1-B11
Method	BLASTN
NCBI GI	g3869073
BLAST score	18

E value	3.9e+00
Match length	294
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	144488
Seq. ID	LIB3168-045-P1-K1-B12
Method	BLASTN
NCBI GI	g3869073
BLAST score	68
E value	6.0e-30
Match length	88
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	144489
Seq. ID	LIB3168-045-P1-K1-B2
Method	BLASTX
NCBI GI	g3157930
BLAST score	530
E value	3.0e-54
Match length	124
% identity	82
NCBI Description	(AC002131) Strong similarity to amino-cyclopropane-carboxylic acid oxidase gb_L27664 from Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from this gene. [Arabidopsis thaliana]

Seq. No.	144490
Seq. ID	LIB3168-045-P1-K1-B3
Method	BLASTX
NCBI GI	g3157930
BLAST score	541
E value	1.0e-55
Match length	110
% identity	93
NCBI Description	(AC002131) Strong similarity to amino-cyclopropane-carboxylic acid oxidase gb_L27664 from Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from this gene. [Arabidopsis thaliana]

Seq. No.	144491
Seq. ID	LIB3168-045-P1-K1-B4
Method	BLASTX
NCBI GI	g112737
BLAST score	491
E value	1.0e-49
Match length	107
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	144492
Seq. ID	LIB3168-045-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	710
E value	3.0e-75
Match length	138
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144493
Seq. ID	LIB3168-045-P1-K1-B6
Method	BLASTN
NCBI GI	g3242970
BLAST score	58
E value	7.0e-24
Match length	362
% identity	84
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	144494
Seq. ID	LIB3168-045-P1-K1-B7
Method	BLASTX
NCBI GI	g4204298
BLAST score	628
E value	1.0e-65
Match length	135
% identity	90
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144495
Seq. ID	LIB3168-045-P1-K1-B8
Method	BLASTN
NCBI GI	g2760173
BLAST score	288
E value	1.0e-161
Match length	431
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	144496
Seq. ID	LIB3168-045-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	747
E value	1.0e-79
Match length	159
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144497
Seq. ID LIB3168-045-P1-K1-C10
Method BLASTX
NCBI GI g1628583
BLAST score 763
E value 2.0e-81
Match length 150
% identity 98
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144498
Seq. ID LIB3168-045-P1-K1-C11
Method BLASTX
NCBI GI g3335169
BLAST score 787
E value 3.0e-84
Match length 147
% identity 99
NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 144499
Seq. ID LIB3168-045-P1-K1-C2
Method BLASTX
NCBI GI g112682
BLAST score 634
E value 2.0e-66
Match length 147
% identity 82
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144500
Seq. ID LIB3168-045-P1-K1-C3
Method BLASTX
NCBI GI g112682
BLAST score 685
E value 2.0e-72
Match length 141
% identity 89
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144501
Seq. ID LIB3168-045-P1-K1-C4
Method BLASTX

NCBI GI	g112741
BLAST score	764
E value	1.0e-81
Match length	144
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144502
Seq. ID	LIB3168-045-P1-K1-C5
Method	BLASTX
NCBI GI	g3603456
BLAST score	687
E value	1.0e-72
Match length	142
% identity	30
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	144503
Seq. ID	LIB3168-045-P1-K1-C6
Method	BLASTN
NCBI GI	g3650026
BLAST score	77
E value	3.0e-35
Match length	138
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144504
Seq. ID	LIB3168-045-P1-K1-C8
Method	BLASTX
NCBI GI	g730526
BLAST score	756
E value	1.0e-80
Match length	149
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	144505
Seq. ID	LIB3168-045-P1-K1-C9
Method	BLASTX
NCBI GI	g730526
BLAST score	160
E value	7.0e-11
Match length	98
% identity	41
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis

thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	144506
Seq. ID	LIB3168-045-P1-K1-D1
Method	BLASTX
NCBI GI	g112741
BLAST score	758
E value	7.0e-81
Match length	145
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144507
Seq. ID	LIB3168-045-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	724
E value	6.0e-77
Match length	145
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144508
Seq. ID	LIB3168-045-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	120
E value	4.0e-06
Match length	134
% identity	66
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144509
Seq. ID	LIB3168-045-P1-K1-D2
Method	BLASTX
NCBI GI	g2529665
BLAST score	531
E value	3.0e-54
Match length	139
% identity	78
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	144510

Seq. ID	LIB3168-045-P1-K1-D3
Method	BLASTX
NCBI GI	g2529665
BLAST score	202
E value	8.0e-16
Match length	61
% identity	70
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	144511
Seq. ID	LIB3168-045-P1-K1-D4
Method	BLASTX
NCBI GI	g112741
BLAST score	749
E value	7.0e-80
Match length	144
% identity	96
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144512
Seq. ID	LIB3168-045-P1-K1-D5
Method	BLASTX
NCBI GI	g112739
BLAST score	533
E value	2.0e-54
Match length	142
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144513
Seq. ID	LIB3168-045-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	455
E value	1.0e-45
Match length	97
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144514
Seq. ID	LIB3168-045-P1-K1-D8
Method	BLASTX

NCBI GI	g1628583
BLAST score	427
E value	4.0e-42
Match length	117
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144515
Seq. ID	LIB3168-045-P1-K1-E1
Method	BLASTX
NCBI GI	g118926
BLAST score	291
E value	4.0e-26
Match length	115
% identity	50
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	144516
Seq. ID	LIB3168-045-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	1.0e-64
Match length	146
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144517
Seq. ID	LIB3168-045-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144518
Seq. ID	LIB3168-045-P1-K1-E2
Method	BLASTX
NCBI GI	g112682
BLAST score	646
E value	9.0e-68
Match length	147
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144519
Seq. ID	LIB3168-045-P1-K1-E3
Method	BLASTX
NCBI GI	g2623303
BLAST score	719
E value	2.0e-76
Match length	141
% identity	98
NCBI Description	(AC002409) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	144520
Seq. ID	LIB3168-045-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	392
E value	5.0e-38
Match length	81
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144521
Seq. ID	LIB3168-045-P1-K1-E6
Method	BLASTX
NCBI GI	g1402904
BLAST score	713
E value	1.0e-75
Match length	144
% identity	96
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	144522
Seq. ID	LIB3168-045-P1-K1-E7
Method	BLASTX
NCBI GI	g112682
BLAST score	612
E value	8.0e-64
Match length	144
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144523
Seq. ID	LIB3168-045-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	684
E value	3.0e-72

Match length 154
% identity 84
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144524
Seq. ID LIB3168-045-P1-K1-F1
Method BLASTX
NCBI GI g112682
BLAST score 609
E value 2.0e-63
Match length 145
% identity 82
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144525
Seq. ID LIB3168-045-P1-K1-F10
Method BLASTX
NCBI GI g112739
BLAST score 409
E value 4.0e-40
Match length 119
% identity 70
NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 144526
Seq. ID LIB3168-045-P1-K1-F11
Method BLASTX
NCBI GI g112739
BLAST score 375
E value 4.0e-36
Match length 113
% identity 68
NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 144527
Seq. ID LIB3168-045-P1-K1-F12
Method BLASTX

NCBI GI g1628583
BLAST score 692
E value 3.0e-73
Match length 136
% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144528
Seq. ID LIB3168-045-P1-K1-F3
Method BLASTX
NCBI GI g881615
BLAST score 722
E value 1.0e-76
Match length 147
% identity 97
NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No. 144529
Seq. ID LIB3168-045-P1-K1-F4
Method BLASTX
NCBI GI g112682
BLAST score 630
E value 6.0e-66
Match length 145
% identity 82
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144530
Seq. ID LIB3168-045-P1-K1-F5
Method BLASTN
NCBI GI g3449329
BLAST score 346
E value 0.0e+00
Match length 446
% identity 95
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No. 144531
Seq. ID LIB3168-045-P1-K1-F6
Method BLASTX
NCBI GI g112682
BLAST score 752
E value 3.0e-80
Match length 144
% identity 99
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144532
Seq. ID	LIB3168-045-P1-K1-F9
Method	BLASTX
NCBI GI	g3386609
BLAST score	88
E value	2.0e-31
Match length	118
% identity	70
NCBI Description	(AC004665) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	144533
Seq. ID	LIB3168-045-P1-K1-G1
Method	BLASTN
NCBI GI	g4580400
BLAST score	423
E value	0.0e+00
Match length	467
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16I21 genomic sequence, complete sequence

Seq. No.	144534
Seq. ID	LIB3168-045-P1-K1-G10
Method	BLASTX
NCBI GI	g3337356
BLAST score	545
E value	5.0e-56
Match length	107
% identity	100
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	144535
Seq. ID	LIB3168-045-P1-K1-G4
Method	BLASTN
NCBI GI	g4063735
BLAST score	133
E value	1.0e-68
Match length	220
% identity	96
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	144536
Seq. ID	LIB3168-045-P1-K1-G5
Method	BLASTX
NCBI GI	g112739
BLAST score	499
E value	2.0e-50
Match length	142
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -

Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144537
Seq. ID	LIB3168-045-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	45
E value	5.0e-69
Match length	148
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144538
Seq. ID	LIB3168-045-P1-K1-G9
Method	BLASTX
NCBI GI	g1628583
BLAST score	492
E value	8.0e-50
Match length	127
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144539
Seq. ID	LIB3168-045-P1-K1-H1
Method	BLASTX
NCBI GI	g112741
BLAST score	773
E value	1.0e-82
Match length	145
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144540
Seq. ID	LIB3168-045-P1-K1-H11
Method	BLASTX
NCBI GI	g99742
BLAST score	548
E value	3.0e-56
Match length	125

% identity	86
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	144541
Seq. ID	LIB3168-045-P1-K1-H12
Method	BLASTX
NCBI GI	g2129577
BLAST score	396
E value	1.0e-38
Match length	78
% identity	96
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	144542
Seq. ID	LIB3168-045-P1-K1-H2
Method	BLASTX
NCBI GI	g3169719
BLAST score	572
E value	5.0e-62
Match length	123
% identity	100
NCBI Description	(AF007109) similar to yeast dcp1 [Arabidopsis thaliana]

Seq. No.	144543
Seq. ID	LIB3168-045-P1-K1-H3
Method	BLASTX
NCBI GI	g1723275
BLAST score	261
E value	1.0e-22
Match length	104
% identity	51
NCBI Description	HYPOTHETICAL 55.6 KD PROTEIN C13F4.15C IN CHROMOSOME I >gi_2130223_pir__S67390 hypothetical protein - fission yeast (Schizosaccharomyces pombe) >gi_3451294_emb_CAA20426_ (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]

Seq. No.	144544
Seq. ID	LIB3168-045-P1-K1-H4
Method	BLASTX
NCBI GI	g2160182
BLAST score	201
E value	1.0e-15
Match length	63
% identity	56
NCBI Description	(AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]

Seq. No.	144545
Seq. ID	LIB3168-045-P1-K1-H5
Method	BLASTN
NCBI GI	g3445196
BLAST score	41
E value	1.0e-13
Match length	154

% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144546
Seq. ID	LIB3168-045-P1-K1-H6
Method	BLASTX
NCBI GI	g3738320
BLAST score	538
E value	4.0e-55
Match length	146
% identity	72
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	144547
Seq. ID	LIB3168-045-P1-K1-H7
Method	BLASTX
NCBI GI	g112681
BLAST score	101
E value	8.0e-66
Match length	132
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144548
Seq. ID	LIB3168-045-P1-K1-H8
Method	BLASTX
NCBI GI	g112682
BLAST score	649
E value	4.0e-68
Match length	151
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144549
Seq. ID	LIB3168-045-P1-K1-H9
Method	BLASTX
NCBI GI	g120675
BLAST score	451
E value	6.0e-45
Match length	107
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	144550
Seq. ID	LIB3168-046-P1-K1-A1
Method	BLASTN
NCBI GI	g3492855
BLAST score	326
E value	0.0e+00
Match length	382
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	144551
Seq. ID	LIB3168-046-P1-K1-A10
Method	BLASTX
NCBI GI	g112681
BLAST score	590
E value	3.0e-61
Match length	144
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144552
Seq. ID	LIB3168-046-P1-K1-A11
Method	BLASTX
NCBI GI	g112737
BLAST score	577
E value	1.0e-59
Match length	142
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144553
Seq. ID	LIB3168-046-P1-K1-A12
Method	BLASTN
NCBI GI	g4454447
BLAST score	37
E value	3.0e-11
Match length	85
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144554
Seq. ID	LIB3168-046-P1-K1-A2
Method	BLASTX
NCBI GI	g112681
BLAST score	120

E value	2.0e-35
Match length	120
% identity	71
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144555
Seq. ID	LIB3168-046-P1-K1-A3
Method	BLASTX
NCBI GI	g1171978
BLAST score	401
E value	4.0e-39
Match length	145
% identity	62
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	144556
Seq. ID	LIB3168-046-P1-K1-A4
Method	BLASTX
NCBI GI	g112682
BLAST score	592
E value	2.0e-61
Match length	123
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144557
Seq. ID	LIB3168-046-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	513
E value	2.0e-52
Match length	111
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144558
Seq. ID	LIB3168-046-P1-K1-A7
Method	BLASTN
NCBI GI	g1592685
BLAST score	66
E value	8.0e-29
Match length	154
% identity	86
NCBI Description	A.thaliana mRNA for oleosin type4 protein

Seq. No.	144559
Seq. ID	LIB3168-046-P1-K1-A8
Method	BLASTN
NCBI GI	g1628582
BLAST score	71
E value	5.0e-32
Match length	159
% identity	75
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	144560
Seq. ID	LIB3168-046-P1-K1-A9
Method	BLASTX
NCBI GI	g112743
BLAST score	621
E value	6.0e-65
Match length	123
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144561
Seq. ID	LIB3168-046-P1-K1-B11
Method	BLASTN
NCBI GI	g4199934
BLAST score	182
E value	3.0e-98
Match length	190
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	144562
Seq. ID	LIB3168-046-P1-K1-B12
Method	BLASTN
NCBI GI	g4432829
BLAST score	422
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144563
Seq. ID	LIB3168-046-P1-K1-B3
Method	BLASTX
NCBI GI	g267073
BLAST score	496
E value	3.0e-50
Match length	107

% identity	85
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	144564
Seq. ID	LIB3168-046-P1-K1-B4
Method	BLASTX
NCBI GI	g3080402
BLAST score	453
E value	3.0e-45
Match length	105
% identity	88
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	144565
Seq. ID	LIB3168-046-P1-K1-B5
Method	BLASTN
NCBI GI	g4079614
BLAST score	63
E value	4.0e-27
Match length	115
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144566
Seq. ID	LIB3168-046-P1-K1-B6
Method	BLASTX
NCBI GI	g112741
BLAST score	671
E value	1.0e-70
Match length	139
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144567
Seq. ID	LIB3168-046-P1-K1-B7
Method	BLASTX
NCBI GI	g112737
BLAST score	305
E value	5.0e-28
Match length	106
% identity	63
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144568
Seq. ID	LIB3168-046-P1-K1-B8
Method	BLASTX
NCBI GI	g126079
BLAST score	122
E value	2.0e-06
Match length	140
% identity	17
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN 76 (LEA 76) >gi_81683_pir__S04130 embryonic abundant protein (clone pLEA76) - rape >gi_17829_emb_CAA33406_ (X15348) LEA76 peptide (AA 1-280) [Brassica napus] >gi_226789_prf__1605299A Lea76 gene [Brassica napus]

Seq. No.	144569
Seq. ID	LIB3168-046-P1-K1-B9
Method	BLASTN
NCBI GI	g2842474
BLAST score	67
E value	9.0e-30
Match length	123
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144570
Seq. ID	LIB3168-046-P1-K1-C1
Method	BLASTN
NCBI GI	g3241924
BLAST score	160
E value	8.0e-85
Match length	180
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	144571
Seq. ID	LIB3168-046-P1-K1-C11
Method	BLASTX
NCBI GI	g3080402
BLAST score	692
E value	3.0e-73
Match length	135
% identity	99
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	144572
Seq. ID	LIB3168-046-P1-K1-C12
Method	BLASTN

NCBI GI	g4220631
BLAST score	410
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	144573
Seq. ID	LIB3168-046-P1-K1-C2
Method	BLASTN
NCBI GI	g4159707
BLAST score	259
E value	1.0e-144
Match length	423
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	144574
Seq. ID	LIB3168-046-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	632
E value	4.0e-66
Match length	144
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144575
Seq. ID	LIB3168-046-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	480
E value	1.0e-48
Match length	92
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144576
Seq. ID	LIB3168-046-P1-K1-C5
Method	BLASTX
NCBI GI	g112682
BLAST score	626
E value	2.0e-65
Match length	143
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	144577
Seq. ID	LIB3168-046-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	456
E value	2.0e-45
Match length	123
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144578
Seq. ID	LIB3168-046-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	427
E value	4.0e-42
Match length	86
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144579
Seq. ID	LIB3168-046-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	551
E value	1.0e-56
Match length	142
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144580
Seq. ID	LIB3168-046-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	552
E value	8.0e-57
Match length	116
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144581
Seq. ID	LIB3168-046-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	445
E value	2.0e-44
Match length	95

% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144582
Seq. ID	LIB3168-046-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	749
E value	7.0e-80
Match length	146
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144583
Seq. ID	LIB3168-046-P1-K1-D11
Method	BLASTX
NCBI GI	g112737
BLAST score	605
E value	5.0e-63
Match length	143
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144584
Seq. ID	LIB3168-046-P1-K1-D2
Method	BLASTN
NCBI GI	g2979540
BLAST score	284
E value	1.0e-158
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144585
Seq. ID	LIB3168-046-P1-K1-D3
Method	BLASTX
NCBI GI	g112682
BLAST score	761
E value	3.0e-81
Match length	146
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144586
Seq. ID	LIB3168-046-P1-K1-D4
Method	BLASTN
NCBI GI	g2760169
BLAST score	41
E value	5.0e-14
Match length	166
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	144587
Seq. ID	LIB3168-046-P1-K1-D5
Method	BLASTX
NCBI GI	g112681
BLAST score	547
E value	3.0e-56
Match length	118
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144588
Seq. ID	LIB3168-046-P1-K1-D6
Method	BLASTX
NCBI GI	g2760606
BLAST score	376
E value	2.0e-36
Match length	77
% identity	95
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	144589
Seq. ID	LIB3168-046-P1-K1-D7
Method	BLASTX
NCBI GI	g3395436
BLAST score	323
E value	8.0e-31
Match length	78
% identity	95
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	144590
Seq. ID	LIB3168-046-P1-K1-D8
Method	BLASTX
NCBI GI	g112682
BLAST score	768
E value	4.0e-82

Match length	145
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144591
Seq. ID	LIB3168-046-P1-K1-D9
Method	BLASTX
NCBI GI	g2500193
BLAST score	228
E value	7.0e-19
Match length	58
% identity	81
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC4 (GTP BINDING PROTEIN ROP2) >gi_1304417 (U45236) Description: rac-like protein; GTP binding protein; Method: conceptual translation supplied by author. [Arabidopsis thaliana] >gi_1777764 (U49972) GTP binding protein Rop2At [Arabidopsis thaliana]

Seq. No.	144592
Seq. ID	LIB3168-046-P1-K1-E1
Method	BLASTN
NCBI GI	g16472
BLAST score	88
E value	1.0e-41
Match length	92
% identity	99
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	144593
Seq. ID	LIB3168-046-P1-K1-E10
Method	BLASTX
NCBI GI	g1419090
BLAST score	347
E value	1.0e-32
Match length	143
% identity	51
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	144594
Seq. ID	LIB3168-046-P1-K1-E12
Method	BLASTX
NCBI GI	g134943
BLAST score	477
E value	5.0e-48
Match length	146
% identity	69
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_99831_pir__S23351 acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) precursor - turnip >gi_17929_emb_CAA43294_ (X60978) acyl-[acyl-carrier-protein] desaturase [Brassica rapa] >gi_1279219_emb_CAA65990_ (X97325) acyl-[acyl-carrier

protein] desaturase [Brassica napus]

Seq. No.	144595
Seq. ID	LIB3168-046-P1-K1-E2
Method	BLASTX
NCBI GI	g1107501
BLAST score	316
E value	2.0e-29
Match length	76
% identity	86
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	144596
Seq. ID	LIB3168-046-P1-K1-E3
Method	BLASTX
NCBI GI	g1946355
BLAST score	627
E value	1.0e-65
Match length	141
% identity	79
NCBI Description	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No.	144597
Seq. ID	LIB3168-046-P1-K1-E4
Method	BLASTN
NCBI GI	g1304416
BLAST score	118
E value	5.0e-60
Match length	170
% identity	93
NCBI Description	Arabidopsis thaliana rac-like protein (ARAC4) mRNA, complete cds

Seq. No.	144598
Seq. ID	LIB3168-046-P1-K1-E5
Method	BLASTX
NCBI GI	g112741
BLAST score	709
E value	3.0e-75
Match length	133
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144599
Seq. ID	LIB3168-046-P1-K1-E6
Method	BLASTX

NCBI GI	g1628583
BLAST score	511
E value	5.0e-52
Match length	124
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144600
Seq. ID	LIB3168-046-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	48
E value	5.0e-55
Match length	146
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144601
Seq. ID	LIB3168-046-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	586
E value	9.0e-61
Match length	145
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144602
Seq. ID	LIB3168-046-P1-K1-E9
Method	BLASTX
NCBI GI	g1848214
BLAST score	117
E value	3.0e-13
Match length	67
% identity	75
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No.	144603
Seq. ID	LIB3168-046-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	779
E value	2.0e-83
Match length	147
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144604
Seq. ID	LIB3168-046-P1-K1-F2
Method	BLASTN
NCBI GI	g2264311
BLAST score	122
E value	2.0e-62
Match length	150
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	144605
Seq. ID	LIB3168-046-P1-K1-F3
Method	BLASTX
NCBI GI	g112682
BLAST score	616
E value	3.0e-64
Match length	144
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144606
Seq. ID	LIB3168-046-P1-K1-F4
Method	BLASTX
NCBI GI	g3769673
BLAST score	570
E value	7.0e-59
Match length	144
% identity	69
NCBI Description	(AF095285) Tic20 [Pisum sativum]

Seq. No.	144607
Seq. ID	LIB3168-046-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	557
E value	2.0e-57
Match length	132
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144608
Seq. ID	LIB3168-046-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	578
E value	9.0e-60
Match length	111

% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144609
Seq. ID	LIB3168-046-P1-K1-F7
Method	BLASTX
NCBI GI	g1076316
BLAST score	552
E value	8.0e-57
Match length	105
% identity	99
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	144610
Seq. ID	LIB3168-046-P1-K1-F9
Method	BLASTN
NCBI GI	g2264314
BLAST score	211
E value	1.0e-115
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	144611
Seq. ID	LIB3168-046-P1-K1-G11
Method	BLASTX
NCBI GI	g1001311
BLAST score	155
E value	3.0e-10
Match length	81
% identity	48
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	144612
Seq. ID	LIB3168-046-P1-K1-G12
Method	BLASTN
NCBI GI	g3985958
BLAST score	67
E value	3.0e-29
Match length	191
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	144613
Seq. ID	LIB3168-046-P1-K1-G2
Method	BLASTN
NCBI GI	g2618603
BLAST score	217
E value	1.0e-118
Match length	378
% identity	97

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	144614
Seq. ID	LIB3168-046-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	313
E value	7.0e-29
Match length	110
% identity	49
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144615
Seq. ID	LIB3168-046-P1-K1-G4
Method	BLASTX
NCBI GI	g2129657
BLAST score	267
E value	2.0e-23
Match length	85
% identity	68
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144616
Seq. ID	LIB3168-046-P1-K1-G5
Method	BLASTX
NCBI GI	g3914467
BLAST score	586
E value	9.0e-61
Match length	144
% identity	82
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	144617
Seq. ID	LIB3168-046-P1-K1-G6
Method	BLASTX
NCBI GI	g112681
BLAST score	315
E value	3.0e-29
Match length	79
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144618
Seq. ID	LIB3168-046-P1-K1-G7
Method	BLASTX

NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144619
Seq. ID	LIB3168-046-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	470
E value	3.0e-47
Match length	122
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144620
Seq. ID	LIB3168-046-P1-K1-G9
Method	BLASTN
NCBI GI	g438450
BLAST score	41
E value	4.0e-14
Match length	96
% identity	90
NCBI Description	Arabidopsis thaliana delta-12 desaturase (Fad2) mRNA, complete cds

Seq. No.	144621
Seq. ID	LIB3168-046-P1-K1-H1
Method	BLASTX
NCBI GI	g3152581
BLAST score	652
E value	2.0e-68
Match length	141
% identity	89
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	144622
Seq. ID	LIB3168-046-P1-K1-H11
Method	BLASTN
NCBI GI	g3763944
BLAST score	244
E value	1.0e-135
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	144623
Seq. ID	LIB3168-046-P1-K1-H12

Method	BLASTX
NCBI GI	g2605714
BLAST score	489
E value	2.0e-49
Match length	115
% identity	83
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	144624
Seq. ID	LIB3168-046-P1-K1-H2
Method	BLASTN
NCBI GI	g2924257
BLAST score	52
E value	2.0e-20
Match length	142
% identity	92
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	144625
Seq. ID	LIB3168-046-P1-K1-H3
Method	BLASTN
NCBI GI	g2864607
BLAST score	393
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	144626
Seq. ID	LIB3168-046-P1-K1-H4
Method	BLASTX
NCBI GI	g112682
BLAST score	532
E value	1.0e-54
Match length	116
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144627
Seq. ID	LIB3168-046-P1-K1-H7
Method	BLASTX
NCBI GI	g2129659
BLAST score	458
E value	9.0e-46
Match length	137
% identity	72
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	144628
Seq. ID	LIB3168-046-P1-K1-H8

Method	BLASTX
NCBI GI	g1352463
BLAST score	445
E value	3.0e-44
Match length	118
% identity	76
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	144629
Seq. ID	LIB3168-047-P1-K1-A1
Method	BLASTX
NCBI GI	g113595
BLAST score	406
E value	1.0e-39
Match length	129
% identity	59
NCBI Description	ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE) >gi_100562_pir__S15024 aldose reductase-related protein - barley >gi_18891_emb_CAA40747_ (X57526) aldose reductase-related protein [Hordeum vulgare]

Seq. No.	144630
Seq. ID	LIB3168-047-P1-K1-A10
Method	BLASTX
NCBI GI	g112739
BLAST score	373
E value	7.0e-36
Match length	112
% identity	69
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144631
Seq. ID	LIB3168-047-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	526
E value	9.0e-54
Match length	134
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144632
Seq. ID	LIB3168-047-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65

Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144633
Seq. ID	LIB3168-047-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	55
E value	5.0e-54
Match length	125
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144634
Seq. ID	LIB3168-047-P1-K1-A3
Method	BLASTX
NCBI GI	g4581109
BLAST score	248
E value	4.0e-21
Match length	113
% identity	40
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	144635
Seq. ID	LIB3168-047-P1-K1-A4
Method	BLASTX
NCBI GI	g2605714
BLAST score	520
E value	5.0e-53
Match length	122
% identity	84
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	144636
Seq. ID	LIB3168-047-P1-K1-A5
Method	BLASTX
NCBI GI	g2702274
BLAST score	331
E value	2.0e-31
Match length	67
% identity	97
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	144637
Seq. ID	LIB3168-047-P1-K1-A6
Method	BLASTX
NCBI GI	g544122
BLAST score	697
E value	8.0e-74
Match length	138
% identity	97

NCBI Description	APOCYTOCHROME F PRECURSOR >gi_629599_pir__S45661 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - turnip chloroplast >gi_441282_emb_CAA54307_ (X77011) cytochrome f [Brassica rapa]
Seq. No.	144638
Seq. ID	LIB3168-047-P1-K1-A7
Method	BLASTX
NCBI GI	g112682
BLAST score	145
E value	7.0e-43
Match length	133
% identity	70
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144639
Seq. ID	LIB3168-047-P1-K1-A8
Method	BLASTN
NCBI GI	g511598
BLAST score	395
E value	0.0e+00
Match length	419
% identity	26
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds
Seq. No.	144640
Seq. ID	LIB3168-047-P1-K1-A9
Method	BLASTX
NCBI GI	g112737
BLAST score	540
E value	2.0e-55
Match length	132
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	144641
Seq. ID	LIB3168-047-P1-K1-B1
Method	BLASTN
NCBI GI	g4455168
BLAST score	386
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	144642
Seq. ID	LIB3168-047-P1-K1-B10
Method	BLASTX
NCBI GI	g2506276
BLAST score	583
E value	2.0e-60
Match length	120
% identity	98
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	144643
Seq. ID	LIB3168-047-P1-K1-B11
Method	BLASTX
NCBI GI	g2982454
BLAST score	298
E value	5.0e-34
Match length	136
% identity	57
NCBI Description	(AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	144644
Seq. ID	LIB3168-047-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144645
Seq. ID	LIB3168-047-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144646
Seq. ID	LIB3168-047-P1-K1-B4
Method	BLASTX
NCBI GI	g112743
BLAST score	694

E value	2.0e-73
Match length	130
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144647
Seq. ID	LIB3168-047-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	225
E value	1.0e-18
Match length	58
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144648
Seq. ID	LIB3168-047-P1-K1-B6
Method	BLASTN
NCBI GI	g2688838
BLAST score	150
E value	1.0e-78
Match length	282
% identity	88
NCBI Description	Thlaspi goesingense ATP phosphoribosyltransferase (THG1) mRNA, complete cds

Seq. No.	144649
Seq. ID	LIB3168-047-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144650
Seq. ID	LIB3168-047-P1-K1-B8
Method	BLASTX
NCBI GI	g2129659
BLAST score	181
E value	3.0e-22
Match length	95
% identity	59
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	144651
Seq. ID	LIB3168-047-P1-K1-B9
Method	BLASTX
NCBI GI	g112682
BLAST score	679
E value	1.0e-71
Match length	141
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144652
Seq. ID	LIB3168-047-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	614
E value	4.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144653
Seq. ID	LIB3168-047-P1-K1-C10
Method	BLASTN
NCBI GI	g2264312
BLAST score	394
E value	0.0e+00
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	144654
Seq. ID	LIB3168-047-P1-K1-C11
Method	BLASTX
NCBI GI	g267070
BLAST score	478
E value	2.0e-48
Match length	91
% identity	98
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]

Seq. No.	144655
Seq. ID	LIB3168-047-P1-K1-C12
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61

Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144656
Seq. ID	LIB3168-047-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	251
E value	5.0e-39
Match length	113
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144657
Seq. ID	LIB3168-047-P1-K1-C3
Method	BLASTX
NCBI GI	g112682
BLAST score	578
E value	7.0e-60
Match length	138
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144658
Seq. ID	LIB3168-047-P1-K1-C4
Method	BLASTX
NCBI GI	g3695390
BLAST score	267
E value	2.0e-23
Match length	77
% identity	66
NCBI Description	(AF096371) contains similarity to Rattus norvegicus cyclin G-associated kinase (SW:P97874) [Arabidopsis thaliana]

Seq. No.	144659
Seq. ID	LIB3168-047-P1-K1-C6
Method	BLASTN
NCBI GI	g3702722
BLAST score	61
E value	6.0e-26
Match length	109
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No. 144660

Seq. ID	LIB3168-047-P1-K1-C7
Method	BLASTX
NCBI GI	g4115365
BLAST score	330
E value	9.0e-31
Match length	123
% identity	71
NCBI Description	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq. No.	144661
Seq. ID	LIB3168-047-P1-K1-C9
Method	BLASTX
NCBI GI	g4454033
BLAST score	253
E value	9.0e-22
Match length	139
% identity	40
NCBI Description	(AL035394) putative potassium transport protein [Arabidopsis thaliana]

Seq. No.	144662
Seq. ID	LIB3168-047-P1-K1-D10
Method	BLASTX
NCBI GI	g464987
BLAST score	471
E value	2.0e-47
Match length	107
% identity	86
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	144663
Seq. ID	LIB3168-047-P1-K1-D11
Method	BLASTX
NCBI GI	g3135274
BLAST score	202
E value	6.0e-16
Match length	80
% identity	53
NCBI Description	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	144664
Seq. ID	LIB3168-047-P1-K1-D12
Method	BLASTX
NCBI GI	g1072480
BLAST score	68
E value	2.0e-46
Match length	119
% identity	83
NCBI Description	cruciferin 1 precursor - rape

Seq. No.	144665
Seq. ID	LIB3168-047-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144666
Seq. ID	LIB3168-047-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	523
E value	2.0e-53
Match length	133
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144667
Seq. ID	LIB3168-047-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	560
E value	9.0e-58
Match length	133
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144668
Seq. ID	LIB3168-047-P1-K1-D5
Method	BLASTN
NCBI GI	g3885325
BLAST score	129
E value	4.0e-66
Match length	177
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144669
Seq. ID	LIB3168-047-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	107
E value	5.0e-20
Match length	55

% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144670
Seq. ID	LIB3168-047-P1-K1-D7
Method	BLASTX
NCBI GI	g1041704
BLAST score	323
E value	6.0e-30
Match length	93
% identity	68
NCBI Description	(U30478) expansin At-EXP5 [Arabidopsis thaliana]

Seq. No.	144671
Seq. ID	LIB3168-047-P1-K1-D8
Method	BLASTX
NCBI GI	g2924779
BLAST score	607
E value	3.0e-63
Match length	121
% identity	99
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	144672
Seq. ID	LIB3168-047-P1-K1-D9
Method	BLASTX
NCBI GI	g1791352
BLAST score	170
E value	5.0e-12
Match length	91
% identity	42
NCBI Description	(U83789) O-diphenol-O-methyltransferase [Capsicum annuum]

Seq. No.	144673
Seq. ID	LIB3168-047-P1-K1-E1
Method	BLASTX
NCBI GI	g82734
BLAST score	596
E value	6.0e-62
Match length	121
% identity	30
NCBI Description	ubiquitin precursor - maize (fragment) >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No.	144674
Seq. ID	LIB3168-047-P1-K1-E12
Method	BLASTX
NCBI GI	g112741
BLAST score	415
E value	9.0e-58
Match length	128

% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	144675
Seq. ID	LIB3168-047-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	543
E value	9.0e-56
Match length	139
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144676
Seq. ID	LIB3168-047-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	447
E value	2.0e-44
Match length	127
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144677
Seq. ID	LIB3168-047-P1-K1-E5
Method	BLASTX
NCBI GI	g3738324
BLAST score	506
E value	2.0e-51
Match length	111
% identity	82
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.	144678
Seq. ID	LIB3168-047-P1-K1-E6
Method	BLASTX
NCBI GI	g112741
BLAST score	475
E value	2.0e-48
Match length	98
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No.	144679
Seq. ID	LIB3168-047-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	681
E value	6.0e-72
Match length	133
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144680
Seq. ID	LIB3168-047-P1-K1-E8
Method	BLASTX
NCBI GI	g4204299
BLAST score	117
E value	4.0e-62
Match length	125
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144681
Seq. ID	LIB3168-047-P1-K1-E9
Method	BLASTX
NCBI GI	g112739
BLAST score	480
E value	2.0e-48
Match length	132
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144682
Seq. ID	LIB3168-047-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	199
E value	1.0e-15
Match length	41
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144683
Seq. ID	LIB3168-047-P1-K1-F10
Method	BLASTX
NCBI GI	g2970654

BLAST score	278
E value	1.0e-24
Match length	107
% identity	57
NCBI Description	(AF052058) ferritin subunit cowpea2 precursor [Vigna unguiculata]

Seq. No.	144684
Seq. ID	LIB3168-047-P1-K1-F12
Method	BLASTX
NCBI GI	g112741
BLAST score	631
E value	4.0e-66
Match length	135
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144685
Seq. ID	LIB3168-047-P1-K1-F2
Method	BLASTX
NCBI GI	g112682
BLAST score	676
E value	2.0e-71
Match length	140
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144686
Seq. ID	LIB3168-047-P1-K1-F4
Method	BLASTX
NCBI GI	g112681
BLAST score	532
E value	2.0e-54
Match length	127
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144687
Seq. ID	LIB3168-047-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	8.0e-70

Match length	139
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144688
Seq. ID	LIB3168-047-P1-K1-F6
Method	BLASTX
NCBI GI	g112739
BLAST score	402
E value	3.0e-39
Match length	116
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144689
Seq. ID	LIB3168-047-P1-K1-F7
Method	BLASTN
NCBI GI	g3985955
BLAST score	338
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	144690
Seq. ID	LIB3168-047-P1-K1-F8
Method	BLASTX
NCBI GI	g82734
BLAST score	617
E value	2.0e-64
Match length	124
% identity	30
NCBI Description	ubiquitin precursor - maize (fragment) >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No.	144691
Seq. ID	LIB3168-047-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	552
E value	8.0e-57
Match length	139
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144692

Seq. ID	LIB3168-047-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	603
E value	9.0e-63
Match length	138
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144693
Seq. ID	LIB3168-047-P1-K1-G10
Method	BLASTN
NCBI GI	g395203
BLAST score	184
E value	2.0e-99
Match length	184
% identity	59
NCBI Description	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

Seq. No.	144694
Seq. ID	LIB3168-047-P1-K1-G12
Method	BLASTX
NCBI GI	g112681
BLAST score	609
E value	2.0e-63
Match length	140
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144695
Seq. ID	LIB3168-047-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	556
E value	3.0e-57
Match length	112
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144696
Seq. ID	LIB3168-047-P1-K1-G4
Method	BLASTX
NCBI GI	g224293
BLAST score	386
E value	2.0e-37
Match length	78
% identity	100

NCBI Description	histone H4 [Triticum aestivum]
Seq. No.	144697
Seq. ID	LIB3168-047-P1-K1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	168
E value	6.0e-12
Match length	39
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144698
Seq. ID	LIB3168-047-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144699
Seq. ID	LIB3168-047-P1-K1-G9
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144700
Seq. ID	LIB3168-047-P1-K1-H10
Method	BLASTX
NCBI GI	g112681
BLAST score	603
E value	8.0e-63
Match length	138
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144701
Seq. ID	LIB3168-047-P1-K1-H11
Method	BLASTX

NCBI GI	g1628583
BLAST score	661
E value	1.0e-69
Match length	128
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144702
Seq. ID	LIB3168-047-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	542
E value	1.0e-55
Match length	138
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144703
Seq. ID	LIB3168-047-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	588
E value	4.0e-61
Match length	127
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144704
Seq. ID	LIB3168-047-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	636
E value	1.0e-66
Match length	127
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144705
Seq. ID	LIB3168-047-P1-K1-H4
Method	BLASTN
NCBI GI	g3869062
BLAST score	42
E value	3.0e-14
Match length	115
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	144706
Seq. ID	LIB3168-047-P1-K1-H6
Method	BLASTX
NCBI GI	g112682
BLAST score	615
E value	3.0e-64
Match length	141
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144707
Seq. ID	LIB3168-047-P1-K1-H8
Method	BLASTX
NCBI GI	g112739
BLAST score	425
E value	6.0e-42
Match length	121
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144708
Seq. ID	LIB3168-047-P1-K1-H9
Method	BLASTX
NCBI GI	g1169476
BLAST score	625
E value	2.0e-65
Match length	121
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	144709
Seq. ID	LIB3168-048-P1-K1-A1
Method	BLASTN
NCBI GI	g4006885
BLAST score	322
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	144710
Seq. ID	LIB3168-048-P1-K1-A11
Method	BLASTX

NCBI GI	g4581146
BLAST score	498
E value	2.0e-50
Match length	119
% identity	87
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	144711
Seq. ID	LIB3168-048-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	533
E value	1.0e-54
Match length	127
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144712
Seq. ID	LIB3168-048-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	656
E value	5.0e-69
Match length	131
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144713
Seq. ID	LIB3168-048-P1-K1-A3
Method	BLASTN
NCBI GI	g4079614
BLAST score	304
E value	1.0e-171
Match length	314
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144714
Seq. ID	LIB3168-048-P1-K1-A4
Method	BLASTX
NCBI GI	g112741
BLAST score	620
E value	7.0e-65
Match length	118
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144715
Seq. ID	LIB3168-048-P1-K1-A5
Method	BLASTN
NCBI GI	g2160132
BLAST score	108
E value	6.0e-54
Match length	191
% identity	93
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	144716
Seq. ID	LIB3168-048-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	556
E value	3.0e-57
Match length	138
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144717
Seq. ID	LIB3168-048-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	309
E value	8.0e-29
Match length	65
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144718
Seq. ID	LIB3168-048-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	665
E value	4.0e-70
Match length	128
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144719
Seq. ID	LIB3168-048-P1-K1-B12
Method	BLASTX
NCBI GI	g131336
BLAST score	339
E value	7.0e-32

Match length	73
% identity	93
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	144720
Seq. ID	LIB3168-048-P1-K1-B2
Method	BLASTN
NCBI GI	g3510341
BLAST score	42
E value	3.0e-14
Match length	213
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	144721
Seq. ID	LIB3168-048-P1-K1-B4
Method	BLASTX
NCBI GI	g1419090
BLAST score	316
E value	4.0e-29
Match length	136
% identity	49
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	144722
Seq. ID	LIB3168-048-P1-K1-B6
Method	BLASTX
NCBI GI	g4651202
BLAST score	294
E value	1.0e-26
Match length	138
% identity	43
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]

Seq. No.	144723
Seq. ID	LIB3168-048-P1-K1-B8
Method	BLASTN
NCBI GI	g4406805
BLAST score	386
E value	0.0e+00
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144724
Seq. ID	LIB3168-048-P1-K1-C1
Method	BLASTX
NCBI GI	g112741
BLAST score	83

E value	6.0e-69
Match length	130
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144725
Seq. ID	LIB3168-048-P1-K1-C12
Method	BLASTX
NCBI GI	g3023848
BLAST score	552
E value	7.0e-57
Match length	109
% identity	29
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	144726
Seq. ID	LIB3168-048-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	596
E value	5.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144727
Seq. ID	LIB3168-048-P1-K1-C4
Method	BLASTX
NCBI GI	g112741
BLAST score	705
E value	9.0e-75
Match length	131
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144728
Seq. ID	LIB3168-048-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	524

E value	2.0e-53
Match length	137
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144729
Seq. ID	LIB3168-048-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	1.0e-60
Match length	115
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144730
Seq. ID	LIB3168-048-P1-K1-D1
Method	BLASTX
NCBI GI	g585922
BLAST score	582
E value	2.0e-60
Match length	139
% identity	80
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

Seq. No.	144731
Seq. ID	LIB3168-048-P1-K1-D2
Method	BLASTX
NCBI GI	g112741
BLAST score	691
E value	4.0e-73
Match length	128
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144732
Seq. ID	LIB3168-048-P1-K1-D3
Method	BLASTN
NCBI GI	g2244991
BLAST score	400
E value	0.0e+00
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	144733

Seq. ID	LIB3168-048-P1-K1-D5
Method	BLASTX
NCBI GI	g112737
BLAST score	405
E value	1.0e-39
Match length	111
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144734
Seq. ID	LIB3168-048-P1-K1-D6
Method	BLASTX
NCBI GI	g3881856
BLAST score	65
E value	6.0e-26
Match length	95
% identity	52
NCBI Description	(Z79759) Similarity to Yeast endosomal P24A protein (SW:EM70_YEAST); cDNA EST CEMSB40F comes from this gene; cDNA EST EMBL:C13538 comes from this gene; cDNA EST yk385b5.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	144735
Seq. ID	LIB3168-048-P1-K1-D7
Method	BLASTN
NCBI GI	g3426033
BLAST score	134
E value	3.0e-69
Match length	198
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144736
Seq. ID	LIB3168-048-P1-K1-D8
Method	BLASTX
NCBI GI	g112681
BLAST score	91
E value	5.0e-60
Match length	126
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144737
Seq. ID	LIB3168-048-P1-K1-D9
Method	BLASTX
NCBI GI	g4204299

BLAST score	723
E value	7.0e-77
Match length	136
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144738
Seq. ID	LIB3168-048-P1-K1-E10
Method	BLASTN
NCBI GI	g3859658
BLAST score	212
E value	1.0e-116
Match length	361
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	144739
Seq. ID	LIB3168-048-P1-K1-E11
Method	BLASTX
NCBI GI	g112682
BLAST score	574
E value	2.0e-59
Match length	134
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144740
Seq. ID	LIB3168-048-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	653
E value	1.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144741
Seq. ID	LIB3168-048-P1-K1-E2
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	144742
Seq. ID	LIB3168-048-P1-K1-E5

Method	BLASTX
NCBI GI	g112737
BLAST score	347
E value	6.0e-33
Match length	66
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144743
Seq. ID	LIB3168-048-P1-K1-E6
Method	BLASTX
NCBI GI	g112739
BLAST score	364
E value	9.0e-35
Match length	121
% identity	61
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144744
Seq. ID	LIB3168-048-P1-K1-E7
Method	BLASTN
NCBI GI	g4217996
BLAST score	85
E value	4.0e-40
Match length	213
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144745
Seq. ID	LIB3168-048-P1-K1-E8
Method	BLASTX
NCBI GI	g112682
BLAST score	511
E value	4.0e-52
Match length	113
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144746
Seq. ID	LIB3168-048-P1-K1-E9

Method	BLASTX
NCBI GI	g2194142
BLAST score	431
E value	1.0e-42
Match length	87
% identity	99
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	144747
Seq. ID	LIB3168-048-P1-K1-F1
Method	BLASTN
NCBI GI	g3608126
BLAST score	371
E value	0.0e+00
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144748
Seq. ID	LIB3168-048-P1-K1-F12
Method	BLASTN
NCBI GI	g4159709
BLAST score	32
E value	1.0e-08
Match length	47
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	144749
Seq. ID	LIB3168-048-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	406
E value	1.0e-39
Match length	146
% identity	68
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144750
Seq. ID	LIB3168-048-P1-K1-G1
Method	BLASTX
NCBI GI	g3281868
BLAST score	724
E value	5.0e-77
Match length	138
% identity	99
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	144751
Seq. ID	LIB3168-048-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583

BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144752
Seq. ID	LIB3168-048-P1-K1-G12
Method	BLASTN
NCBI GI	g2264304
BLAST score	74
E value	2.0e-33
Match length	438
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	144753
Seq. ID	LIB3168-048-P1-K1-G2
Method	BLASTX
NCBI GI	g1169515
BLAST score	609
E value	2.0e-63
Match length	116
% identity	98
NCBI Description	EM-LIKE PROTEIN GEA1 >gi_2119768_pir__S34819 embryonic abundant protein Em1 - Arabidopsis thaliana >gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1 protein [Arabidopsis thaliana]

Seq. No.	144754
Seq. ID	LIB3168-048-P1-K1-G4
Method	BLASTN
NCBI GI	g4662640
BLAST score	194
E value	1.0e-105
Match length	340
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	144755
Seq. ID	LIB3168-048-P1-K1-G5
Method	BLASTX
NCBI GI	g112741
BLAST score	60
E value	3.0e-30
Match length	75
% identity	93
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144756
Seq. ID	LIB3168-048-P1-K1-G6
Method	BLASTX
NCBI GI	g4512684
BLAST score	384
E value	4.0e-37
Match length	90
% identity	86
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	144757
Seq. ID	LIB3168-048-P1-K1-H10
Method	BLASTX
NCBI GI	g112682
BLAST score	564
E value	3.0e-58
Match length	132
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144758
Seq. ID	LIB3168-048-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	644
E value	1.0e-67
Match length	137
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144759
Seq. ID	LIB3168-048-P1-K1-H2
Method	BLASTX
NCBI GI	g4006897
BLAST score	371
E value	1.0e-35
Match length	76
% identity	99
NCBI Description	(Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.	144760
Seq. ID	LIB3168-048-P1-K1-H3
Method	BLASTX
NCBI GI	g112681
BLAST score	473

E value	1.0e-47
Match length	136
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144761
Seq. ID	LIB3168-048-P1-K1-H5
Method	BLASTX
NCBI GI	g1619602
BLAST score	187
E value	5.0e-14
Match length	71
% identity	58
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	144762
Seq. ID	LIB3168-048-P1-K1-H6
Method	BLASTN
NCBI GI	g2454181
BLAST score	51
E value	1.0e-19
Match length	106
% identity	92
NCBI Description	Arabidopsis thaliana pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	144763
Seq. ID	LIB3168-048-P1-K1-H8
Method	BLASTX
NCBI GI	g267073
BLAST score	282
E value	5.0e-43
Match length	92
% identity	97
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	144764
Seq. ID	LIB3168-048-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	542
E value	1.0e-55
Match length	137
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144765

Seq. ID	LIB3168-050-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144766
Seq. ID	LIB3168-050-P1-K1-A11
Method	BLASTN
NCBI GI	g16231
BLAST score	49
E value	1.0e-18
Match length	105
% identity	90
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	144767
Seq. ID	LIB3168-050-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	317
E value	2.0e-52
Match length	140
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144768
Seq. ID	LIB3168-050-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	683
E value	4.0e-72
Match length	137
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144769
Seq. ID	LIB3168-050-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	353
E value	6.0e-34
Match length	70
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144770
Seq. ID	LIB3168-050-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61
Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144771
Seq. ID	LIB3168-050-P1-K1-A7
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	2.0e-60
Match length	123
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144772
Seq. ID	LIB3168-050-P1-K1-A8
Method	BLASTX
NCBI GI	g112741
BLAST score	702
E value	2.0e-74
Match length	132
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144773
Seq. ID	LIB3168-050-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	1.0e-63
Match length	129
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144774
Seq. ID	LIB3168-050-P1-K1-B1
Method	BLASTX
NCBI GI	g112741
BLAST score	725
E value	4.0e-77
Match length	135
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144775
Seq. ID	LIB3168-050-P1-K1-B10
Method	BLASTX
NCBI GI	g2829918
BLAST score	305
E value	8.0e-28
Match length	87
% identity	66
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	144776
Seq. ID	LIB3168-050-P1-K1-B11
Method	BLASTN
NCBI GI	g2337888
BLAST score	336
E value	0.0e+00
Match length	407
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	144777
Seq. ID	LIB3168-050-P1-K1-B12
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	2.0e-60
Match length	136
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144778
Seq. ID	LIB3168-050-P1-K1-B2

Method	BLASTN
NCBI GI	g16236
BLAST score	44
E value	1.0e-15
Match length	147
% identity	91
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	144779
Seq. ID	LIB3168-050-P1-K1-B3
Method	BLASTX
NCBI GI	g2911067
BLAST score	718
E value	3.0e-76
Match length	143
% identity	94
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	144780
Seq. ID	LIB3168-050-P1-K1-B4
Method	BLASTX
NCBI GI	g112681
BLAST score	644
E value	1.0e-67
Match length	127
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144781
Seq. ID	LIB3168-050-P1-K1-B5
Method	BLASTX
NCBI GI	g112737
BLAST score	283
E value	2.0e-46
Match length	128
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144782
Seq. ID	LIB3168-050-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	516
E value	1.0e-52

Match length	141
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144783
Seq. ID	LIB3168-050-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	587
E value	5.0e-61
Match length	116
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144784
Seq. ID	LIB3168-050-P1-K1-C10
Method	BLASTX
NCBI GI	g112681
BLAST score	454
E value	2.0e-45
Match length	112
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144785
Seq. ID	LIB3168-050-P1-K1-C11
Method	BLASTX
NCBI GI	g1118137
BLAST score	169
E value	7.0e-12
Match length	125
% identity	8
NCBI Description	(U41746) coded for by C. elegans cDNA yk68a8.5 [Caenorhabditis elegans]

Seq. No.	144786
Seq. ID	LIB3168-050-P1-K1-C4
Method	BLASTX
NCBI GI	g119143
BLAST score	385
E value	6.0e-57
Match length	123
% identity	94
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana]

	>gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]
Seq. No.	144787
Seq. ID	LIB3168-050-P1-K1-C5
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	1.0e-61
Match length	133
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA52494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144788
Seq. ID	LIB3168-050-P1-K1-C6
Method	BLASTN
NCBI GI	g4406752
BLAST score	275
E value	1.0e-153
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	144789
Seq. ID	LIB3168-050-P1-K1-C7
Method	BLASTX
NCBI GI	g82051
BLAST score	323
E value	6.0e-30
Match length	127
% identity	52
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]
Seq. No.	144790
Seq. ID	LIB3168-050-P1-K1-C8
Method	BLASTX
NCBI GI	g2623962
BLAST score	462
E value	3.0e-46
Match length	97
% identity	91
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]
Seq. No.	144791

Seq. ID	LIB3168-050-P1-K1-C9
Method	BLASTX
NCBI GI	g140292
BLAST score	309
E value	3.0e-28
Match length	70
% identity	87
NCBI Description	HYPOTHETICAL 21.5 KD PROTEIN (ORF 184) >gi_82208_pir__A05197 hypothetical protein 184 - common tobacco chloroplast >gi_11843_emb_CAA77363_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225211_prf__1211235AR ORF 184 [Nicotiana tabacum]

Seq. No.	144792
Seq. ID	LIB3168-050-P1-K1-D1
Method	BLASTX
NCBI GI	g112741
BLAST score	709
E value	3.0e-75
Match length	132
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144793
Seq. ID	LIB3168-050-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	707
E value	5.0e-75
Match length	134
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144794
Seq. ID	LIB3168-050-P1-K1-D12
Method	BLASTX
NCBI GI	g112737
BLAST score	534
E value	1.0e-54
Match length	134
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144795
Seq. ID	LIB3168-050-P1-K1-D2
Method	BLASTX
NCBI GI	g2129657
BLAST score	239
E value	4.0e-20
Match length	97
% identity	57
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144796
Seq. ID	LIB3168-050-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	588
E value	1.0e-62
Match length	138
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144797
Seq. ID	LIB3168-050-P1-K1-D5
Method	BLASTN
NCBI GI	g1313927
BLAST score	45
E value	4.0e-16
Match length	181
% identity	83
NCBI Description	B.oleracea mRNA for IFA binding protein (sp10)

Seq. No.	144798
Seq. ID	LIB3168-050-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	496
E value	3.0e-50
Match length	128
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144799
Seq. ID	LIB3168-050-P1-K1-D7
Method	BLASTX
NCBI GI	g2129657
BLAST score	352
E value	2.0e-33
Match length	102
% identity	75
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis

thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144800
Seq. ID	LIB3168-050-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	561
E value	7.0e-58
Match length	139
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144801
Seq. ID	LIB3168-050-P1-K1-D9
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	137
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144802
Seq. ID	LIB3168-050-P1-K1-E1
Method	BLASTX
NCBI GI	g112681
BLAST score	351
E value	1.0e-52
Match length	142
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144803
Seq. ID	LIB3168-050-P1-K1-E10
Method	BLASTX
NCBI GI	g112741
BLAST score	635
E value	1.0e-66
Match length	118
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144804
Seq. ID	LIB3168-050-P1-K1-E11
Method	BLASTX
NCBI GI	g2493696
BLAST score	618
E value	1.0e-64
Match length	134
% identity	91
NCBI Description	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi_1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]

Seq. No.	144805
Seq. ID	LIB3168-050-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	618
E value	1.0e-64
Match length	119
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144806
Seq. ID	LIB3168-050-P1-K1-E2
Method	BLASTX
NCBI GI	g112682
BLAST score	604
E value	7.0e-63
Match length	140
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144807
Seq. ID	LIB3168-050-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	1.0e-60
Match length	123
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144808
Seq. ID	LIB3168-050-P1-K1-E4

Method	BLASTX
NCBI GI	g1628583
BLAST score	565
E value	2.0e-58
Match length	112
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144809
Seq. ID	LIB3168-050-P1-K1-E5
Method	BLASTX
NCBI GI	g112737
BLAST score	554
E value	5.0e-57
Match length	135
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144810
Seq. ID	LIB3168-050-P1-K1-E6
Method	BLASTX
NCBI GI	g112741
BLAST score	721
E value	1.0e-76
Match length	134
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144811
Seq. ID	LIB3168-050-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144812
Seq. ID	LIB3168-050-P1-K1-E8
Method	BLASTX

NCBI GI	g112682
BLAST score	51
E value	7.0e-10
Match length	75
% identity	49
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144813
Seq. ID	LIB3168-050-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	171
E value	5.0e-54
Match length	137
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144814
Seq. ID	LIB3168-050-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	679
E value	1.0e-71
Match length	143
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144815
Seq. ID	LIB3168-050-P1-K1-F10
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	7.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144816
Seq. ID	LIB3168-050-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583

BLAST score 386
E value 2.0e-37
Match length 97
% identity 79
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144817
Seq. ID LIB3168-050-P1-K1-F12
Method BLASTX
NCBI GI g112681
BLAST score 747
E value 1.0e-79
Match length 142
% identity 99
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144818
Seq. ID LIB3168-050-P1-K1-F2
Method BLASTX
NCBI GI g1628583
BLAST score 730
E value 1.0e-77
Match length 139
% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144819
Seq. ID LIB3168-050-P1-K1-F3
Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144820
Seq. ID LIB3168-050-P1-K1-F4
Method BLASTX
NCBI GI g112682
BLAST score 595
E value 8.0e-62
Match length 138
% identity 82
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144821
Seq. ID	LIB3168-050-P1-K1-F5
Method	BLASTX
NCBI GI	g112741
BLAST score	717
E value	4.0e-76
Match length	135
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144822
Seq. ID	LIB3168-050-P1-K1-F6
Method	BLASTX
NCBI GI	g112682
BLAST score	194
E value	7.0e-15
Match length	38
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144823
Seq. ID	LIB3168-050-P1-K1-F7
Method	BLASTN
NCBI GI	g2264311
BLAST score	314
E value	1.0e-176
Match length	343
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	144824
Seq. ID	LIB3168-050-P1-K1-F9
Method	BLASTX
NCBI GI	g2454184
BLAST score	548
E value	2.0e-56
Match length	112
% identity	99
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	144825
Seq. ID	LIB3168-050-P1-K1-G10

Method	BLASTX
NCBI GI	g112682
BLAST score	163
E value	9.0e-12
Match length	47
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144826
Seq. ID	LIB3168-050-P1-K1-G11
Method	BLASTX
NCBI GI	g1076361
BLAST score	655
E value	7.0e-69
Match length	138
% identity	87
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129660_pir__S69197 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) (clone TE 1-7) - Arabidopsis thaliana >gi_804946_emb_CAA85389_ (Z36912) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	144827
Seq. ID	LIB3168-050-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	692
E value	3.0e-73
Match length	132
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144828
Seq. ID	LIB3168-050-P1-K1-G2
Method	BLASTX
NCBI GI	g461838
BLAST score	283
E value	2.0e-47
Match length	116
% identity	78
NCBI Description	CRUCIFERIN PGCRURSE5 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_282895_pir__S26223 cruciferin - radish >gi_21118_emb_CAA42478_ (X59808) cruciferin [Raphanus sativus]

Seq. No.	144829
Seq. ID	LIB3168-050-P1-K1-G4
Method	BLASTX
NCBI GI	g112682
BLAST score	537

E value	4.0e-55
Match length	117
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144830
Seq. ID	LIB3168-050-P1-K1-G5
Method	BLASTX
NCBI GI	g112741
BLAST score	692
E value	3.0e-73
Match length	135
% identity	96
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144831
Seq. ID	LIB3168-050-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144832
Seq. ID	LIB3168-050-P1-K1-H1
Method	BLASTN
NCBI GI	g4159703
BLAST score	221
E value	1.0e-121
Match length	328
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	144833
Seq. ID	LIB3168-050-P1-K1-H10
Method	BLASTX
NCBI GI	g112741
BLAST score	695
E value	1.0e-73
Match length	130
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144834
Seq. ID	LIB3168-050-P1-K1-H11
Method	BLASTX
NCBI GI	g112681
BLAST score	592
E value	2.0e-61
Match length	112
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144835
Seq. ID	LIB3168-050-P1-K1-H2
Method	BLASTX
NCBI GI	g112741
BLAST score	687
E value	1.0e-72
Match length	128
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144836
Seq. ID	LIB3168-050-P1-K1-H3
Method	BLASTX
NCBI GI	g2129657
BLAST score	366
E value	5.0e-35
Match length	104
% identity	76
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	144837
Seq. ID	LIB3168-050-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	530
E value	2.0e-54
Match length	100

% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144838
Seq. ID	LIB3168-050-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144839
Seq. ID	LIB3168-050-P1-K1-H9
Method	BLASTX
NCBI GI	g112741
BLAST score	705
E value	9.0e-75
Match length	131
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144840
Seq. ID	LIB3168-051-P1-K1-A1
Method	BLASTN
NCBI GI	g4191760
BLAST score	202
E value	1.0e-110
Match length	382
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	144841
Seq. ID	LIB3168-051-P1-K1-A10
Method	BLASTN
NCBI GI	g3928074
BLAST score	391
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144842
Seq. ID	LIB3168-051-P1-K1-A11

Method	BLASTX
NCBI GI	g3335169
BLAST score	613
E value	5.0e-64
Match length	117
% identity	99
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	144843
Seq. ID	LIB3168-051-P1-K1-A12
Method	BLASTN
NCBI GI	g2645198
BLAST score	45
E value	4.0e-16
Match length	162
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144844
Seq. ID	LIB3168-051-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	245
E value	6.0e-21
Match length	52
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144845
Seq. ID	LIB3168-051-P1-K1-A4
Method	BLASTN
NCBI GI	g4582411
BLAST score	59
E value	3.0e-25
Match length	71
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	144846
Seq. ID	LIB3168-051-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	683
E value	4.0e-72
Match length	130
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144847

Seq. ID	LIB3168-051-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	464
E value	2.0e-46
Match length	112
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144848
Seq. ID	LIB3168-051-P1-K1-A8
Method	BLASTN
NCBI GI	g3402695
BLAST score	334
E value	0.0e+00
Match length	397
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144849
Seq. ID	LIB3168-051-P1-K1-A9
Method	BLASTX
NCBI GI	g4204299
BLAST score	619
E value	9.0e-65
Match length	122
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144850
Seq. ID	LIB3168-051-P1-K1-B1
Method	BLASTX
NCBI GI	g4539335
BLAST score	156
E value	2.0e-10
Match length	42
% identity	60
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	144851
Seq. ID	LIB3168-051-P1-K1-B10
Method	BLASTX
NCBI GI	g3367573
BLAST score	562
E value	4.0e-58
Match length	110
% identity	97
NCBI Description	(AL031135) homeodomain - like protein [Arabidopsis thaliana]

Seq. No.	144852
Seq. ID	LIB3168-051-P1-K1-B11
Method	BLASTX

NCBI GI	g112737
BLAST score	545
E value	5.0e-56
Match length	132
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144853
Seq. ID	LIB3168-051-P1-K1-B12
Method	BLASTX
NCBI GI	g1170317
BLAST score	573
E value	2.0e-60
Match length	118
% identity	96
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA REDUCTASE 2) (HMGR2) >gi_388558 (L19262) 3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis thaliana] >gi_2262168 (AC002329) 3-hydroxy-3-methylglutaryl-CoA reductase (HMG2 protein) [Arabidopsis thaliana]

Seq. No.	144854
Seq. ID	LIB3168-051-P1-K1-B4
Method	BLASTX
NCBI GI	g4056505
BLAST score	284
E value	2.0e-25
Match length	134
% identity	49
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	144855
Seq. ID	LIB3168-051-P1-K1-B5
Method	BLASTX
NCBI GI	g112737
BLAST score	162
E value	4.0e-11
Match length	66
% identity	58
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144856
Seq. ID	LIB3168-051-P1-K1-B7
Method	BLASTX

NCBI GI	g1628583
BLAST score	661
E value	1.0e-69
Match length	140
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144857
Seq. ID	LIB3168-051-P1-K1-B8
Method	BLASTX
NCBI GI	g3250695
BLAST score	237
E value	5.0e-20
Match length	114
% identity	52
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	144858
Seq. ID	LIB3168-051-P1-K1-B9
Method	BLASTX
NCBI GI	g3264805
BLAST score	355
E value	8.0e-34
Match length	79
% identity	92
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	144859
Seq. ID	LIB3168-051-P1-K1-C1
Method	BLASTN
NCBI GI	g2623294
BLAST score	331
E value	0.0e+00
Match length	387
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144860
Seq. ID	LIB3168-051-P1-K1-C10
Method	BLASTN
NCBI GI	g4580365
BLAST score	421
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	144861
Seq. ID	LIB3168-051-P1-K1-C11
Method	BLASTN
NCBI GI	g2262155

BLAST score	239
E value	1.0e-132
Match length	389
% identity	98
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	144862
Seq. ID	LIB3168-051-P1-K1-C12
Method	BLASTX
NCBI GI	g170354
BLAST score	612
E value	8.0e-64
Match length	124
% identity	22
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	144863
Seq. ID	LIB3168-051-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	167
E value	1.0e-11
Match length	116
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144864
Seq. ID	LIB3168-051-P1-K1-C4
Method	BLASTN
NCBI GI	g829157
BLAST score	55
E value	4.0e-22
Match length	74
% identity	93
NCBI Description	Arabidopsis thaliana 3-hydroxy-3-methylglutaryl-CoA reductase (HMG2) gene, complete cds

Seq. No.	144865
Seq. ID	LIB3168-051-P1-K1-C5
Method	BLASTX
NCBI GI	g2739010
BLAST score	273
E value	4.0e-24
Match length	75
% identity	68
NCBI Description	(AF022464) CYP77A3p [Glycine max]

Seq. No.	144866
Seq. ID	LIB3168-051-P1-K1-C6
Method	BLASTX
NCBI GI	g112737
BLAST score	247
E value	4.0e-26
Match length	86

% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144867
Seq. ID	LIB3168-051-P1-K1-C7
Method	BLASTX
NCBI GI	g4512631
BLAST score	213
E value	4.0e-17
Match length	79
% identity	58
NCBI Description	(AC004793) Contains similarity to gi_3249080 T13D8.24 MYB transcription factor homolog from A. thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	144868
Seq. ID	LIB3168-051-P1-K1-C8
Method	BLASTX
NCBI GI	g2244749
BLAST score	587
E value	6.0e-61
Match length	114
% identity	97
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	144869
Seq. ID	LIB3168-051-P1-K1-C9
Method	BLASTX
NCBI GI	g4678924
BLAST score	152
E value	5.0e-10
Match length	63
% identity	46
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	144870
Seq. ID	LIB3168-051-P1-K1-D1
Method	BLASTN
NCBI GI	g2605713
BLAST score	175
E value	6.0e-94
Match length	225
% identity	96
NCBI Description	Arabidopsis thaliana beta-tonoplast intrinsic protein (beta-TIP) mRNA, complete cds

Seq. No.	144871
Seq. ID	LIB3168-051-P1-K1-D10
Method	BLASTN
NCBI GI	g3236234
BLAST score	339

E value	0.0e+00
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144872
Seq. ID	LIB3168-051-P1-K1-D11
Method	BLASTX
NCBI GI	g1071913
BLAST score	360
E value	3.0e-34
Match length	139
% identity	57
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	144873
Seq. ID	LIB3168-051-P1-K1-D12
Method	BLASTX
NCBI GI	g3264805
BLAST score	635
E value	1.0e-66
Match length	138
% identity	90
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	144874
Seq. ID	LIB3168-051-P1-K1-D2
Method	BLASTX
NCBI GI	g3264778
BLAST score	171
E value	4.0e-12
Match length	59
% identity	57
NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	144875
Seq. ID	LIB3168-051-P1-K1-D3
Method	BLASTX
NCBI GI	g16245
BLAST score	328
E value	2.0e-30
Match length	100
% identity	70
NCBI Description	(X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana]

Seq. No.	144876
Seq. ID	LIB3168-051-P1-K1-D4
Method	BLASTX
NCBI GI	g3860277
BLAST score	462

E value	3.0e-46
Match length	134
% identity	71
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	144877
Seq. ID	LIB3168-051-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144878
Seq. ID	LIB3168-051-P1-K1-D6
Method	BLASTN
NCBI GI	g2959729
BLAST score	386
E value	0.0e+00
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	144879
Seq. ID	LIB3168-051-P1-K1-D7
Method	BLASTX
NCBI GI	g1070654
BLAST score	345
E value	8.0e-46
Match length	98
% identity	86
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	144880
Seq. ID	LIB3168-051-P1-K1-E1
Method	BLASTX
NCBI GI	g4204299
BLAST score	82
E value	1.0e-01
Match length	136
% identity	51
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144881
Seq. ID	LIB3168-051-P1-K1-E10
Method	BLASTX
NCBI GI	g112682
BLAST score	742
E value	4.0e-79
Match length	140

% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144882
Seq. ID	LIB3168-051-P1-K1-E11
Method	BLASTX
NCBI GI	g2369714
BLAST score	548
E value	2.0e-56
Match length	138
% identity	75
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	144883
Seq. ID	LIB3168-051-P1-K1-E12
Method	BLASTX
NCBI GI	g2129633
BLAST score	448
E value	1.0e-44
Match length	114
% identity	82
NCBI Description	LEA protein Le25 homolog - Arabidopsis thaliana >gi_984050_emb_CAA61676_ (X89505) LEA protein Le25 homolog [Arabidopsis thaliana]
Seq. No.	144884
Seq. ID	LIB3168-051-P1-K1-E4
Method	BLASTX
NCBI GI	g2244998
BLAST score	152
E value	7.0e-10
Match length	89
% identity	35
NCBI Description	(Z97341) similarity to probable transcriptional adaptor ADA2 [Arabidopsis thaliana]
Seq. No.	144885
Seq. ID	LIB3168-051-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144886
Seq. ID	LIB3168-051-P1-K1-E8
Method	BLASTN
NCBI GI	g4432793
BLAST score	238

E value	1.0e-131
Match length	286
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T19K21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144887
Seq. ID	LIB3168-051-P1-K1-E9
Method	BLASTX
NCBI GI	g4204298
BLAST score	464
E value	1.0e-46
Match length	88
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144888
Seq. ID	LIB3168-051-P1-K1-F10
Method	BLASTN
NCBI GI	g3004543
BLAST score	219
E value	1.0e-120
Match length	244
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144889
Seq. ID	LIB3168-051-P1-K1-F11
Method	BLASTX
NCBI GI	g4406775
BLAST score	206
E value	3.0e-16
Match length	82
% identity	49
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	144890
Seq. ID	LIB3168-051-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	688
E value	9.0e-73
Match length	132
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144891
Seq. ID	LIB3168-051-P1-K1-F2
Method	BLASTX
NCBI GI	g1864017
BLAST score	455
E value	1.0e-45
Match length	93

% identity	95
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	144892
Seq. ID	LIB3168-051-P1-K1-F5
Method	BLASTX
NCBI GI	g112739
BLAST score	380
E value	1.0e-36
Match length	116
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144893
Seq. ID	LIB3168-051-P1-K1-F6
Method	BLASTX
NCBI GI	g1352681
BLAST score	232
E value	3.0e-19
Match length	70
% identity	64
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	144894
Seq. ID	LIB3168-051-P1-K1-F7
Method	BLASTX
NCBI GI	g112681
BLAST score	660
E value	2.0e-69
Match length	131
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144895
Seq. ID	LIB3168-051-P1-K1-F8
Method	BLASTX
NCBI GI	g112682
BLAST score	556
E value	3.0e-57
Match length	131
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144896
Seq. ID	LIB3168-051-P1-K1-F9
Method	BLASTN
NCBI GI	g2262155
BLAST score	388
E value	0.0e+00
Match length	392
% identity	100
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	144897
Seq. ID	LIB3168-051-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	412
E value	2.0e-40
Match length	112
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144898
Seq. ID	LIB3168-051-P1-K1-G11
Method	BLASTX
NCBI GI	g112739
BLAST score	466
E value	1.0e-46
Match length	130
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	144899
Seq. ID	LIB3168-051-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	606
E value	3.0e-63
Match length	119
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144900
Seq. ID	LIB3168-051-P1-K1-G2
Method	BLASTX

NCBI GI g4185141
BLAST score 545
E value 5.0e-56
Match length 122
% identity 85
NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No. 144901
Seq. ID LIB3168-051-P1-K1-G3
Method BLASTX
NCBI GI g1628583
BLAST score 492
E value 9.0e-56
Match length 119
% identity 96
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 144902
Seq. ID LIB3168-051-P1-K1-G6
Method BLASTN
NCBI GI g511598
BLAST score 398
E value 0.0e+00
Match length 426
% identity 28
NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No. 144903
Seq. ID LIB3168-051-P1-K1-G7
Method BLASTX
NCBI GI g112682
BLAST score 533
E value 4.0e-59
Match length 117
% identity 94
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 144904
Seq. ID LIB3168-051-P1-K1-G8
Method BLASTX
NCBI GI g3924597
BLAST score 699
E value 5.0e-74
Match length 137
% identity 97
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No. 144905
Seq. ID LIB3168-051-P1-K1-G9

Method	BLASTN
NCBI GI	g3335356
BLAST score	148
E value	9.0e-78
Match length	242
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144906
Seq. ID	LIB3168-051-P1-K1-H10
Method	BLASTX
NCBI GI	g2160151
BLAST score	616
E value	3.0e-64
Match length	124
% identity	96
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	144907
Seq. ID	LIB3168-051-P1-K1-H11
Method	BLASTX
NCBI GI	g112741
BLAST score	576
E value	9.0e-60
Match length	107
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144908
Seq. ID	LIB3168-051-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	9.0e-66
Match length	127
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144909
Seq. ID	LIB3168-051-P1-K1-H5
Method	BLASTX
NCBI GI	g131325
BLAST score	689
E value	7.0e-73
Match length	135
% identity	98
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K

>gi_72687_pir__F2NTG psbG protein - common tobacco chloroplast

Seq. No.	144910
Seq. ID	LIB3168-051-P1-K1-H6
Method	BLASTX
NCBI GI	g1076303
BLAST score	45
E value	4.0e-31
Match length	73
% identity	100
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	144911
Seq. ID	LIB3168-051-P1-K1-H7
Method	BLASTX
NCBI GI	g112741
BLAST score	621
E value	7.0e-65
Match length	131
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144912
Seq. ID	LIB3168-051-P1-K1-H8
Method	BLASTX
NCBI GI	g112737
BLAST score	625
E value	2.0e-65
Match length	134
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144913
Seq. ID	LIB3168-051-P1-K1-H9
Method	BLASTX
NCBI GI	g112682
BLAST score	658
E value	3.0e-69
Match length	137
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144914
Seq. ID	LIB3168-052-P1-K1-A1
Method	BLASTX
NCBI GI	g4220533
BLAST score	587
E value	6.0e-61
Match length	119
% identity	99
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	144915
Seq. ID	LIB3168-052-P1-K1-A10
Method	BLASTN
NCBI GI	g4589444
BLAST score	212
E value	1.0e-116
Match length	244
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	144916
Seq. ID	LIB3168-052-P1-K1-A2
Method	BLASTX
NCBI GI	g3935154
BLAST score	302
E value	2.0e-27
Match length	90
% identity	62
NCBI Description	(AC005106) T25N20.18 [Arabidopsis thaliana]

Seq. No.	144917
Seq. ID	LIB3168-052-P1-K1-A3
Method	BLASTX
NCBI GI	g3929364
BLAST score	548
E value	2.0e-56
Match length	120
% identity	90
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	144918
Seq. ID	LIB3168-052-P1-K1-A4
Method	BLASTX
NCBI GI	g112682

BLAST score	587
E value	6.0e-61
Match length	108
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144919
Seq. ID	LIB3168-052-P1-K1-A5
Method	BLASTX
NCBI GI	g2792155
BLAST score	202
E value	9.0e-16
Match length	76
% identity	46
NCBI Description	(AJ223291) chalcone reductase [Sesbania rostrata]

Seq. No.	144920
Seq. ID	LIB3168-052-P1-K1-A7
Method	BLASTX
NCBI GI	g112741
BLAST score	639
E value	5.0e-67
Match length	119
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	144921
Seq. ID	LIB3168-052-P1-K1-A8
Method	BLASTX
NCBI GI	g4584110
BLAST score	324
E value	4.0e-30
Match length	122
% identity	52
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	144922
Seq. ID	LIB3168-052-P1-K1-B10
Method	BLASTN
NCBI GI	g2264309
BLAST score	394
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	144923
Seq. ID	LIB3168-052-P1-K1-B11
Method	BLASTX
NCBI GI	g99992
BLAST score	320
E value	1.0e-29
Match length	104
% identity	43
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) precursor - alfalfa (clone B2) >gi_166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No.	144924
Seq. ID	LIB3168-052-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	593
E value	1.0e-61
Match length	116
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144925
Seq. ID	LIB3168-052-P1-K1-B3
Method	BLASTN
NCBI GI	g4580732
BLAST score	44
E value	1.0e-15
Match length	202
% identity	82
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F5J5, complete sequence

Seq. No.	144926
Seq. ID	LIB3168-052-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	657
E value	4.0e-69
Match length	129
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144927
Seq. ID	LIB3168-052-P1-K1-B5
Method	BLASTX
NCBI GI	g112681
BLAST score	549
E value	2.0e-56
Match length	129
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144928
Seq. ID	LIB3168-052-P1-K1-B6
Method	BLASTX
NCBI GI	g2281099
BLAST score	711
E value	2.0e-75
Match length	133
% identity	100
NCBI Description	(AC002333) stearoyl-ACP desaturase [Arabidopsis thaliana]

Seq. No.	144929
Seq. ID	LIB3168-052-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	673
E value	5.0e-71
Match length	129
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144930
Seq. ID	LIB3168-052-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	380
E value	4.0e-37
Match length	75
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144931
Seq. ID	LIB3168-052-P1-K1-C10
Method	BLASTN
NCBI GI	g3402695
BLAST score	210
E value	1.0e-114
Match length	363
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	144932
Seq. ID	LIB3168-052-P1-K1-C11
Method	BLASTN
NCBI GI	g4376087
BLAST score	200
E value	1.0e-108
Match length	355
% identity	97

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	144933
Seq. ID	LIB3168-052-P1-K1-C12
Method	BLASTX
NCBI GI	g112739
BLAST score	416
E value	7.0e-41
Match length	119
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	144934
Seq. ID	LIB3168-052-P1-K1-C2
Method	BLASTN
NCBI GI	g4079614
BLAST score	92
E value	1.0e-44
Match length	96
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	144935
Seq. ID	LIB3168-052-P1-K1-C3
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	4.0e-62
Match length	126
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144936
Seq. ID	LIB3168-052-P1-K1-C4
Method	BLASTX
NCBI GI	g66179
BLAST score	629
E value	7.0e-66
Match length	134
% identity	87
NCBI Description	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common tobacco chloroplast >gi_225255_prf__1211235CP NADH dehydrogenase 4-like ORF 509B [Nicotiana tabacum]
Seq. No.	144937

Seq. ID	LIB3168-052-P1-K1-C5
Method	BLASTN
NCBI GI	g4159704
BLAST score	48
E value	7.0e-18
Match length	64
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	144938
Seq. ID	LIB3168-052-P1-K1-C6
Method	BLASTX
NCBI GI	g4101589
BLAST score	362
E value	1.0e-34
Match length	120
% identity	53
NCBI Description	(AF005050) aspartyl aminopeptidase [Homo sapiens]

Seq. No.	144939
Seq. ID	LIB3168-052-P1-K1-C7
Method	BLASTN
NCBI GI	g4199934
BLAST score	248
E value	1.0e-137
Match length	288
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	144940
Seq. ID	LIB3168-052-P1-K1-C8
Method	BLASTX
NCBI GI	g112681
BLAST score	341
E value	3.0e-32
Match length	107
% identity	68
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144941
Seq. ID	LIB3168-052-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	674
E value	4.0e-71
Match length	129
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144942
Seq. ID	LIB3168-052-P1-K1-D11
Method	BLASTX
NCBI GI	g4160402
BLAST score	242
E value	1.0e-20
Match length	112
% identity	53
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No.	144943
Seq. ID	LIB3168-052-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	4.0e-56
Match length	126
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144944
Seq. ID	LIB3168-052-P1-K1-D2
Method	BLASTX
NCBI GI	g3885334
BLAST score	701
E value	3.0e-74
Match length	132
% identity	100
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	144945
Seq. ID	LIB3168-052-P1-K1-D3
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	6.0e-09
Match length	48
% identity	64
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	144946
Seq. ID	LIB3168-052-P1-K1-D4
Method	BLASTN
NCBI GI	g2618601
BLAST score	392
E value	0.0e+00
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	144947
Seq. ID	LIB3168-052-P1-K1-D5

Method	BLASTX
NCBI GI	g1628583
BLAST score	622
E value	4.0e-65
Match length	125
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144948
Seq. ID	LIB3168-052-P1-K1-D7
Method	BLASTX
NCBI GI	g112682
BLAST score	544
E value	6.0e-56
Match length	116
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144949
Seq. ID	LIB3168-052-P1-K1-D8
Method	BLASTN
NCBI GI	g3243214
BLAST score	103
E value	1.0e-50
Match length	311
% identity	84
NCBI Description	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	144950
Seq. ID	LIB3168-052-P1-K1-D9
Method	BLASTX
NCBI GI	g2851581
BLAST score	643
E value	2.0e-67
Match length	130
% identity	98
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	144951
Seq. ID	LIB3168-052-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	560
E value	7.0e-58
Match length	116
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144952
Seq. ID	LIB3168-052-P1-K1-E10
Method	BLASTX
NCBI GI	g3927825
BLAST score	684
E value	3.0e-72
Match length	132
% identity	98
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	144953
Seq. ID	LIB3168-052-P1-K1-E11
Method	BLASTX
NCBI GI	g1172873
BLAST score	250
E value	2.0e-21
Match length	106
% identity	51
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	144954
Seq. ID	LIB3168-052-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	364
E value	8.0e-35
Match length	109
% identity	69
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144955
Seq. ID	LIB3168-052-P1-K1-E3
Method	BLASTX
NCBI GI	g1871182
BLAST score	444
E value	3.0e-44
Match length	83
% identity	98
NCBI Description	(U90439) phospholipase D isolog [Arabidopsis thaliana]

Seq. No.	144956
Seq. ID	LIB3168-052-P1-K1-E5
Method	BLASTN
NCBI GI	g4159707
BLAST score	277
E value	1.0e-154
Match length	409

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	144957
Seq. ID	LIB3168-052-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	652
E value	1.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144958
Seq. ID	LIB3168-052-P1-K1-E8
Method	BLASTX
NCBI GI	g4204298
BLAST score	576
E value	1.0e-59
Match length	128
% identity	87
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	144959
Seq. ID	LIB3168-052-P1-K1-E9
Method	BLASTX
NCBI GI	g4587564
BLAST score	642
E value	2.0e-67
Match length	127
% identity	100
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	144960
Seq. ID	LIB3168-052-P1-K1-F1
Method	BLASTX
NCBI GI	g3808062
BLAST score	161
E value	5.0e-11
Match length	68
% identity	44
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	144961
Seq. ID	LIB3168-052-P1-K1-F10
Method	BLASTX
NCBI GI	g112682
BLAST score	569
E value	8.0e-59
Match length	133

% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	144962
Seq. ID	LIB3168-052-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	479
E value	2.0e-48
Match length	99
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144963
Seq. ID	LIB3168-052-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144964
Seq. ID	LIB3168-052-P1-K1-F2
Method	BLASTX
NCBI GI	g2129657
BLAST score	315
E value	5.0e-29
Match length	97
% identity	71
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	144965
Seq. ID	LIB3168-052-P1-K1-F3
Method	BLASTX
NCBI GI	g132901
BLAST score	320
E value	1.0e-29
Match length	66
% identity	86
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L33 >gi_71356_pir__R5NT33 ribosomal protein L33 - common tobacco chloroplast >gi_11850_emb_CAA77370_ (Z00044) ribosomal protein L33 [Nicotiana tabacum] >gi_225219_prf__1211235BA ribosomal protein L33 [Nicotiana tabacum]

Seq. No.	144966
Seq. ID	LIB3168-052-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	487
E value	3.0e-49
Match length	133
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144967
Seq. ID	LIB3168-052-P1-K1-F6
Method	BLASTX
NCBI GI	g3157937
BLAST score	109
E value	8.0e-57
Match length	123
% identity	94
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	144968
Seq. ID	LIB3168-052-P1-K1-F7
Method	BLASTX
NCBI GI	g2160151
BLAST score	483
E value	9.0e-49
Match length	109
% identity	87
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	144969
Seq. ID	LIB3168-052-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	205
E value	4.0e-16
Match length	65
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144970
Seq. ID	LIB3168-052-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583
BLAST score	651

E value	2.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144971
Seq. ID	LIB3168-052-P1-K1-G11
Method	BLASTX
NCBI GI	g1402906
BLAST score	531
E value	2.0e-54
Match length	125
% identity	82
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	144972
Seq. ID	LIB3168-052-P1-K1-G12
Method	BLASTX
NCBI GI	g112743
BLAST score	589
E value	4.0e-61
Match length	126
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	144973
Seq. ID	LIB3168-052-P1-K1-G2
Method	BLASTN
NCBI GI	g3128139
BLAST score	390
E value	0.0e+00
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	144974
Seq. ID	LIB3168-052-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144975
Seq. ID	LIB3168-052-P1-K1-G6
Method	BLASTX
NCBI GI	g1109699
BLAST score	561
E value	7.0e-58
Match length	109
% identity	99
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	144976
Seq. ID	LIB3168-052-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	585
E value	1.0e-60
Match length	127
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	144977
Seq. ID	LIB3168-052-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	443
E value	4.0e-44
Match length	120
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144978
Seq. ID	LIB3168-052-P1-K1-G9
Method	BLASTX
NCBI GI	g1628583
BLAST score	146
E value	3.0e-09
Match length	66
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144979
Seq. ID	LIB3168-052-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	486
E value	3.0e-49

Match length	100
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144980
Seq. ID	LIB3168-052-P1-K1-H12
Method	BLASTN
NCBI GI	g3449331
BLAST score	369
E value	0.0e+00
Match length	381
% identity	27
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	144981
Seq. ID	LIB3168-052-P1-K1-H3
Method	BLASTN
NCBI GI	g3869062
BLAST score	46
E value	1.0e-16
Match length	149
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	144982
Seq. ID	LIB3168-052-P1-K1-H4
Method	BLASTX
NCBI GI	g2924258
BLAST score	669
E value	1.0e-70
Match length	131
% identity	98
NCBI Description	(Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No.	144983
Seq. ID	LIB3168-052-P1-K1-H5
Method	BLASTX
NCBI GI	g3695380
BLAST score	213
E value	4.0e-17
Match length	134
% identity	22
NCBI Description	(AF096370) partial CDS; contains similarity to Nicotiana tabacum membrane-associated salt-inducible protein (GB:U08285) [Arabidopsis thaliana]

Seq. No.	144984
Seq. ID	LIB3168-052-P1-K1-H7
Method	BLASTX
NCBI GI	g1172969
BLAST score	169
E value	4.0e-12
Match length	36

% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L16) >gi_629552_pir__S49033 ribosomal protein L11.e - Arabidopsis thaliana >gi_550544_emb_CAA57394_ (X81798) ribosomal protein L16 [Arabidopsis thaliana]
Seq. No.	144985
Seq. ID	LIB3168-052-P1-K1-H8
Method	BLASTN
NCBI GI	g4558674
BLAST score	57
E value	3.0e-23
Match length	258
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7B19 genomic sequence, complete sequence
Seq. No.	144986
Seq. ID	LIB3168-052-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	407
E value	8.0e-40
Match length	77
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	144987
Seq. ID	LIB3168-053-P1-K1-A10
Method	BLASTN
NCBI GI	g2160132
BLAST score	421
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	144988
Seq. ID	LIB3168-053-P1-K1-A12
Method	BLASTX
NCBI GI	g3860165
BLAST score	528
E value	5.0e-54
Match length	142
% identity	22
NCBI Description	(AF098963) disease resistance protein RPP1-WsB [Arabidopsis thaliana]
Seq. No.	144989
Seq. ID	LIB3168-053-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	532
E value	2.0e-54

Match length	135
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144990
Seq. ID	LIB3168-053-P1-K1-A3
Method	BLASTX
NCBI GI	g3121836
BLAST score	174
E value	1.0e-12
Match length	30
% identity	97
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2181182_emb_CAA63969_ (X94306) CDP-diacylglycerol synthetase [Arabidopsis thaliana]

Seq. No.	144991
Seq. ID	LIB3168-053-P1-K1-A4
Method	BLASTX
NCBI GI	g112681
BLAST score	409
E value	4.0e-40
Match length	126
% identity	71
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144992
Seq. ID	LIB3168-053-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	527
E value	7.0e-54
Match length	125
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	144993
Seq. ID	LIB3168-053-P1-K1-A6
Method	BLASTN
NCBI GI	g2842474
BLAST score	66
E value	1.0e-28
Match length	90
% identity	93

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	144994
Seq. ID	LIB3168-053-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	553
E value	5.0e-57
Match length	111
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144995
Seq. ID	LIB3168-053-P1-K1-A8
Method	BLASTX
NCBI GI	g2317731
BLAST score	691
E value	4.0e-73
Match length	130
% identity	99
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	144996
Seq. ID	LIB3168-053-P1-K1-A9
Method	BLASTX
NCBI GI	g1173218
BLAST score	468
E value	5.0e-47
Match length	99
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	144997
Seq. ID	LIB3168-053-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	412
E value	2.0e-40
Match length	112
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144998
Seq. ID	LIB3168-053-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	503
E value	3.0e-51
Match length	103

% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	144999
Seq. ID	LIB3168-053-P1-K1-B11
Method	BLASTX
NCBI GI	g4249382
BLAST score	498
E value	2.0e-50
Match length	120
% identity	77
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	145000
Seq. ID	LIB3168-053-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	533
E value	1.0e-54
Match length	105
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145001
Seq. ID	LIB3168-053-P1-K1-B3
Method	BLASTX
NCBI GI	g112681
BLAST score	488
E value	2.0e-49
Match length	121
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145002
Seq. ID	LIB3168-053-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145003
Seq. ID	LIB3168-053-P1-K1-B5

Method	BLASTX
NCBI GI	g1628583
BLAST score	443
E value	8.0e-69
Match length	142
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145004
Seq. ID	LIB3168-053-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145005
Seq. ID	LIB3168-053-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	329
E value	6.0e-31
Match length	95
% identity	69
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145006
Seq. ID	LIB3168-053-P1-K1-B8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	9.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	145007
Seq. ID	LIB3168-053-P1-K1-B9
Method	BLASTX
NCBI GI	g112737
BLAST score	588
E value	5.0e-61
Match length	140
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145008
Seq. ID	LIB3168-053-P1-K1-C1
Method	BLASTX
NCBI GI	g112743
BLAST score	590
E value	3.0e-61
Match length	131
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145009
Seq. ID	LIB3168-053-P1-K1-C10
Method	BLASTN
NCBI GI	g3668073
BLAST score	413
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145010
Seq. ID	LIB3168-053-P1-K1-C12
Method	BLASTN
NCBI GI	g2832611
BLAST score	204
E value	1.0e-111
Match length	248
% identity	70
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	145011
Seq. ID	LIB3168-053-P1-K1-C2
Method	BLASTX
NCBI GI	g112682
BLAST score	584
E value	1.0e-60
Match length	124
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145012
Seq. ID	LIB3168-053-P1-K1-C3

Method	BLASTX
NCBI GI	g2129659
BLAST score	412
E value	2.0e-40
Match length	129
% identity	69
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145013
Seq. ID	LIB3168-053-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145014
Seq. ID	LIB3168-053-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145015
Seq. ID	LIB3168-053-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145016
Seq. ID	LIB3168-053-P1-K1-C9
Method	BLASTX
NCBI GI	g112681
BLAST score	607
E value	3.0e-63
Match length	121
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	145017
Seq. ID	LIB3168-053-P1-K1-D1
Method	BLASTN
NCBI GI	g3659491
BLAST score	241
E value	1.0e-133
Match length	433
% identity	100
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	145018
Seq. ID	LIB3168-053-P1-K1-D10
Method	BLASTX
NCBI GI	g2129767
BLAST score	617
E value	2.0e-64
Match length	126
% identity	91
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	145019
Seq. ID	LIB3168-053-P1-K1-D12
Method	BLASTX
NCBI GI	g1592677
BLAST score	230
E value	5.0e-19
Match length	117
% identity	44
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No.	145020
Seq. ID	LIB3168-053-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	172
E value	3.0e-12
Match length	64
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145021
Seq. ID	LIB3168-053-P1-K1-D5
Method	BLASTN
NCBI GI	g4587986
BLAST score	161
E value	2.0e-85
Match length	273
% identity	95
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	145022
Seq. ID	LIB3168-053-P1-K1-D7
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	8.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145023
Seq. ID	LIB3168-053-P1-K1-D8
Method	BLASTX
NCBI GI	g4102582
BLAST score	409
E value	5.0e-40
Match length	139
% identity	38
NCBI Description	(AF013115) CAO [Arabidopsis thaliana]

Seq. No.	145024
Seq. ID	LIB3168-053-P1-K1-D9
Method	BLASTX
NCBI GI	g3892057
BLAST score	726
E value	3.0e-77
Match length	142
% identity	63
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	145025
Seq. ID	LIB3168-053-P1-K1-E1
Method	BLASTX
NCBI GI	g2244953
BLAST score	611
E value	1.0e-63
Match length	132
% identity	90
NCBI Description	(Z97340) ATsEH homolog [Arabidopsis thaliana]

Seq. No.	145026
Seq. ID	LIB3168-053-P1-K1-E12
Method	BLASTX
NCBI GI	g112741
BLAST score	721
E value	1.0e-76
Match length	134
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145027
Seq. ID	LIB3168-053-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	601
E value	1.0e-62
Match length	113
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145028
Seq. ID	LIB3168-053-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	429
E value	1.0e-42
Match length	91
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145029
Seq. ID	LIB3168-053-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	551
E value	1.0e-56
Match length	139
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145030
Seq. ID	LIB3168-053-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	652
E value	2.0e-68
Match length	129
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145031
Seq. ID	LIB3168-053-P1-K1-F11
Method	BLASTN

NCBI GI g3335170
BLAST score 115
E value 7.0e-58
Match length 410
% identity 97
NCBI Description Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No. 145032
Seq. ID LIB3168-053-P1-K1-F12
Method BLASTX
NCBI GI g2129657
BLAST score 346
E value 1.0e-32
Match length 99
% identity 75
NCBI Description oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No. 145033
Seq. ID LIB3168-053-P1-K1-F2
Method BLASTX
NCBI GI g112741
BLAST score 519
E value 5.0e-53
Match length 113
% identity 87
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 145034
Seq. ID LIB3168-053-P1-K1-F3
Method BLASTX
NCBI GI g1628583
BLAST score 436
E value 9.0e-56
Match length 117
% identity 97
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 145035
Seq. ID LIB3168-053-P1-K1-F4
Method BLASTX
NCBI GI g1628583
BLAST score 497
E value 2.0e-50
Match length 100
% identity 94

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145036
Seq. ID	LIB3168-053-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	4.0e-62
Match length	126
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145037
Seq. ID	LIB3168-053-P1-K1-F6
Method	BLASTN
NCBI GI	g2358139
BLAST score	98
E value	1.0e-47
Match length	98
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	145038
Seq. ID	LIB3168-053-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	348
E value	4.0e-33
Match length	73
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145039
Seq. ID	LIB3168-053-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	44
E value	6.0e-39
Match length	96
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145040
Seq. ID	LIB3168-053-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583

BLAST score	712
E value	1.0e-75
Match length	140
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145041
Seq. ID	LIB3168-053-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	740
E value	8.0e-79
Match length	141
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145042
Seq. ID	LIB3168-053-P1-K1-G11
Method	BLASTX
NCBI GI	g3335171
BLAST score	605
E value	5.0e-63
Match length	141
% identity	83
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	145043
Seq. ID	LIB3168-053-P1-K1-G2
Method	BLASTX
NCBI GI	g2499606
BLAST score	435
E value	5.0e-43
Match length	102
% identity	82
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No.	145044
Seq. ID	LIB3168-053-P1-K1-G3
Method	BLASTX
NCBI GI	g112682
BLAST score	667
E value	3.0e-70
Match length	146
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145045

Seq. ID	LIB3168-053-P1-K1-G4
Method	BLASTX
NCBI GI	g112741
BLAST score	296
E value	3.0e-73
Match length	137
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145046
Seq. ID	LIB3168-053-P1-K1-G5
Method	BLASTN
NCBI GI	g3650026
BLAST score	185
E value	1.0e-99
Match length	272
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145047
Seq. ID	LIB3168-053-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	614
E value	4.0e-64
Match length	119
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145048
Seq. ID	LIB3168-053-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	580
E value	4.0e-60
Match length	139
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145049
Seq. ID	LIB3168-053-P1-K1-G8
Method	BLASTX

NCBI GI	g112682
BLAST score	609
E value	2.0e-63
Match length	140
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145050
Seq. ID	LIB3168-053-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	586
E value	9.0e-61
Match length	138
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145051
Seq. ID	LIB3168-053-P1-K1-H1
Method	BLASTN
NCBI GI	g3298610
BLAST score	411
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	145052
Seq. ID	LIB3168-053-P1-K1-H10
Method	BLASTX
NCBI GI	g3341697
BLAST score	360
E value	3.0e-34
Match length	95
% identity	72
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	145053
Seq. ID	LIB3168-053-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	577
E value	1.0e-59
Match length	143
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145054
Seq. ID	LIB3168-053-P1-K1-H12
Method	BLASTX
NCBI GI	g112681
BLAST score	550
E value	1.0e-56
Match length	136
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145055
Seq. ID	LIB3168-053-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	631
E value	5.0e-66
Match length	144
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145056
Seq. ID	LIB3168-053-P1-K1-H4
Method	BLASTX
NCBI GI	g112741
BLAST score	595
E value	6.0e-62
Match length	109
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145057
Seq. ID	LIB3168-053-P1-K1-H5
Method	BLASTX
NCBI GI	g112741
BLAST score	507
E value	2.0e-51
Match length	93
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145058
Seq. ID	LIB3168-053-P1-K1-H6
Method	BLASTX
NCBI GI	g1107501
BLAST score	384
E value	4.0e-37
Match length	140
% identity	58
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	145059
Seq. ID	LIB3168-053-P1-K1-H7
Method	BLASTX
NCBI GI	g3335171
BLAST score	523
E value	2.0e-53
Match length	122
% identity	84
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	145060
Seq. ID	LIB3168-053-P1-K1-H9
Method	BLASTN
NCBI GI	g2351067
BLAST score	276
E value	1.0e-154
Match length	348
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	145061
Seq. ID	LIB3168-054-P1-K1-A1
Method	BLASTN
NCBI GI	g4678315
BLAST score	164
E value	2.0e-87
Match length	180
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	145062
Seq. ID	LIB3168-054-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	585
E value	1.0e-60
Match length	117
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145063
Seq. ID	LIB3168-054-P1-K1-A2
Method	BLASTX
NCBI GI	g112681
BLAST score	548
E value	2.0e-56
Match length	113
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145064
Seq. ID	LIB3168-054-P1-K1-A3
Method	BLASTN
NCBI GI	g3927822
BLAST score	110
E value	2.0e-55
Match length	122
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145065
Seq. ID	LIB3168-054-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	379
E value	1.0e-36
Match length	108
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145066
Seq. ID	LIB3168-054-P1-K1-A5
Method	BLASTX
NCBI GI	g112682
BLAST score	578
E value	7.0e-60
Match length	137
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145067
Seq. ID	LIB3168-054-P1-K1-A6
Method	BLASTX

NCBI GI	g1628583
BLAST score	494
E value	3.0e-50
Match length	96
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145068
Seq. ID	LIB3168-054-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	3.0e-56
Match length	104
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145069
Seq. ID	LIB3168-054-P1-K1-A8
Method	BLASTN
NCBI GI	g1468974
BLAST score	251
E value	1.0e-139
Match length	275
% identity	98
NCBI Description	Arabidopsis thaliana blue light photoreceptor/photolyase homolog (PHH1) mRNA, complete cds

Seq. No.	145070
Seq. ID	LIB3168-054-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	362
E value	6.0e-35
Match length	79
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145071
Seq. ID	LIB3168-054-P1-K1-B1
Method	BLASTX
NCBI GI	g112682
BLAST score	730
E value	1.0e-77
Match length	142
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145072
Seq. ID	LIB3168-054-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	369
E value	1.0e-35
Match length	90
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145073
Seq. ID	LIB3168-054-P1-K1-B11
Method	BLASTX
NCBI GI	g3273743
BLAST score	526
E value	7.0e-54
Match length	105
% identity	96
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	145074
Seq. ID	LIB3168-054-P1-K1-B2
Method	BLASTX
NCBI GI	g3786017
BLAST score	432
E value	5.0e-43
Match length	84
% identity	100
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	145075
Seq. ID	LIB3168-054-P1-K1-B4
Method	BLASTX
NCBI GI	g112737
BLAST score	561
E value	7.0e-58
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145076
Seq. ID	LIB3168-054-P1-K1-B5
Method	BLASTN

NCBI GI g1592685
BLAST score 74
E value 2.0e-33
Match length 102
% identity 94
NCBI Description A.thaliana mRNA for oleosin type4 protein

Seq. No. 145077
Seq. ID LIB3168-054-P1-K1-B6
Method BLASTX
NCBI GI g112682
BLAST score 350
E value 1.0e-33
Match length 66
% identity 97
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 145078
Seq. ID LIB3168-054-P1-K1-B7
Method BLASTN
NCBI GI g1628582
BLAST score 169
E value 2.0e-90
Match length 225
% identity 97
NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No. 145079
Seq. ID LIB3168-054-P1-K1-B8
Method BLASTX
NCBI GI g112741
BLAST score 415
E value 4.0e-41
Match length 79
% identity 99
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 145080
Seq. ID LIB3168-054-P1-K1-B9
Method BLASTX
NCBI GI g1628583
BLAST score 440
E value 6.0e-44
Match length 92
% identity 93
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145081
Seq. ID	LIB3168-054-P1-K1-C1
Method	BLASTX
NCBI GI	g1363488
BLAST score	384
E value	3.0e-37
Match length	80
% identity	95
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	145082
Seq. ID	LIB3168-054-P1-K1-C10
Method	BLASTX
NCBI GI	g112682
BLAST score	664
E value	6.0e-70
Match length	135
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145083
Seq. ID	LIB3168-054-P1-K1-C11
Method	BLASTX
NCBI GI	g112681
BLAST score	470
E value	3.0e-47
Match length	131
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145084
Seq. ID	LIB3168-054-P1-K1-C3
Method	BLASTX
NCBI GI	g112682
BLAST score	660
E value	2.0e-69
Match length	127
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145085
Seq. ID	LIB3168-054-P1-K1-C4
Method	BLASTN
NCBI GI	g4589408
BLAST score	408
E value	0.0e+00
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F14A1, complete sequence

Seq. No.	145086
Seq. ID	LIB3168-054-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	451
E value	3.0e-45
Match length	88
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145087
Seq. ID	LIB3168-054-P1-K1-C7
Method	BLASTX
NCBI GI	g2160151
BLAST score	333
E value	2.0e-31
Match length	84
% identity	81
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	145088
Seq. ID	LIB3168-054-P1-K1-C9
Method	BLASTX
NCBI GI	g131529
BLAST score	75
E value	5.2e-01
Match length	80
% identity	22
NCBI Description	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) >gi_53553_emb_CAA36321_ (X52101) 25kDa nuclear protein [Mus musculus]

Seq. No.	145089
Seq. ID	LIB3168-054-P1-K1-D10
Method	BLASTX
NCBI GI	g3688175
BLAST score	540
E value	2.0e-55
Match length	124
% identity	83
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme)

[Arabidopsis thaliana]

Seq. No.	145090
Seq. ID	LIB3168-054-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	515
E value	2.0e-52
Match length	138
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145091
Seq. ID	LIB3168-054-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	636
E value	1.0e-66
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145092
Seq. ID	LIB3168-054-P1-K1-D3
Method	BLASTX
NCBI GI	g112741
BLAST score	530
E value	3.0e-54
Match length	113
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145093
Seq. ID	LIB3168-054-P1-K1-D6
Method	BLASTX
NCBI GI	g2160146
BLAST score	309
E value	2.0e-28
Match length	113
% identity	65
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this gene. [Arabidopsis thaliana]

Seq. No. 145094

Seq. ID	LIB3168-054-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	433
E value	3.0e-43
Match length	86
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145095
Seq. ID	LIB3168-054-P1-K1-D8
Method	BLASTX
NCBI GI	g112682
BLAST score	621
E value	6.0e-65
Match length	132
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145096
Seq. ID	LIB3168-054-P1-K1-E1
Method	BLASTX
NCBI GI	g112737
BLAST score	611
E value	1.0e-63
Match length	127
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145097
Seq. ID	LIB3168-054-P1-K1-E10
Method	BLASTX
NCBI GI	g1065515
BLAST score	141
E value	6.0e-09
Match length	77
% identity	39
NCBI Description	(U40420) weak similarity to procollagen alpha chain 1(V) chain [Caenorhabditis elegans]

Seq. No.	145098
Seq. ID	LIB3168-054-P1-K1-E11
Method	BLASTN
NCBI GI	g2264313
BLAST score	34

E value	2.0e-09
Match length	94
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	145099
Seq. ID	LIB3168-054-P1-K1-E12
Method	BLASTN
NCBI GI	g4220640
BLAST score	41
E value	6.0e-14
Match length	85
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	145100
Seq. ID	LIB3168-054-P1-K1-E2
Method	BLASTX
NCBI GI	g464987
BLAST score	591
E value	2.0e-61
Match length	114
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	145101
Seq. ID	LIB3168-054-P1-K1-E4
Method	BLASTN
NCBI GI	g2842474
BLAST score	90
E value	4.0e-43
Match length	146
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145102
Seq. ID	LIB3168-054-P1-K1-E5
Method	BLASTX
NCBI GI	g112681
BLAST score	327
E value	9.0e-31
Match length	79
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145103
Seq. ID	LIB3168-054-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	607
E value	3.0e-63
Match length	135
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145104
Seq. ID	LIB3168-054-P1-K1-E8
Method	BLASTX
NCBI GI	g4204271
BLAST score	242
E value	2.0e-20
Match length	46
% identity	96
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]

Seq. No.	145105
Seq. ID	LIB3168-054-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	560
E value	8.0e-58
Match length	128
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145106
Seq. ID	LIB3168-054-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	644
E value	1.0e-67
Match length	137
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145107
Seq. ID	LIB3168-054-P1-K1-F10
Method	BLASTX
NCBI GI	g4204298
BLAST score	385
E value	2.0e-37
Match length	93
% identity	80

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	145108
Seq. ID	LIB3168-054-P1-K1-F3
Method	BLASTN
NCBI GI	g16131
BLAST score	125
E value	3.0e-64
Match length	153
% identity	95
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment
Seq. No.	145109
Seq. ID	LIB3168-054-P1-K1-F4
Method	BLASTX
NCBI GI	g166570
BLAST score	178
E value	3.0e-13
Match length	68
% identity	54
NCBI Description	(L04173) glycine rich protein [Arabidopsis thaliana]
Seq. No.	145110
Seq. ID	LIB3168-054-P1-K1-F5
Method	BLASTN
NCBI GI	g3758832
BLAST score	42
E value	2.0e-14
Match length	70
% identity	90
NCBI Description	Medicago truncatula mRNA for MtN6 gene
Seq. No.	145111
Seq. ID	LIB3168-054-P1-K1-F6
Method	BLASTN
NCBI GI	g3046852
BLAST score	186
E value	1.0e-100
Match length	253
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]
Seq. No.	145112
Seq. ID	LIB3168-054-P1-K1-F7
Method	BLASTX
NCBI GI	g4138179
BLAST score	246
E value	2.0e-21
Match length	52
% identity	92
NCBI Description	(AJ223969) elongation factor 1 alpha subunit [Malus domestica]
Seq. No.	145113

Seq. ID	LIB3168-054-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	374
E value	4.0e-36
Match length	106
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145114
Seq. ID	LIB3168-054-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	542
E value	1.0e-55
Match length	137
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145115
Seq. ID	LIB3168-054-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583
BLAST score	713
E value	1.0e-75
Match length	136
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145116
Seq. ID	LIB3168-054-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	643
E value	1.0e-67
Match length	125
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145117
Seq. ID	LIB3168-054-P1-K1-G11
Method	BLASTX
NCBI GI	g4191814
BLAST score	233
E value	2.0e-19
Match length	137
% identity	36
NCBI Description	(AB008680) alpha' subunit of beta-conglycinin [Glycine max]

Seq. No.	145118
Seq. ID	LIB3168-054-P1-K1-G2
Method	BLASTN
NCBI GI	g438450
BLAST score	68
E value	8.0e-30
Match length	148
% identity	94
NCBI Description	Arabidopsis thaliana delta-12 desaturase (Fad2) mRNA, complete cds

Seq. No.	145119
Seq. ID	LIB3168-054-P1-K1-G3
Method	BLASTX
NCBI GI	g112737
BLAST score	554
E value	5.0e-57
Match length	134
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145120
Seq. ID	LIB3168-054-P1-K1-G4
Method	BLASTN
NCBI GI	g2924257
BLAST score	48
E value	3.0e-18
Match length	130
% identity	91
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	145121
Seq. ID	LIB3168-054-P1-K1-G5
Method	BLASTX
NCBI GI	g112682
BLAST score	509
E value	7.0e-52
Match length	111
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145122
Seq. ID	LIB3168-054-P1-K1-G6
Method	BLASTX
NCBI GI	g112681
BLAST score	703
E value	2.0e-74

Match length	135
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145123
Seq. ID	LIB3168-054-P1-K1-G7
Method	BLASTX
NCBI GI	g2160146
BLAST score	427
E value	3.0e-42
Match length	104
% identity	85
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this gene. [Arabidopsis thaliana]

Seq. No.	145124
Seq. ID	LIB3168-054-P1-K1-G8
Method	BLASTX
NCBI GI	g112741
BLAST score	362
E value	1.0e-34
Match length	67
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145125
Seq. ID	LIB3168-054-P1-K1-G9
Method	BLASTX
NCBI GI	g3258637
BLAST score	287
E value	9.0e-26
Match length	104
% identity	59
NCBI Description	(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No.	145126
Seq. ID	LIB3168-054-P1-K1-H1
Method	BLASTX
NCBI GI	g1172873
BLAST score	577
E value	8.0e-60
Match length	115
% identity	99
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_

(D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	145127
Seq. ID	LIB3168-054-P1-K1-H11
Method	BLASTN
NCBI GI	g4757414
BLAST score	394
E value	0.0e+00
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	145128
Seq. ID	LIB3168-054-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	472
E value	1.0e-47
Match length	103
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145129
Seq. ID	LIB3168-054-P1-K1-H3
Method	BLASTN
NCBI GI	g3510347
BLAST score	193
E value	1.0e-104
Match length	328
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	145130
Seq. ID	LIB3168-054-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	510
E value	6.0e-52
Match length	111
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145131
Seq. ID	LIB3168-054-P1-K1-H6
Method	BLASTX
NCBI GI	g2129657
BLAST score	290
E value	4.0e-26
Match length	90
% identity	69
NCBI Description	oleosin isoform - Arabidopsis thaliana

	>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	145132
Seq. ID	LIB3168-054-P1-K1-H8
Method	BLASTX
NCBI GI	g112737
BLAST score	507
E value	2.0e-51
Match length	133
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	145133
Seq. ID	LIB3168-054-P1-K1-H9
Method	BLASTX
NCBI GI	g4204299
BLAST score	625
E value	2.0e-65
Match length	121
% identity	98
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	145134
Seq. ID	LIB3168-055-P1-K1-A10
Method	BLASTX
NCBI GI	g2129657
BLAST score	213
E value	4.0e-17
Match length	75
% identity	63
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	145135
Seq. ID	LIB3168-055-P1-K1-A11
Method	BLASTN
NCBI GI	g4159712
BLAST score	309
E value	1.0e-173
Match length	333
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence
Seq. No.	145136
Seq. ID	LIB3168-055-P1-K1-A12

Method	BLASTX
NCBI GI	g4263771
BLAST score	293
E value	2.0e-26
Match length	72
% identity	72
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	145137
Seq. ID	LIB3168-055-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	499
E value	1.0e-50
Match length	98
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145138
Seq. ID	LIB3168-055-P1-K1-A3
Method	BLASTX
NCBI GI	g2983690
BLAST score	144
E value	4.0e-09
Match length	96
% identity	38
NCBI Description	(AE000730) hypothetical protein [Aquifex aeolicus]

Seq. No.	145139
Seq. ID	LIB3168-055-P1-K1-A4
Method	BLASTX
NCBI GI	g2129657
BLAST score	182
E value	9.0e-14
Match length	70
% identity	59
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145140
Seq. ID	LIB3168-055-P1-K1-A5
Method	BLASTX
NCBI GI	g112739
BLAST score	338
E value	8.0e-32
Match length	105
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -

	Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	145141
Seq. ID	LIB3168-055-P1-K1-A6
Method	BLASTX
NCBI GI	g552956
BLAST score	346
E value	8.0e-33
Match length	77
% identity	87
NCBI Description	(M10124) ATPase subunit I [Nicotiana tabacum] >gi_224351_prf__1102209E ORF 5 [Nicotiana sp.]
Seq. No.	145142
Seq. ID	LIB3168-055-P1-K1-A7
Method	BLASTX
NCBI GI	g112682
BLAST score	696
E value	1.0e-73
Match length	147
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145143
Seq. ID	LIB3168-055-P1-K1-A8
Method	BLASTX
NCBI GI	g2129657
BLAST score	149
E value	5.0e-10
Match length	72
% identity	50
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	145144
Seq. ID	LIB3168-055-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	387
E value	9.0e-38
Match length	89
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145145

Seq. ID	LIB3168-055-P1-K1-B1
Method	BLASTX
NCBI GI	g131276
BLAST score	591
E value	2.0e-61
Match length	128
% identity	89
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72704_pir__QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi_11856_emb_CAA77373_ (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi_225224_prf__1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

Seq. No.	145146
Seq. ID	LIB3168-055-P1-K1-B10
Method	BLASTN
NCBI GI	g2642152
BLAST score	342
E value	0.0e+00
Match length	362
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145147
Seq. ID	LIB3168-055-P1-K1-B11
Method	BLASTX
NCBI GI	g4741962
BLAST score	240
E value	2.0e-20
Match length	63
% identity	47
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	145148
Seq. ID	LIB3168-055-P1-K1-B12
Method	BLASTX
NCBI GI	g2129657
BLAST score	140
E value	5.0e-09
Match length	30
% identity	83
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145149
Seq. ID	LIB3168-055-P1-K1-B2
Method	BLASTX
NCBI GI	g2244749
BLAST score	563
E value	4.0e-58
Match length	106
% identity	100
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	145150
Seq. ID	LIB3168-055-P1-K1-B3
Method	BLASTN
NCBI GI	g2244747
BLAST score	64
E value	1.0e-27
Match length	191
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	145151
Seq. ID	LIB3168-055-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	629
E value	6.0e-66
Match length	122
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145152
Seq. ID	LIB3168-055-P1-K1-B5
Method	BLASTN
NCBI GI	g2645198
BLAST score	379
E value	0.0e+00
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145153
Seq. ID	LIB3168-055-P1-K1-B6
Method	BLASTN
NCBI GI	g4388816
BLAST score	177
E value	6.0e-95
Match length	349
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145154
Seq. ID	LIB3168-055-P1-K1-B7
Method	BLASTX
NCBI GI	g112737
BLAST score	455
E value	1.0e-45
Match length	114
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145155
Seq. ID	LIB3168-055-P1-K1-B8
Method	BLASTX
NCBI GI	g4204298
BLAST score	271
E value	2.0e-24
Match length	65
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145156
Seq. ID	LIB3168-055-P1-K1-B9
Method	BLASTX
NCBI GI	g2146735
BLAST score	271
E value	7.0e-24
Match length	52
% identity	98
NCBI Description	glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone E5) - Arabidopsis thaliana (fragment) >gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No.	145157
Seq. ID	LIB3168-055-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	528
E value	5.0e-54
Match length	114
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145158
Seq. ID	LIB3168-055-P1-K1-C12
Method	BLASTN
NCBI GI	g2924505
BLAST score	307
E value	1.0e-172
Match length	336
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	145159
Seq. ID	LIB3168-055-P1-K1-C2
Method	BLASTN
NCBI GI	g3510344
BLAST score	218

E value	1.0e-119
Match length	349
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	145160
Seq. ID	LIB3168-055-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	516
E value	1.0e-52
Match length	132
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145161
Seq. ID	LIB3168-055-P1-K1-C4
Method	BLASTX
NCBI GI	g112739
BLAST score	43
E value	7.0e-18
Match length	65
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145162
Seq. ID	LIB3168-055-P1-K1-C5
Method	BLASTN
NCBI GI	g4512656
BLAST score	92
E value	3.0e-44
Match length	278
% identity	75
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	145163
Seq. ID	LIB3168-055-P1-K1-C6
Method	BLASTX
NCBI GI	g231586
BLAST score	156
E value	2.0e-10
Match length	77
% identity	49
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

Seq. No.	145164
Seq. ID	LIB3168-055-P1-K1-C7
Method	BLASTX
NCBI GI	g131375
BLAST score	144
E value	5.0e-09
Match length	26
% identity	100
NCBI Description	PHOTOSYSTEM II REACTION CENTRE N PROTEIN >gi_72720_pir__F2RZN photosystem II protein psbN - rice chloroplast >gi_82632_pir__S14142 photosystem II protein psbN - wheat chloroplast >gi_100123_pir__S12130 photosystem II protein psbN - Appalachian evening primrose chloroplast >gi_100737_pir__JN0417 photosystem II protein psbN - rye chloroplast >gi_485419_pir__S12133 photosystem II protein psbN - Hooker's evening primrose chloroplast >gi_1363584_pir__S58579 photosystem II protein psbN - maize chloroplast >gi_11208_emb_CAA39389_ (X55899) psbN product, unknown protein [Oenothera argillicola] >gi_12015_emb_CAA33975_ (X15901) PSII low MW protein [Oryza sativa] >gi_12359_emb_CAA38543_ (X54749) photosystem II polypeptide [Triticum aestivum] >gi_14148_emb_CAA39392_ (X55900) psbN product, unknown protein [Oenothera elata subsp. hookeri] >gi_902249_emb_CAA60313_ (X86563) PSII low MW protein [Zea mays] >gi_2143325_emb_CAA73767_ (Y13328) PSII subunit [Populus deltoides] >gi_226637_prf__1603356BL photosystem II low MW protein [Oryza sativa]

Seq. No.	145165
Seq. ID	LIB3168-055-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	477
E value	7.0e-58
Match length	118
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145166
Seq. ID	LIB3168-055-P1-K1-C9
Method	BLASTN
NCBI GI	g1526561
BLAST score	35
E value	3.0e-10
Match length	47
% identity	94
NCBI Description	Raphanus sativus mRNA for glutamine synthetase, complete cds

Seq. No.	145167
Seq. ID	LIB3168-055-P1-K1-D10
Method	BLASTX
NCBI GI	g112681

BLAST score	342
E value	1.0e-32
Match length	81
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145168
Seq. ID	LIB3168-055-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	505
E value	2.0e-51
Match length	98
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145169
Seq. ID	LIB3168-055-P1-K1-D3
Method	BLASTX
NCBI GI	g2605714
BLAST score	338
E value	6.0e-32
Match length	65
% identity	100
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	145170
Seq. ID	LIB3168-055-P1-K1-D4
Method	BLASTX
NCBI GI	g2894574
BLAST score	538
E value	3.0e-55
Match length	102
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	145171
Seq. ID	LIB3168-055-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	361
E value	7.0e-35
Match length	77
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145172
Seq. ID	LIB3168-055-P1-K1-D8
Method	BLASTX
NCBI GI	g112739
BLAST score	333
E value	3.0e-31
Match length	104
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145173
Seq. ID	LIB3168-055-P1-K1-D9
Method	BLASTX
NCBI GI	g3036819
BLAST score	410
E value	3.0e-40
Match length	115
% identity	77
NCBI Description	(AJ000058) MCM3 homolog [Arabidopsis thaliana]

Seq. No.	145174
Seq. ID	LIB3168-055-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	64
E value	4.0e-13
Match length	59
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145175
Seq. ID	LIB3168-055-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	282
E value	3.0e-25
Match length	55
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145176
Seq. ID	LIB3168-055-P1-K1-E12
Method	BLASTN
NCBI GI	g2842474
BLAST score	53
E value	5.0e-21
Match length	97

% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145177
Seq. ID	LIB3168-055-P1-K1-E2
Method	BLASTX
NCBI GI	g3169182
BLAST score	394
E value	2.0e-38
Match length	78
% identity	96
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	145178
Seq. ID	LIB3168-055-P1-K1-E3
Method	BLASTX
NCBI GI	g3128211
BLAST score	434
E value	5.0e-43
Match length	113
% identity	71
NCBI Description	(AC004077) putative cytochrome p450 protein [Arabidopsis thaliana] >gi_3337377 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	145179
Seq. ID	LIB3168-055-P1-K1-E4
Method	BLASTN
NCBI GI	g4662640
BLAST score	96
E value	1.0e-46
Match length	174
% identity	42
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	145180
Seq. ID	LIB3168-055-P1-K1-E5
Method	BLASTN
NCBI GI	g3133272
BLAST score	22
E value	1.5e-02
Match length	428
% identity	32
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	145181
Seq. ID	LIB3168-055-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	333
E value	1.0e-31
Match length	66
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145182
Seq. ID	LIB3168-055-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	594
E value	7.0e-62
Match length	114
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145183
Seq. ID	LIB3168-055-P1-K1-E8
Method	BLASTX
NCBI GI	g112741
BLAST score	565
E value	5.0e-58
Match length	112
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145184
Seq. ID	LIB3168-055-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	566
E value	2.0e-58
Match length	119
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145185
Seq. ID	LIB3168-055-P1-K1-F1
Method	BLASTX
NCBI GI	g132110
BLAST score	534
E value	7.0e-55
Match length	107
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_

	(X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	145186
Seq. ID	LIB3168-055-P1-K1-F10
Method	BLASTN
NCBI GI	g2264316
BLAST score	195
E value	1.0e-106
Match length	203
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.	145187
Seq. ID	LIB3168-055-P1-K1-F11
Method	BLASTX
NCBI GI	g4510348
BLAST score	193
E value	9.0e-15
Match length	57
% identity	61
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.	145188
Seq. ID	LIB3168-055-P1-K1-F4
Method	BLASTX
NCBI GI	g4467147
BLAST score	568
E value	9.0e-59
Match length	117
% identity	97
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]
Seq. No.	145189
Seq. ID	LIB3168-055-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	575
E value	1.0e-59
Match length	124
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145190
Seq. ID	LIB3168-055-P1-K1-F6
Method	BLASTX
NCBI GI	g2605714
BLAST score	365
E value	6.0e-35
Match length	100
% identity	74
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No.	145191
Seq. ID	LIB3168-055-P1-K1-F7
Method	BLASTX
NCBI GI	g2827528
BLAST score	356
E value	4.0e-37
Match length	107
% identity	68
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	145192
Seq. ID	LIB3168-055-P1-K1-F8
Method	BLASTX
NCBI GI	g112682
BLAST score	386
E value	1.0e-37
Match length	88
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145193
Seq. ID	LIB3168-055-P1-K1-G10
Method	BLASTX
NCBI GI	g1703723
BLAST score	586
E value	9.0e-61
Match length	129
% identity	88
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_733448 (U23082) CF1 ATP synthase beta subunit [Spinacia oleracea]

Seq. No.	145194
Seq. ID	LIB3168-055-P1-K1-G11
Method	BLASTX
NCBI GI	g112739
BLAST score	363
E value	7.0e-35
Match length	90
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145195
Seq. ID	LIB3168-055-P1-K1-G12
Method	BLASTX
NCBI GI	g3738338

BLAST score	414
E value	1.0e-40
Match length	128
% identity	59
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	145196
Seq. ID	LIB3168-055-P1-K1-G2
Method	BLASTX
NCBI GI	g112739
BLAST score	349
E value	2.0e-33
Match length	68
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145197
Seq. ID	LIB3168-055-P1-K1-G3
Method	BLASTX
NCBI GI	g112741
BLAST score	271
E value	5.0e-24
Match length	51
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145198
Seq. ID	LIB3168-055-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	526
E value	9.0e-54
Match length	135
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145199
Seq. ID	LIB3168-055-P1-K1-G5
Method	BLASTX
NCBI GI	g112737
BLAST score	650
E value	3.0e-68

Match length	139
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145200
Seq. ID	LIB3168-055-P1-K1-G6
Method	BLASTX
NCBI GI	g226120
BLAST score	238
E value	6.0e-20
Match length	116
% identity	41
NCBI Description	vicilin gene B [Saguinus oedipus]

Seq. No.	145201
Seq. ID	LIB3168-055-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	244
E value	4.0e-21
Match length	47
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145202
Seq. ID	LIB3168-055-P1-K1-H1
Method	BLASTN
NCBI GI	g4539402
BLAST score	38
E value	4.0e-12
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	145203
Seq. ID	LIB3168-055-P1-K1-H10
Method	BLASTX
NCBI GI	g4263771
BLAST score	285
E value	2.0e-25
Match length	75
% identity	69
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	145204
Seq. ID	LIB3168-055-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	415
E value	4.0e-41
Match length	82
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145205
Seq. ID	LIB3168-055-P1-K1-H12
Method	BLASTX
NCBI GI	g4204265
BLAST score	288
E value	8.0e-26
Match length	109
% identity	57
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	145206
Seq. ID	LIB3168-055-P1-K1-H2
Method	BLASTN
NCBI GI	g12255
BLAST score	32
E value	5.0e-09
Match length	40
% identity	95
NCBI Description	Spinach plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No.	145207
Seq. ID	LIB3168-055-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	350
E value	3.0e-33
Match length	74
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145208
Seq. ID	LIB3168-055-P1-K1-H5
Method	BLASTX
NCBI GI	g112681
BLAST score	492
E value	9.0e-50
Match length	140
% identity	75
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

	>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145209
Seq. ID	LIB3168-056-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	480
E value	2.0e-48
Match length	133
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145210
Seq. ID	LIB3168-056-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	685
E value	2.0e-72
Match length	137
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145211
Seq. ID	LIB3168-056-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	629
E value	7.0e-66
Match length	133
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145212
Seq. ID	LIB3168-056-P1-K1-A2
Method	BLASTN
NCBI GI	g1628582
BLAST score	58
E value	4.0e-24
Match length	117
% identity	53
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds
Seq. No.	145213
Seq. ID	LIB3168-056-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583

BLAST score	137
E value	3.0e-08
Match length	110
% identity	57
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145214
Seq. ID	LIB3168-056-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	625
E value	2.0e-65
Match length	139
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145215
Seq. ID	LIB3168-056-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	464
E value	9.0e-47
Match length	96
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145216
Seq. ID	LIB3168-056-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	585
E value	9.0e-61
Match length	116
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145217
Seq. ID	LIB3168-056-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	668
E value	2.0e-70
Match length	126
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145218
Seq. ID	LIB3168-056-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	711
E value	2.0e-75
Match length	136
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145219
Seq. ID	LIB3168-056-P1-K1-B12
Method	BLASTX
NCBI GI	g112737
BLAST score	561
E value	7.0e-58
Match length	135
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145220
Seq. ID	LIB3168-056-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	134
E value	2.0e-09
Match length	62
% identity	61
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145221
Seq. ID	LIB3168-056-P1-K1-B4
Method	BLASTN
NCBI GI	g4538895
BLAST score	348
E value	0.0e+00
Match length	411
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	145222
Seq. ID	LIB3168-056-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	441

E value	5.0e-44
Match length	90
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145223
Seq. ID	LIB3168-056-P1-K1-B6
Method	BLASTX
NCBI GI	g112682
BLAST score	641
E value	3.0e-67
Match length	135
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145224
Seq. ID	LIB3168-056-P1-K1-C1
Method	BLASTX
NCBI GI	g112737
BLAST score	566
E value	2.0e-58
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145225
Seq. ID	LIB3168-056-P1-K1-C10
Method	BLASTX
NCBI GI	g112741
BLAST score	463
E value	2.0e-46
Match length	130
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145226
Seq. ID	LIB3168-056-P1-K1-C11
Method	BLASTN
NCBI GI	g2739359

BLAST score	286
E value	1.0e-160
Match length	355
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145227
Seq. ID	LIB3168-056-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	489
E value	2.0e-49
Match length	109
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145228
Seq. ID	LIB3168-056-P1-K1-C4
Method	BLASTX
NCBI GI	g112737
BLAST score	245
E value	6.0e-21
Match length	95
% identity	60
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145229
Seq. ID	LIB3168-056-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	603
E value	9.0e-63
Match length	115
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145230
Seq. ID	LIB3168-056-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	463
E value	2.0e-46
Match length	96
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145231
Seq. ID	LIB3168-056-P1-K1-C7
Method	BLASTN
NCBI GI	g2708736
BLAST score	313
E value	1.0e-176
Match length	321
% identity	99
NCBI Description	Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	145232
Seq. ID	LIB3168-056-P1-K1-C8
Method	BLASTN
NCBI GI	g4406805
BLAST score	340
E value	0.0e+00
Match length	348
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145233
Seq. ID	LIB3168-056-P1-K1-C9
Method	BLASTX
NCBI GI	g112682
BLAST score	601
E value	1.0e-62
Match length	140
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145234
Seq. ID	LIB3168-056-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	73
E value	2.0e-17
Match length	69
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145235
Seq. ID	LIB3168-056-P1-K1-D3
Method	BLASTN
NCBI GI	g4079614
BLAST score	40
E value	2.0e-13
Match length	122

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% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145236
Seq. ID	LIB3168-056-P1-K1-D5
Method	BLASTN
NCBI GI	g725259
BLAST score	182
E value	7.0e-98
Match length	294
% identity	90
NCBI Description	Arabidopsis thaliana oleosin mRNA, complete cds

Seq. No.	145237
Seq. ID	LIB3168-056-P1-K1-D6
Method	BLASTX
NCBI GI	g112681
BLAST score	628
E value	1.0e-65
Match length	124
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145238
Seq. ID	LIB3168-056-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	195
E value	1.0e-15
Match length	67
% identity	68
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145239
Seq. ID	LIB3168-056-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	652
E value	1.0e-68
Match length	126
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145240
Seq. ID	LIB3168-056-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	574

E value	2.0e-59
Match length	141
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145241
Seq. ID	LIB3168-056-P1-K1-E10
Method	BLASTX
NCBI GI	g4204298
BLAST score	570
E value	6.0e-59
Match length	124
% identity	89
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145242
Seq. ID	LIB3168-056-P1-K1-E11
Method	BLASTX
NCBI GI	g3434973
BLAST score	444
E value	3.0e-44
Match length	106
% identity	80
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No.	145243
Seq. ID	LIB3168-056-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	420
E value	1.0e-41
Match length	91
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145244
Seq. ID	LIB3168-056-P1-K1-E3
Method	BLASTX
NCBI GI	g112681
BLAST score	536
E value	6.0e-55
Match length	128
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145245
Seq. ID	LIB3168-056-P1-K1-E5

Method	BLASTX
NCBI GI	g4204299
BLAST score	106
E value	2.0e-21
Match length	93
% identity	69
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145246
Seq. ID	LIB3168-056-P1-K1-E6
Method	BLASTX
NCBI GI	g112743
BLAST score	636
E value	1.0e-66
Match length	135
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145247
Seq. ID	LIB3168-056-P1-K1-E8
Method	BLASTX
NCBI GI	g3913194
BLAST score	153
E value	8.0e-13
Match length	71
% identity	52
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 3 (CAD) >gi_548323 (L36456) cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]

Seq. No.	145248
Seq. ID	LIB3168-056-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	555
E value	4.0e-57
Match length	134
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145249
Seq. ID	LIB3168-056-P1-K1-F1
Method	BLASTX
NCBI GI	g112737
BLAST score	580

E value	4.0e-60
Match length	139
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145250
Seq. ID	LIB3168-056-P1-K1-F10
Method	BLASTN
NCBI GI	g4512656
BLAST score	263
E value	1.0e-146
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	145251
Seq. ID	LIB3168-056-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	338
E value	2.0e-32
Match length	70
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145252
Seq. ID	LIB3168-056-P1-K1-F2
Method	BLASTX
NCBI GI	g112741
BLAST score	480
E value	2.0e-48
Match length	101
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145253
Seq. ID	LIB3168-056-P1-K1-F3
Method	BLASTX
NCBI GI	g4585998
BLAST score	319
E value	2.0e-29
Match length	121

% identity	53
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	145254
Seq. ID	LIB3168-056-P1-K1-F4
Method	BLASTN
NCBI GI	g4757403
BLAST score	262
E value	1.0e-145
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	145255
Seq. ID	LIB3168-056-P1-K1-F6
Method	BLASTX
NCBI GI	g1755162
BLAST score	328
E value	7.0e-31
Match length	79
% identity	86
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	145256
Seq. ID	LIB3168-056-P1-K1-F7
Method	BLASTX
NCBI GI	g112737
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145257
Seq. ID	LIB3168-056-P1-K1-F8
Method	BLASTX
NCBI GI	g112737
BLAST score	187
E value	1.0e-14
Match length	52
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145258

Seq. ID	LIB3168-056-P1-K1-F9
Method	BLASTN
NCBI GI	g2880038
BLAST score	244
E value	1.0e-135
Match length	336
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145259
Seq. ID	LIB3168-056-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	528
E value	5.0e-54
Match length	106
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145260
Seq. ID	LIB3168-056-P1-K1-G11
Method	BLASTX
NCBI GI	g112741
BLAST score	596
E value	4.0e-62
Match length	112
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145261
Seq. ID	LIB3168-056-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145262
Seq. ID	LIB3168-056-P1-K1-G2
Method	BLASTX
NCBI GI	g4510383
BLAST score	498
E value	2.0e-50
Match length	142

% identity	71
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	145263
Seq. ID	LIB3168-056-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	42
E value	6.0e-34
Match length	95
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145264
Seq. ID	LIB3168-056-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	84
E value	2.0e-20
Match length	81
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145265
Seq. ID	LIB3168-056-P1-K1-G5
Method	BLASTX
NCBI GI	g112682
BLAST score	578
E value	7.0e-60
Match length	135
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145266
Seq. ID	LIB3168-056-P1-K1-G6
Method	BLASTX
NCBI GI	g112741
BLAST score	243
E value	6.0e-21
Match length	76
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145267
Seq. ID	LIB3168-056-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	551
E value	1.0e-56
Match length	137
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145268
Seq. ID	LIB3168-056-P1-K1-G9
Method	BLASTX
NCBI GI	g112681
BLAST score	645
E value	1.0e-67
Match length	136
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145269
Seq. ID	LIB3168-056-P1-K1-H10
Method	BLASTX
NCBI GI	g3805854
BLAST score	69
E value	6.0e-19
Match length	53
% identity	96
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	145270
Seq. ID	LIB3168-056-P1-K1-H11
Method	BLASTN
NCBI GI	g3449318
BLAST score	345
E value	0.0e+00
Match length	396
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana]

Seq. No.	145271
Seq. ID	LIB3168-056-P1-K1-H7
Method	BLASTX
NCBI GI	g2129657
BLAST score	151
E value	9.0e-11

Match length	51
% identity	78
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145272
Seq. ID	LIB3168-056-P1-K1-H8
Method	BLASTX
NCBI GI	g2129657
BLAST score	222
E value	4.0e-18
Match length	89
% identity	60
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145273
Seq. ID	LIB3168-056-P1-K1-H9
Method	BLASTX
NCBI GI	g2924779
BLAST score	601
E value	1.0e-62
Match length	123
% identity	98
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	145274
Seq. ID	LIB3168-057-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	455
E value	1.0e-45
Match length	91
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145275
Seq. ID	LIB3168-057-P1-K1-A11
Method	BLASTX
NCBI GI	g3273743
BLAST score	448
E value	8.0e-45
Match length	87
% identity	97
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	145276
Seq. ID	LIB3168-057-P1-K1-A12
Method	BLASTN
NCBI GI	g4587641
BLAST score	179
E value	5.0e-96
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	145277
Seq. ID	LIB3168-057-P1-K1-A4
Method	BLASTX
NCBI GI	g2914710
BLAST score	288
E value	7.0e-26
Match length	55
% identity	93
NCBI Description	(AC003974) putative beta-D-galactosidase [Arabidopsis thaliana]

Seq. No.	145278
Seq. ID	LIB3168-057-P1-K1-A5
Method	BLASTN
NCBI GI	g992642
BLAST score	79
E value	4.0e-37
Match length	83
% identity	99
NCBI Description	Arabidopsis thaliana cyclophilin (ATCYP1) gene, complete cds

Seq. No.	145279
Seq. ID	LIB3168-057-P1-K1-A6
Method	BLASTN
NCBI GI	g3093275
BLAST score	94
E value	1.0e-45
Match length	123
% identity	98
NCBI Description	Arabidopsis thaliana cda1 gene

Seq. No.	145280
Seq. ID	LIB3168-057-P1-K1-A7
Method	BLASTN
NCBI GI	g3193282
BLAST score	34
E value	5.0e-10
Match length	81
% identity	91
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	145281
Seq. ID	LIB3168-057-P1-K1-A9
Method	BLASTX

NCBI GI	g1628583
BLAST score	472
E value	2.0e-47
Match length	102
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145282
Seq. ID	LIB3168-057-P1-K1-B1
Method	BLASTX
NCBI GI	g2129532
BLAST score	263
E value	5.0e-23
Match length	80
% identity	70
NCBI Description	acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) - Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis thaliana]

Seq. No.	145283
Seq. ID	LIB3168-057-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	438
E value	1.0e-43
Match length	104
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145284
Seq. ID	LIB3168-057-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	445
E value	2.0e-44
Match length	96
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145285
Seq. ID	LIB3168-057-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	191
E value	4.0e-15
Match length	55
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145286
Seq. ID	LIB3168-057-P1-K1-B2
Method	BLASTX
NCBI GI	g1854386
BLAST score	455
E value	2.0e-45
Match length	123
% identity	71
NCBI Description	(AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No.	145287
Seq. ID	LIB3168-057-P1-K1-B3
Method	BLASTX
NCBI GI	g3269284
BLAST score	348
E value	7.0e-33
Match length	115
% identity	65
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	145288
Seq. ID	LIB3168-057-P1-K1-B5
Method	BLASTN
NCBI GI	g4079614
BLAST score	82
E value	1.0e-38
Match length	122
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145289
Seq. ID	LIB3168-057-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	530
E value	2.0e-54
Match length	103
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145290
Seq. ID	LIB3168-057-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	441
E value	4.0e-44
Match length	87
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	145291
Seq. ID	LIB3168-057-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	655
E value	6.0e-69
Match length	127
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145292
Seq. ID	LIB3168-057-P1-K1-B9
Method	BLASTX
NCBI GI	g112737
BLAST score	374
E value	4.0e-36
Match length	90
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145293
Seq. ID	LIB3168-057-P1-K1-C1
Method	BLASTN
NCBI GI	g1069997
BLAST score	53
E value	6.0e-21
Match length	85
% identity	92
NCBI Description	B.napus chloroplast accD gene

Seq. No.	145294
Seq. ID	LIB3168-057-P1-K1-C10
Method	BLASTX
NCBI GI	g112737
BLAST score	457
E value	9.0e-46
Match length	111
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145295

Seq. ID	LIB3168-057-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	395
E value	2.0e-38
Match length	116
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145296
Seq. ID	LIB3168-057-P1-K1-C12
Method	BLASTX
NCBI GI	g1592679
BLAST score	310
E value	9.0e-29
Match length	81
% identity	80
NCBI Description	(X91915) LEA D113 homologue type1 [Arabidopsis thaliana]

Seq. No.	145297
Seq. ID	LIB3168-057-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	305
E value	6.0e-28
Match length	91
% identity	67
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145298
Seq. ID	LIB3168-057-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	353
E value	1.0e-33
Match length	92
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145299
Seq. ID	LIB3168-057-P1-K1-C5
Method	BLASTN
NCBI GI	g395200
BLAST score	157
E value	3.0e-83
Match length	224
% identity	82
NCBI Description	A.thaliana 2S albumin gene isoforms 3 and 4, complete CDS's

Seq. No.	145300
Seq. ID	LIB3168-057-P1-K1-C6
Method	BLASTN
NCBI GI	g4490701
BLAST score	151
E value	1.0e-79
Match length	175
% identity	36
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	145301
Seq. ID	LIB3168-057-P1-K1-C7
Method	BLASTX
NCBI GI	g3273751
BLAST score	72
E value	1.0e-30
Match length	89
% identity	83
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	145302
Seq. ID	LIB3168-057-P1-K1-C8
Method	BLASTN
NCBI GI	g4490701
BLAST score	62
E value	4.0e-27
Match length	74
% identity	69
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	145303
Seq. ID	LIB3168-057-P1-K1-C9
Method	BLASTN
NCBI GI	g4388816
BLAST score	239
E value	1.0e-132
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145304
Seq. ID	LIB3168-057-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	271
E value	2.0e-27
Match length	70
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145305

Seq. ID	LIB3168-057-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	516
E value	9.0e-53
Match length	95
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145306
Seq. ID	LIB3168-057-P1-K1-D3
Method	BLASTX
NCBI GI	g112681
BLAST score	527
E value	7.0e-54
Match length	142
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145307
Seq. ID	LIB3168-057-P1-K1-D4
Method	BLASTN
NCBI GI	g4755185
BLAST score	232
E value	1.0e-128
Match length	264
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	145308
Seq. ID	LIB3168-057-P1-K1-D5
Method	BLASTX
NCBI GI	g129867
BLAST score	404
E value	7.0e-40
Match length	81
% identity	98
NCBI Description	CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE) >gi_2924273_emb_CAA77425_ (Z00044) cytochrome b/f complex subunit IV [Nicotiana tabacum]

Seq. No.	145309
Seq. ID	LIB3168-057-P1-K1-D7
Method	BLASTX
NCBI GI	g112682
BLAST score	538
E value	4.0e-55
Match length	132

% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145310
Seq. ID	LIB3168-057-P1-K1-D9
Method	BLASTX
NCBI GI	g112682
BLAST score	752
E value	3.0e-80
Match length	143
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145311
Seq. ID	LIB3168-057-P1-K1-E10
Method	BLASTX
NCBI GI	g2160185
BLAST score	189
E value	3.0e-14
Match length	71
% identity	48
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]
Seq. No.	145312
Seq. ID	LIB3168-057-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	570
E value	6.0e-59
Match length	142
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145313
Seq. ID	LIB3168-057-P1-K1-E2
Method	BLASTX
NCBI GI	g112681
BLAST score	178
E value	3.0e-13
Match length	94
% identity	36
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145314
Seq. ID	LIB3168-057-P1-K1-E4
Method	BLASTN
NCBI GI	g2760173
BLAST score	343
E value	0.0e+00
Match length	374
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	145315
Seq. ID	LIB3168-057-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	1.0e-60
Match length	116
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145316
Seq. ID	LIB3168-057-P1-K1-E6
Method	BLASTX
NCBI GI	g112737
BLAST score	351
E value	2.0e-33
Match length	84
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145317
Seq. ID	LIB3168-057-P1-K1-E7
Method	BLASTX
NCBI GI	g112741
BLAST score	454
E value	2.0e-45
Match length	127
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145318

Seq. ID	LIB3168-057-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	237
E value	2.0e-20
Match length	54
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145319
Seq. ID	LIB3168-057-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	193
E value	3.0e-15
Match length	51
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145320
Seq. ID	LIB3168-057-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	343
E value	2.0e-43
Match length	118
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145321
Seq. ID	LIB3168-057-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	488
E value	3.0e-49
Match length	131
% identity	73
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145322
Seq. ID	LIB3168-057-P1-K1-F12
Method	BLASTX
NCBI GI	g112682
BLAST score	279
E value	2.0e-61
Match length	142
% identity	87

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145323
Seq. ID	LIB3168-057-P1-K1-F2
Method	BLASTX
NCBI GI	g1706749
BLAST score	432
E value	9.0e-43
Match length	85
% identity	98
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]

Seq. No.	145324
Seq. ID	LIB3168-057-P1-K1-F3
Method	BLASTX
NCBI GI	g112682
BLAST score	192
E value	3.0e-15
Match length	59
% identity	63
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145325
Seq. ID	LIB3168-057-P1-K1-F4
Method	BLASTX
NCBI GI	g112741
BLAST score	508
E value	7.0e-52
Match length	95
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145326
Seq. ID	LIB3168-057-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	222
E value	1.0e-43
Match length	104
% identity	90

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145327
Seq. ID	LIB3168-057-P1-K1-F6
Method	BLASTN
NCBI GI	g3059018
BLAST score	194
E value	1.0e-105
Match length	295
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	145328
Seq. ID	LIB3168-057-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	81
E value	4.0e-54
Match length	122
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145329
Seq. ID	LIB3168-057-P1-K1-F8
Method	BLASTX
NCBI GI	g4432846
BLAST score	548
E value	2.0e-56
Match length	108
% identity	96
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	145330
Seq. ID	LIB3168-057-P1-K1-F9
Method	BLASTX
NCBI GI	g3367515
BLAST score	478
E value	4.0e-48
Match length	97
% identity	95
NCBI Description	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No.	145331
Seq. ID	LIB3168-057-P1-K1-G1
Method	BLASTX
NCBI GI	g112682
BLAST score	603
E value	8.0e-63

Match length	125
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145332
Seq. ID	LIB3168-057-P1-K1-G10
Method	BLASTX
NCBI GI	g2194142
BLAST score	438
E value	2.0e-43
Match length	90
% identity	98
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No.	145333
Seq. ID	LIB3168-057-P1-K1-G12
Method	BLASTX
NCBI GI	g112682
BLAST score	564
E value	3.0e-58
Match length	132
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145334
Seq. ID	LIB3168-057-P1-K1-G3
Method	BLASTX
NCBI GI	g112681
BLAST score	373
E value	7.0e-38
Match length	95
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145335
Seq. ID	LIB3168-057-P1-K1-G5
Method	BLASTN
NCBI GI	g2281648
BLAST score	168
E value	1.0e-89
Match length	192
% identity	97
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	145336
Seq. ID	LIB3168-057-P1-K1-G6
Method	BLASTX
NCBI GI	g112681
BLAST score	689
E value	7.0e-73
Match length	140
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145337
Seq. ID	LIB3168-057-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	645
E value	1.0e-67
Match length	138
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145338
Seq. ID	LIB3168-057-P1-K1-G8
Method	BLASTX
NCBI GI	g2865177
BLAST score	434
E value	6.0e-43
Match length	107
% identity	79
NCBI Description	(AB010946) AtRer1B [Arabidopsis thaliana]

Seq. No.	145339
Seq. ID	LIB3168-057-P1-K1-G9
Method	BLASTX
NCBI GI	g112739
BLAST score	599
E value	3.0e-62
Match length	139
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145340
Seq. ID	LIB3168-057-P1-K1-H12
Method	BLASTX
NCBI GI	g4587686

BLAST score	663
E value	7.0e-70
Match length	134
% identity	98
NCBI Description	(AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No.	145341
Seq. ID	LIB3168-057-P1-K1-H7
Method	BLASTX
NCBI GI	g112681
BLAST score	498
E value	2.0e-50
Match length	106
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145342
Seq. ID	LIB3168-057-P1-K1-H8
Method	BLASTN
NCBI GI	g16231
BLAST score	116
E value	5.0e-59
Match length	128
% identity	98
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145343
Seq. ID	LIB3168-057-P1-K1-H9
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	137
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145344
Seq. ID	LIB3168-058-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	697
E value	8.0e-74
Match length	139
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145345
Seq. ID	LIB3168-058-P1-K1-A11
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61
Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145346
Seq. ID	LIB3168-058-P1-K1-A12
Method	BLASTX
NCBI GI	g3402716
BLAST score	172
E value	2.0e-12
Match length	42
% identity	71
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	145347
Seq. ID	LIB3168-058-P1-K1-A2
Method	BLASTX
NCBI GI	g2262167
BLAST score	124
E value	2.0e-33
Match length	87
% identity	89
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	145348
Seq. ID	LIB3168-058-P1-K1-A4
Method	BLASTX
NCBI GI	g2129657
BLAST score	292
E value	2.0e-26
Match length	93
% identity	69
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145349
Seq. ID	LIB3168-058-P1-K1-A6
Method	BLASTX
NCBI GI	g2129657
BLAST score	246
E value	5.0e-21

Match length	93
% identity	59
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145350
Seq. ID	LIB3168-058-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	601
E value	1.0e-62
Match length	130
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145351
Seq. ID	LIB3168-058-P1-K1-B1
Method	BLASTN
NCBI GI	g4582444
BLAST score	64
E value	8.0e-28
Match length	92
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	145352
Seq. ID	LIB3168-058-P1-K1-B10
Method	BLASTX
NCBI GI	g112681
BLAST score	737
E value	2.0e-78
Match length	140
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145353
Seq. ID	LIB3168-058-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	670
E value	1.0e-70
Match length	140
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145354

Seq. ID	LIB3168-058-P1-K1-B12
Method	BLASTX
NCBI GI	g112739
BLAST score	438
E value	2.0e-43
Match length	124
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145355
Seq. ID	LIB3168-058-P1-K1-B3
Method	BLASTX
NCBI GI	g112681
BLAST score	733
E value	5.0e-78
Match length	138
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145356
Seq. ID	LIB3168-058-P1-K1-B4
Method	BLASTX
NCBI GI	g112741
BLAST score	531
E value	2.0e-54
Match length	98
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145357
Seq. ID	LIB3168-058-P1-K1-B5
Method	BLASTN
NCBI GI	g3036791
BLAST score	366
E value	0.0e+00
Match length	410
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No. 145358

Seq. ID	LIB3168-058-P1-K1-B6
Method	BLASTX
NCBI GI	g112681
BLAST score	472
E value	2.0e-47
Match length	125
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145359
Seq. ID	LIB3168-058-P1-K1-B9
Method	BLASTN
NCBI GI	g4159712
BLAST score	309
E value	1.0e-173
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	145360
Seq. ID	LIB3168-058-P1-K1-C1
Method	BLASTX
NCBI GI	g1169476
BLAST score	639
E value	5.0e-67
Match length	122
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	145361
Seq. ID	LIB3168-058-P1-K1-C10
Method	BLASTN
NCBI GI	g3859658
BLAST score	51
E value	1.0e-19
Match length	318
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	145362
Seq. ID	LIB3168-058-P1-K1-C11
Method	BLASTN
NCBI GI	g16231
BLAST score	66
E value	9.0e-29
Match length	106
% identity	92
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage

protein CRA1 gene, exons 1-4

Seq. No.	145363
Seq. ID	LIB3168-058-P1-K1-C12
Method	BLASTX
NCBI GI	g112743
BLAST score	642
E value	2.0e-67
Match length	135
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145364
Seq. ID	LIB3168-058-P1-K1-C2
Method	BLASTX
NCBI GI	g1899025
BLAST score	346
E value	1.0e-32
Match length	136
% identity	52
NCBI Description	(U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232 (AC005169) hexokinase [Arabidopsis thaliana]

Seq. No.	145365
Seq. ID	LIB3168-058-P1-K1-C3
Method	BLASTN
NCBI GI	g2244991
BLAST score	275
E value	1.0e-153
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	145366
Seq. ID	LIB3168-058-P1-K1-C4
Method	BLASTX
NCBI GI	g584882
BLAST score	161
E value	1.0e-30
Match length	71
% identity	93
NCBI Description	CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL CYCLASE) >gi_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No.	145367
Seq. ID	LIB3168-058-P1-K1-C5
Method	BLASTX
NCBI GI	g4262226
BLAST score	231

E value	3.0e-19
Match length	73
% identity	59
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	145368
Seq. ID	LIB3168-058-P1-K1-C6
Method	BLASTX
NCBI GI	g1109699
BLAST score	731
E value	8.0e-78
Match length	138
% identity	100
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	145369
Seq. ID	LIB3168-058-P1-K1-C7
Method	BLASTN
NCBI GI	g1628582
BLAST score	177
E value	6.0e-95
Match length	289
% identity	91
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145370
Seq. ID	LIB3168-058-P1-K1-D1
Method	BLASTX
NCBI GI	g140321
BLAST score	282
E value	2.0e-25
Match length	63
% identity	84
NCBI Description	HYPOTHETICAL 7.5 KD PROTEIN (ORF 63) >gi_81507_pir__S01447 hypothetical protein 63 - spinach chloroplast >gi_12247_emb_CAA30744_ (X07908) ORF 63 [Spinacia oleracea]

Seq. No.	145371
Seq. ID	LIB3168-058-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	586
E value	7.0e-61
Match length	116
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145372
Seq. ID	LIB3168-058-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	342
E value	2.0e-32
Match length	81

% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145373
Seq. ID	LIB3168-058-P1-K1-D2
Method	BLASTN
NCBI GI	g2351062
BLAST score	397
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.	145374
Seq. ID	LIB3168-058-P1-K1-D3
Method	BLASTN
NCBI GI	g4159704
BLAST score	171
E value	3.0e-91
Match length	267
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence
Seq. No.	145375
Seq. ID	LIB3168-058-P1-K1-D4
Method	BLASTX
NCBI GI	g3258637
BLAST score	308
E value	3.0e-28
Match length	109
% identity	61
NCBI Description	(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
Seq. No.	145376
Seq. ID	LIB3168-058-P1-K1-D5
Method	BLASTX
NCBI GI	g1169598
BLAST score	442
E value	6.0e-44
Match length	94
% identity	86
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]
Seq. No.	145377
Seq. ID	LIB3168-058-P1-K1-D9
Method	BLASTX
NCBI GI	g82051
BLAST score	327
E value	2.0e-30

Match length	124
% identity	53
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	145378
Seq. ID	LIB3168-058-P1-K1-E1
Method	BLASTX
NCBI GI	g4220479
BLAST score	583
E value	2.0e-60
Match length	129
% identity	90
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	145379
Seq. ID	LIB3168-058-P1-K1-E12
Method	BLASTX
NCBI GI	g3152587
BLAST score	300
E value	6.0e-29
Match length	92
% identity	74
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	145380
Seq. ID	LIB3168-058-P1-K1-E2
Method	BLASTX
NCBI GI	g112737
BLAST score	545
E value	5.0e-56
Match length	132
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145381
Seq. ID	LIB3168-058-P1-K1-E3
Method	BLASTX
NCBI GI	g112737
BLAST score	536
E value	6.0e-55
Match length	130
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145382
Seq. ID	LIB3168-058-P1-K1-E4
Method	BLASTX
NCBI GI	g4454032
BLAST score	238
E value	5.0e-20
Match length	74
% identity	57
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	145383
Seq. ID	LIB3168-058-P1-K1-E6
Method	BLASTX
NCBI GI	g112737
BLAST score	251
E value	6.0e-22
Match length	48
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145384
Seq. ID	LIB3168-058-P1-K1-F10
Method	BLASTX
NCBI GI	g119150
BLAST score	267
E value	6.0e-24
Match length	56
% identity	91
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No.	145385
Seq. ID	LIB3168-058-P1-K1-F11
Method	BLASTN
NCBI GI	g3355463
BLAST score	185
E value	1.0e-99
Match length	330
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145386
Seq. ID	LIB3168-058-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	590
E value	3.0e-61
Match length	126
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145387
Seq. ID	LIB3168-058-P1-K1-F2
Method	BLASTX
NCBI GI	g3935169
BLAST score	322
E value	7.0e-30
Match length	68
% identity	96
NCBI Description	(AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No.	145388
Seq. ID	LIB3168-058-P1-K1-F3
Method	BLASTN
NCBI GI	g3510343
BLAST score	235
E value	1.0e-129
Match length	317
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	145389
Seq. ID	LIB3168-058-P1-K1-F4
Method	BLASTX
NCBI GI	g1169476
BLAST score	627
E value	1.0e-65
Match length	120
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	145390
Seq. ID	LIB3168-058-P1-K1-F5
Method	BLASTX
NCBI GI	g112737
BLAST score	554
E value	5.0e-57
Match length	134
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145391
Seq. ID	LIB3168-058-P1-K1-F6
Method	BLASTN
NCBI GI	g4199934
BLAST score	230
E value	1.0e-126
Match length	378
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	145392
Seq. ID	LIB3168-058-P1-K1-G11
Method	BLASTX
NCBI GI	g112737
BLAST score	359
E value	2.0e-34
Match length	83
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145393
Seq. ID	LIB3168-058-P1-K1-G12
Method	BLASTX
NCBI GI	g112737
BLAST score	455
E value	2.0e-45
Match length	115
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145394
Seq. ID	LIB3168-058-P1-K1-G2
Method	BLASTN
NCBI GI	g4159708
BLAST score	287
E value	1.0e-160
Match length	315
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	145395
Seq. ID	LIB3168-058-P1-K1-G3
Method	BLASTX
NCBI GI	g112682
BLAST score	556
E value	3.0e-57
Match length	131
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145396
Seq. ID	LIB3168-058-P1-K1-G4
Method	BLASTN
NCBI GI	g16473
BLAST score	406
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	145397
Seq. ID	LIB3168-058-P1-K1-G5
Method	BLASTN
NCBI GI	g2341023
BLAST score	71
E value	4.0e-32
Match length	119
% identity	95
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	145398
Seq. ID	LIB3168-058-P1-K1-G9
Method	BLASTX
NCBI GI	g112681
BLAST score	502
E value	6.0e-51
Match length	137
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145399
Seq. ID	LIB3168-058-P1-K1-H1
Method	BLASTX
NCBI GI	g2129657
BLAST score	430
E value	2.0e-42
Match length	117

% identity 78
NCBI Description oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No. 145400
Seq. ID LIB3168-058-P1-K1-H12
Method BLASTX
NCBI GI g3785980
BLAST score 331
E value 7.0e-31
Match length 59
% identity 100
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 145401
Seq. ID LIB3168-058-P1-K1-H2
Method BLASTX
NCBI GI g1628583
BLAST score 524
E value 1.0e-53
Match length 102
% identity 99
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 145402
Seq. ID LIB3168-058-P1-K1-H3
Method BLASTX
NCBI GI g1628583
BLAST score 252
E value 9.0e-22
Match length 49
% identity 98
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 145403
Seq. ID LIB3168-058-P1-K1-H4
Method BLASTX
NCBI GI g1168258
BLAST score 610
E value 1.0e-63
Match length 135
% identity 90
NCBI Description ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 145404
Seq. ID LIB3168-058-P1-K1-H5
Method BLASTX
NCBI GI g1709970
BLAST score 185

E value	6.0e-14
Match length	50
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	145405
Seq. ID	LIB3168-058-P1-K1-H9
Method	BLASTN
NCBI GI	g166609
BLAST score	113
E value	8.0e-57
Match length	290
% identity	84
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145406
Seq. ID	LIB3168-059-P1-K1-A10
Method	BLASTX
NCBI GI	g480450
BLAST score	450
E value	8.0e-45
Match length	102
% identity	89
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	145407
Seq. ID	LIB3168-059-P1-K1-A11
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	7.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145408
Seq. ID	LIB3168-059-P1-K1-A12
Method	BLASTN
NCBI GI	g3885325
BLAST score	280
E value	1.0e-156
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145409
Seq. ID	LIB3168-059-P1-K1-A2
Method	BLASTX
NCBI GI	g112681

BLAST score	51
E value	1.0e-14
Match length	89
% identity	60
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145410
Seq. ID	LIB3168-059-P1-K1-A3
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	3.0e-62
Match length	114
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145411
Seq. ID	LIB3168-059-P1-K1-A4
Method	BLASTX
NCBI GI	g3915961
BLAST score	677
E value	2.0e-71
Match length	143
% identity	91
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	145412
Seq. ID	LIB3168-059-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	616
E value	3.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145413
Seq. ID	LIB3168-059-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145414
Seq. ID	LIB3168-059-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	648
E value	4.0e-68
Match length	128
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145415
Seq. ID	LIB3168-059-P1-K1-A8
Method	BLASTX
NCBI GI	g3451074
BLAST score	372
E value	1.0e-35
Match length	136
% identity	58
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	145416
Seq. ID	LIB3168-059-P1-K1-B1
Method	BLASTX
NCBI GI	g112743
BLAST score	686
E value	2.0e-72
Match length	128
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145417
Seq. ID	LIB3168-059-P1-K1-B11
Method	BLASTX
NCBI GI	g2633047
BLAST score	182
E value	2.0e-13
Match length	126
% identity	30
NCBI Description	(Z99107) similar to metabolite transporter [Bacillus subtilis] >gi_2633058_emb_CAB12563_ (Z99108) similar to metabolite transporter [Bacillus subtilis]

Seq. No.	145418

Seq. ID	LIB3168-059-P1-K1-B12
Method	BLASTX
NCBI GI	g112739
BLAST score	446
E value	2.0e-44
Match length	126
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145419
Seq. ID	LIB3168-059-P1-K1-B2
Method	BLASTX
NCBI GI	g3402711
BLAST score	412
E value	2.0e-40
Match length	121
% identity	44
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	145420
Seq. ID	LIB3168-059-P1-K1-B3
Method	BLASTX
NCBI GI	g1173345
BLAST score	80
E value	6.0e-29
Match length	116
% identity	60
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase - Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	145421
Seq. ID	LIB3168-059-P1-K1-B4
Method	BLASTN
NCBI GI	g2864607
BLAST score	250
E value	1.0e-138
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	145422
Seq. ID	LIB3168-059-P1-K1-B5
Method	BLASTX
NCBI GI	g3451075

BLAST score	77
E value	6.0e-23
Match length	102
% identity	55
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	145423
Seq. ID	LIB3168-059-P1-K1-B7
Method	BLASTN
NCBI GI	g3449320
BLAST score	259
E value	1.0e-144
Match length	354
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	145424
Seq. ID	LIB3168-059-P1-K1-B8
Method	BLASTN
NCBI GI	g4159703
BLAST score	124
E value	2.0e-63
Match length	296
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	145425
Seq. ID	LIB3168-059-P1-K1-B9
Method	BLASTX
NCBI GI	g1490554
BLAST score	304
E value	1.0e-27
Match length	63
% identity	98
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	145426
Seq. ID	LIB3168-059-P1-K1-C1
Method	BLASTN
NCBI GI	g3540210
BLAST score	218
E value	1.0e-119
Match length	309
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145427
Seq. ID	LIB3168-059-P1-K1-C11
Method	BLASTX
NCBI GI	g112739
BLAST score	461
E value	4.0e-46
Match length	129

% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145428
Seq. ID	LIB3168-059-P1-K1-C12
Method	BLASTX
NCBI GI	g2828267
BLAST score	595
E value	7.0e-62
Match length	141
% identity	86
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	145429
Seq. ID	LIB3168-059-P1-K1-C2
Method	BLASTX
NCBI GI	g2851581
BLAST score	249
E value	3.0e-21
Match length	48
% identity	100
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	145430
Seq. ID	LIB3168-059-P1-K1-C3
Method	BLASTX
NCBI GI	g464621
BLAST score	499
E value	1.0e-50
Match length	120
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	145431
Seq. ID	LIB3168-059-P1-K1-C4
Method	BLASTX
NCBI GI	g112739
BLAST score	225
E value	1.0e-18
Match length	61
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145432
Seq. ID	LIB3168-059-P1-K1-C7
Method	BLASTX
NCBI GI	g112681
BLAST score	542
E value	1.0e-55
Match length	141
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145433
Seq. ID	LIB3168-059-P1-K1-C8
Method	BLASTN
NCBI GI	g2827538
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	145434
Seq. ID	LIB3168-059-P1-K1-C9
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	137
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145435
Seq. ID	LIB3168-059-P1-K1-D1
Method	BLASTN
NCBI GI	g3080352
BLAST score	259
E value	1.0e-144
Match length	347
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	145436
Seq. ID	LIB3168-059-P1-K1-D10

Method	BLASTX
NCBI GI	g99688
BLAST score	724
E value	5.0e-77
Match length	138
% identity	100
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	145437
Seq. ID	LIB3168-059-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	8.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145438
Seq. ID	LIB3168-059-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	1.0e-63
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145439
Seq. ID	LIB3168-059-P1-K1-D2
Method	BLASTN
NCBI GI	g4689466
BLAST score	307
E value	1.0e-172
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	145440
Seq. ID	LIB3168-059-P1-K1-D3
Method	BLASTN
NCBI GI	g3510347
BLAST score	328
E value	0.0e+00
Match length	404
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	145441
Seq. ID	LIB3168-059-P1-K1-D4
Method	BLASTX
NCBI GI	g4204298
BLAST score	528
E value	5.0e-54
Match length	100
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145442
Seq. ID	LIB3168-059-P1-K1-D5
Method	BLASTX
NCBI GI	g112741
BLAST score	720
E value	2.0e-76
Match length	135
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145443
Seq. ID	LIB3168-059-P1-K1-D6
Method	BLASTX
NCBI GI	g2924279
BLAST score	260
E value	7.0e-23
Match length	81
% identity	68
NCBI Description	(Z00044) NADH dehydrogenase ND4 subunit [Nicotiana tabacum]

Seq. No.	145444
Seq. ID	LIB3168-059-P1-K1-D8
Method	BLASTX
NCBI GI	g131336
BLAST score	339
E value	8.0e-32
Match length	73
% identity	93
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	145445
Seq. ID	LIB3168-059-P1-K1-D9
Method	BLASTN
NCBI GI	g2924257

BLAST score	39
E value	1.0e-12
Match length	131
% identity	82
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	145446
Seq. ID	LIB3168-059-P1-K1-E1
Method	BLASTX
NCBI GI	g112682
BLAST score	585
E value	1.0e-60
Match length	140
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145447
Seq. ID	LIB3168-059-P1-K1-E10
Method	BLASTX
NCBI GI	g1402904
BLAST score	644
E value	1.0e-67
Match length	123
% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	145448
Seq. ID	LIB3168-059-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	382
E value	7.0e-37
Match length	76
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145449
Seq. ID	LIB3168-059-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	485
E value	5.0e-49
Match length	97
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145450
Seq. ID	LIB3168-059-P1-K1-E2
Method	BLASTX

NCBI GI	g112737
BLAST score	299
E value	4.0e-27
Match length	129
% identity	52
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145451
Seq. ID	LIB3168-059-P1-K1-E3
Method	BLASTX
NCBI GI	g3023848
BLAST score	622
E value	5.0e-65
Match length	126
% identity	60
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	145452
Seq. ID	LIB3168-059-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	69
E value	9.0e-35
Match length	83
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145453
Seq. ID	LIB3168-059-P1-K1-E6
Method	BLASTX
NCBI GI	g112739
BLAST score	480
E value	2.0e-48
Match length	132
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145454
Seq. ID	LIB3168-059-P1-K1-E8
Method	BLASTX

NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145455
Seq. ID	LIB3168-059-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145456
Seq. ID	LIB3168-059-P1-K1-F1
Method	BLASTN
NCBI GI	g4406805
BLAST score	387
E value	0.0e+00
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145457
Seq. ID	LIB3168-059-P1-K1-F11
Method	BLASTN
NCBI GI	g3128142
BLAST score	48
E value	7.0e-18
Match length	105
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	145458
Seq. ID	LIB3168-059-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145459
Seq. ID	LIB3168-059-P1-K1-F3

Method	BLASTX
NCBI GI	g1628583
BLAST score	456
E value	8.0e-46
Match length	96
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145460
Seq. ID	LIB3168-059-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145461
Seq. ID	LIB3168-059-P1-K1-F6
Method	BLASTX
NCBI GI	g529353
BLAST score	373
E value	7.0e-36
Match length	110
% identity	57
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	145462
Seq. ID	LIB3168-059-P1-K1-F7
Method	BLASTX
NCBI GI	g4512615
BLAST score	439
E value	8.0e-44
Match length	98
% identity	88
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	145463
Seq. ID	LIB3168-059-P1-K1-F8
Method	BLASTX
NCBI GI	g4768831
BLAST score	160
E value	8.0e-11
Match length	90
% identity	34
NCBI Description	(AF116827) unknown [Homo sapiens]

Seq. No.	145464
Seq. ID	LIB3168-059-P1-K1-F9
Method	BLASTX

NCBI GI	g4510397
BLAST score	740
E value	8.0e-79
Match length	141
% identity	100
NCBI Description	(AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No.	145465
Seq. ID	LIB3168-059-P1-K1-G1
Method	BLASTX
NCBI GI	g3913418
BLAST score	714
E value	9.0e-76
Match length	142
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	145466
Seq. ID	LIB3168-059-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	541
E value	2.0e-55
Match length	117
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145467
Seq. ID	LIB3168-059-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	374
E value	5.0e-36
Match length	76
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145468
Seq. ID	LIB3168-059-P1-K1-G4
Method	BLASTX
NCBI GI	g112682
BLAST score	614
E value	5.0e-64
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145469
Seq. ID	LIB3168-059-P1-K1-G5
Method	BLASTX
NCBI GI	g112743
BLAST score	653
E value	1.0e-68
Match length	137
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145470
Seq. ID	LIB3168-059-P1-K1-G6
Method	BLASTX
NCBI GI	g3510249
BLAST score	680
E value	8.0e-72
Match length	134
% identity	99
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	145471
Seq. ID	LIB3168-059-P1-K1-G7
Method	BLASTX
NCBI GI	g4567249
BLAST score	551
E value	1.0e-56
Match length	119
% identity	87
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	145472
Seq. ID	LIB3168-059-P1-K1-G9
Method	BLASTX
NCBI GI	g2464905
BLAST score	480
E value	2.0e-48
Match length	131
% identity	74
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	145473
Seq. ID	LIB3168-059-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	627
E value	1.0e-65
Match length	124
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145474
Seq. ID	LIB3168-059-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	529
E value	3.0e-54
Match length	112
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145475
Seq. ID	LIB3168-059-P1-K1-H11
Method	BLASTX
NCBI GI	g112737
BLAST score	538
E value	3.0e-55
Match length	116
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145476
Seq. ID	LIB3168-059-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	6.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145477
Seq. ID	LIB3168-059-P1-K1-H2
Method	BLASTX
NCBI GI	g2129657
BLAST score	52
E value	1.0e-29
Match length	100
% identity	80
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145478
Seq. ID	LIB3168-059-P1-K1-H4
Method	BLASTX

NCBI GI	g1628583
BLAST score	162
E value	5.0e-11
Match length	79
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145479
Seq. ID	LIB3168-059-P1-K1-H7
Method	BLASTX
NCBI GI	g4204299
BLAST score	514
E value	2.0e-52
Match length	102
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145480
Seq. ID	LIB3168-059-P1-K1-H9
Method	BLASTN
NCBI GI	g2264304
BLAST score	77
E value	4.0e-35
Match length	464
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	145481
Seq. ID	LIB3168-060-P1-K1-A1
Method	BLASTX
NCBI GI	g112681
BLAST score	763
E value	2.0e-81
Match length	143
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145482
Seq. ID	LIB3168-060-P1-K1-A12
Method	BLASTX
NCBI GI	g2497702
BLAST score	187
E value	5.0e-14
Match length	113
% identity	42
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	145483
Seq. ID	LIB3168-060-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	425
E value	7.0e-42
Match length	115
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145484
Seq. ID	LIB3168-060-P1-K1-A3
Method	BLASTX
NCBI GI	g112741
BLAST score	721
E value	1.0e-76
Match length	134
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145485
Seq. ID	LIB3168-060-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	204
E value	2.0e-16
Match length	69
% identity	62
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145486
Seq. ID	LIB3168-060-P1-K1-A5
Method	BLASTN
NCBI GI	g3928861
BLAST score	386
E value	0.0e+00
Match length	433
% identity	97
NCBI Description	Arabidopsis thaliana disease resistance protein RPP8 (RPP8) gene, complete cds

Seq. No.	145487
Seq. ID	LIB3168-060-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	676

E value	2.0e-71
Match length	132
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145488
Seq. ID	LIB3168-060-P1-K1-A9
Method	BLASTX
NCBI GI	g112737
BLAST score	592
E value	2.0e-61
Match length	141
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145489
Seq. ID	LIB3168-060-P1-K1-B1
Method	BLASTX
NCBI GI	g112739
BLAST score	474
E value	1.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145490
Seq. ID	LIB3168-060-P1-K1-B10
Method	BLASTX
NCBI GI	g3024526
BLAST score	621
E value	7.0e-65
Match length	121
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	145491
Seq. ID	LIB3168-060-P1-K1-B11
Method	BLASTN
NCBI GI	g4063756
BLAST score	245
E value	1.0e-135

Match length	274
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145492
Seq. ID	LIB3168-060-P1-K1-B12
Method	BLASTX
NCBI GI	g3702328
BLAST score	514
E value	2.0e-52
Match length	93
% identity	100
NCBI Description	(AC005397) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No.	145493
Seq. ID	LIB3168-060-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	187
E value	2.0e-14
Match length	60
% identity	67
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145494
Seq. ID	LIB3168-060-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	445
E value	3.0e-44
Match length	129
% identity	70
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145495
Seq. ID	LIB3168-060-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145496
Seq. ID	LIB3168-060-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	661
E value	1.0e-69

Match length	128
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145497
Seq. ID	LIB3168-060-P1-K1-B6
Method	BLASTX
NCBI GI	g112737
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145498
Seq. ID	LIB3168-060-P1-K1-B8
Method	BLASTX
NCBI GI	g112682
BLAST score	584
E value	1.0e-60
Match length	137
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145499
Seq. ID	LIB3168-060-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	567
E value	1.0e-58
Match length	141
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145500
Seq. ID	LIB3168-060-P1-K1-C1
Method	BLASTX
NCBI GI	g112739
BLAST score	357
E value	5.0e-34
Match length	109
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

	PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	145501
Seq. ID	LIB3168-060-P1-K1-C10
Method	BLASTX
NCBI GI	g112741
BLAST score	721
E value	1.0e-76
Match length	134
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	145502
Seq. ID	LIB3168-060-P1-K1-C11
Method	BLASTN
NCBI GI	g343498
BLAST score	237
E value	1.0e-130
Match length	311
% identity	96
NCBI Description	Tobacco chloroplast Arg-tRNA and Asn-tRNA 4.5S and 5S rRNA genes
Seq. No.	145503
Seq. ID	LIB3168-060-P1-K1-C4
Method	BLASTX
NCBI GI	g112741
BLAST score	275
E value	2.0e-24
Match length	123
% identity	52
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	145504
Seq. ID	LIB3168-060-P1-K1-C5
Method	BLASTX
NCBI GI	g4263771
BLAST score	300
E value	3.0e-27
Match length	76

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% identity	71
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	145505
Seq. ID	LIB3168-060-P1-K1-C6
Method	BLASTN
NCBI GI	g4097693
BLAST score	72
E value	1.0e-32
Match length	152
% identity	88
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	145506
Seq. ID	LIB3168-060-P1-K1-C7
Method	BLASTX
NCBI GI	g1107501
BLAST score	400
E value	5.0e-39
Match length	99
% identity	85
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	145507
Seq. ID	LIB3168-060-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	655
E value	6.0e-69
Match length	128
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145508
Seq. ID	LIB3168-060-P1-K1-C9
Method	BLASTX
NCBI GI	g4490736
BLAST score	695
E value	1.0e-73
Match length	140
% identity	64
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	145509
Seq. ID	LIB3168-060-P1-K1-D1
Method	BLASTX
NCBI GI	g112739

BLAST score	416
E value	7.0e-41
Match length	119
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145510
Seq. ID	LIB3168-060-P1-K1-D10
Method	BLASTX
NCBI GI	g112741
BLAST score	716
E value	5.0e-76
Match length	133
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145511
Seq. ID	LIB3168-060-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	429
E value	2.0e-42
Match length	116
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145512
Seq. ID	LIB3168-060-P1-K1-D2
Method	BLASTX
NCBI GI	g2129657
BLAST score	623
E value	4.0e-65
Match length	126
% identity	99
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145513
Seq. ID	LIB3168-060-P1-K1-D3
Method	BLASTN
NCBI GI	g2244829

BLAST score	306
E value	1.0e-172
Match length	366
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	145514
Seq. ID	LIB3168-060-P1-K1-D4
Method	BLASTN
NCBI GI	g3150396
BLAST score	371
E value	0.0e+00
Match length	379
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145515
Seq. ID	LIB3168-060-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	532
E value	2.0e-54
Match length	134
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145516
Seq. ID	LIB3168-060-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	464
E value	1.0e-46
Match length	120
% identity	63
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145517
Seq. ID	LIB3168-060-P1-K1-D8
Method	BLASTN
NCBI GI	g2564048
BLAST score	402
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	145518
Seq. ID	LIB3168-060-P1-K1-D9
Method	BLASTX
NCBI GI	g112681

BLAST score	475
E value	8.0e-48
Match length	130
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145519
Seq. ID	LIB3168-060-P1-K1-E1
Method	BLASTX
NCBI GI	g112739
BLAST score	338
E value	7.0e-32
Match length	105
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145520
Seq. ID	LIB3168-060-P1-K1-E11
Method	BLASTX
NCBI GI	g112737
BLAST score	580
E value	4.0e-60
Match length	139
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145521
Seq. ID	LIB3168-060-P1-K1-E2
Method	BLASTX
NCBI GI	g1706749
BLAST score	527
E value	7.0e-54
Match length	110
% identity	97
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]

Seq. No.	145522
Seq. ID	LIB3168-060-P1-K1-E3

Method	BLASTN
NCBI GI	g3128142
BLAST score	159
E value	2.0e-84
Match length	225
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	145523
Seq. ID	LIB3168-060-P1-K1-E4
Method	BLASTN
NCBI GI	g4512656
BLAST score	165
E value	1.0e-87
Match length	373
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	145524
Seq. ID	LIB3168-060-P1-K1-E5
Method	BLASTX
NCBI GI	g112682
BLAST score	551
E value	1.0e-56
Match length	130
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145525
Seq. ID	LIB3168-060-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	524
E value	1.0e-53
Match length	108
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145526
Seq. ID	LIB3168-060-P1-K1-E7
Method	BLASTX
NCBI GI	g133438
BLAST score	630
E value	6.0e-66
Match length	133
% identity	86
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN >gi_81504_pir__B29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - spinach chloroplast >gi_295120

(M55297) RNA polymerase [Spinacia oleracea]

Seq. No.	145527
Seq. ID	LIB3168-060-P1-K1-E8
Method	BLASTN
NCBI GI	g3212102
BLAST score	365
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	145528
Seq. ID	LIB3168-060-P1-K1-E9
Method	BLASTX
NCBI GI	g112743
BLAST score	635
E value	2.0e-66
Match length	135
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145529
Seq. ID	LIB3168-060-P1-K1-F1
Method	BLASTX
NCBI GI	g4581520
BLAST score	260
E value	1.0e-22
Match length	122
% identity	46
NCBI Description	(AL049559) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	145530
Seq. ID	LIB3168-060-P1-K1-F11
Method	BLASTN
NCBI GI	g2264321
BLAST score	68
E value	3.0e-30
Match length	132
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	145531
Seq. ID	LIB3168-060-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	318
E value	2.0e-29
Match length	76

% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145532
Seq. ID	LIB3168-060-P1-K1-F2
Method	BLASTX
NCBI GI	g112741
BLAST score	718
E value	3.0e-76
Match length	135
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145533
Seq. ID	LIB3168-060-P1-K1-F3
Method	BLASTX
NCBI GI	g112739
BLAST score	467
E value	8.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145534
Seq. ID	LIB3168-060-P1-K1-F4
Method	BLASTN
NCBI GI	g3056579
BLAST score	419
E value	0.0e+00
Match length	419
% identity	46
NCBI Description	Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	145535
Seq. ID	LIB3168-060-P1-K1-F5
Method	BLASTX
NCBI GI	g1345973
BLAST score	498
E value	2.0e-50
Match length	108
% identity	83
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	145536
Seq. ID	LIB3168-060-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	606
E value	4.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145537
Seq. ID	LIB3168-060-P1-K1-F7
Method	BLASTX
NCBI GI	g99751
BLAST score	260
E value	3.0e-29
Match length	74
% identity	80
NCBI Description	phosphoprotein phosphatase (EC 3.1.3.16) 1A catalytic chain - Arabidopsis thaliana >gi_16433_emb_CAA78153_ (Z12163) protein phosphatase 1A [Arabidopsis thaliana]

Seq. No.	145538
Seq. ID	LIB3168-060-P1-K1-F8
Method	BLASTX
NCBI GI	g3386613
BLAST score	538
E value	4.0e-55
Match length	141
% identity	78
NCBI Description	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	145539
Seq. ID	LIB3168-060-P1-K1-F9
Method	BLASTX
NCBI GI	g3445201
BLAST score	723
E value	7.0e-77
Match length	138
% identity	99
NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]

Seq. No.	145540
Seq. ID	LIB3168-060-P1-K1-G10
Method	BLASTX

NCBI GI	g2129659
BLAST score	446
E value	2.0e-44
Match length	113
% identity	82
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145541
Seq. ID	LIB3168-060-P1-K1-G11
Method	BLASTX
NCBI GI	g112739
BLAST score	416
E value	7.0e-41
Match length	119
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145542
Seq. ID	LIB3168-060-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	630
E value	5.0e-66
Match length	121
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145543
Seq. ID	LIB3168-060-P1-K1-G2
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61
Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145544
Seq. ID	LIB3168-060-P1-K1-G3
Method	BLASTX
NCBI GI	g112681
BLAST score	545
E value	2.0e-57
Match length	138

% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145545
Seq. ID	LIB3168-060-P1-K1-G4
Method	BLASTN
NCBI GI	g3292807
BLAST score	421
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)
Seq. No.	145546
Seq. ID	LIB3168-060-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	595
E value	6.0e-62
Match length	116
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145547
Seq. ID	LIB3168-060-P1-K1-G6
Method	BLASTX
NCBI GI	g112681
BLAST score	538
E value	4.0e-55
Match length	139
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145548
Seq. ID	LIB3168-060-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	8.0e-64
Match length	119
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145549

Seq. ID	LIB3168-060-P1-K1-G9
Method	BLASTX
NCBI GI	g4204265
BLAST score	441
E value	8.0e-44
Match length	139
% identity	65
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	145550
Seq. ID	LIB3168-060-P1-K1-H10
Method	BLASTX
NCBI GI	g112681
BLAST score	656
E value	5.0e-69
Match length	137
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145551
Seq. ID	LIB3168-060-P1-K1-H2
Method	BLASTX
NCBI GI	g112682
BLAST score	608
E value	2.0e-63
Match length	121
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145552
Seq. ID	LIB3168-060-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	404
E value	2.0e-39
Match length	112
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145553
Seq. ID	LIB3168-060-P1-K1-H5
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	2.0e-67
Match length	126
% identity	98

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145554
Seq. ID	LIB3168-060-P1-K1-H7
Method	BLASTX
NCBI GI	g1352347
BLAST score	91
E value	9.0e-33
Match length	116
% identity	74
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	145555
Seq. ID	LIB3168-060-P1-K1-H8
Method	BLASTX
NCBI GI	g112739
BLAST score	383
E value	5.0e-37
Match length	115
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145556
Seq. ID	LIB3168-061-P1-K1-A1
Method	BLASTN
NCBI GI	g4191771
BLAST score	51
E value	4.0e-20
Match length	91
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145557
Seq. ID	LIB3168-061-P1-K1-A10
Method	BLASTX
NCBI GI	g112741
BLAST score	433
E value	5.0e-43
Match length	104
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145558
Seq. ID	LIB3168-061-P1-K1-A11
Method	BLASTX
NCBI GI	g1854445
BLAST score	406
E value	9.0e-40
Match length	103
% identity	76
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	145559
Seq. ID	LIB3168-061-P1-K1-A2
Method	BLASTX
NCBI GI	g112682
BLAST score	436
E value	1.0e-43
Match length	87
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145560
Seq. ID	LIB3168-061-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	350
E value	4.0e-33
Match length	115
% identity	65
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145561
Seq. ID	LIB3168-061-P1-K1-A6
Method	BLASTX
NCBI GI	g4204299
BLAST score	72
E value	1.3e+00
Match length	120
% identity	72
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145562
Seq. ID	LIB3168-061-P1-K1-A7
Method	BLASTN
NCBI GI	g166609
BLAST score	99
E value	1.0e-48

Match length	177
% identity	88
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145563
Seq. ID	LIB3168-061-P1-K1-A9
Method	BLASTX
NCBI GI	g4538979
BLAST score	454
E value	2.0e-45
Match length	89
% identity	96
NCBI Description	(AL049487) putative protein [Arabidopsis thaliana]

Seq. No.	145564
Seq. ID	LIB3168-061-P1-K1-B11
Method	BLASTX
NCBI GI	g2129918
BLAST score	308
E value	3.0e-28
Match length	70
% identity	81
NCBI Description	BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337) BPF-1 [Petroselinum crispum] >gi_441310_emb_CAA44518_ (X62653) BPF-1 [Petroselinum crispum]

Seq. No.	145565
Seq. ID	LIB3168-061-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	191
E value	1.0e-14
Match length	86
% identity	50
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145566
Seq. ID	LIB3168-061-P1-K1-B2
Method	BLASTX
NCBI GI	g4056502
BLAST score	602
E value	9.0e-63
Match length	122
% identity	96
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	145567
Seq. ID	LIB3168-061-P1-K1-B4
Method	BLASTN
NCBI GI	g4097693
BLAST score	49
E value	4.0e-19
Match length	103
% identity	84

NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	145568
Seq. ID	LIB3168-061-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	552
E value	8.0e-57
Match length	135
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145569
Seq. ID	LIB3168-061-P1-K1-B9
Method	BLASTX
NCBI GI	g1107501
BLAST score	312
E value	7.0e-29
Match length	71
% identity	89
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	145570
Seq. ID	LIB3168-061-P1-K1-C1
Method	BLASTX
NCBI GI	g112682
BLAST score	260
E value	8.0e-23
Match length	55
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145571
Seq. ID	LIB3168-061-P1-K1-C10
Method	BLASTN
NCBI GI	g3046852
BLAST score	64
E value	7.0e-28
Match length	157
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	145572
Seq. ID	LIB3168-061-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583

BLAST score	473
E value	2.0e-47
Match length	99
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145573
Seq. ID	LIB3168-061-P1-K1-C2
Method	BLASTN
NCBI GI	g16231
BLAST score	74
E value	6.0e-34
Match length	94
% identity	95
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145574
Seq. ID	LIB3168-061-P1-K1-C3
Method	BLASTX
NCBI GI	g2078350
BLAST score	161
E value	2.0e-11
Match length	70
% identity	54
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	145575
Seq. ID	LIB3168-061-P1-K1-C4
Method	BLASTN
NCBI GI	g336274
BLAST score	91
E value	8.0e-44
Match length	204
% identity	86
NCBI Description	Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA, tRNA-Arg, and tRNA-Asn genes

Seq. No.	145576
Seq. ID	LIB3168-061-P1-K1-C6
Method	BLASTX
NCBI GI	g112681
BLAST score	148
E value	5.0e-10
Match length	33
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145577
Seq. ID	LIB3168-061-P1-K1-C8

Method	BLASTX
NCBI GI	g112739
BLAST score	421
E value	2.0e-41
Match length	115
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145578
Seq. ID	LIB3168-061-P1-K1-C9
Method	BLASTN
NCBI GI	g3449313
BLAST score	70
E value	1.0e-31
Match length	94
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	145579
Seq. ID	LIB3168-061-P1-K1-D1
Method	BLASTX
NCBI GI	g112682
BLAST score	53
E value	1.0e-14
Match length	57
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145580
Seq. ID	LIB3168-061-P1-K1-D11
Method	BLASTX
NCBI GI	g112737
BLAST score	304
E value	2.0e-28
Match length	69
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145581
Seq. ID	LIB3168-061-P1-K1-D2

Method	BLASTX
NCBI GI	g4415923
BLAST score	273
E value	1.0e-24
Match length	76
% identity	72
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	145582
Seq. ID	LIB3168-061-P1-K1-D4
Method	BLASTN
NCBI GI	g4490701
BLAST score	103
E value	7.0e-51
Match length	187
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	145583
Seq. ID	LIB3168-061-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	186
E value	2.0e-14
Match length	37
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145584
Seq. ID	LIB3168-061-P1-K1-D9
Method	BLASTN
NCBI GI	g166609
BLAST score	108
E value	8.0e-54
Match length	206
% identity	86
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145585
Seq. ID	LIB3168-061-P1-K1-E1
Method	BLASTX
NCBI GI	g4204299
BLAST score	456
E value	9.0e-46
Match length	104
% identity	89
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145586
Seq. ID	LIB3168-061-P1-K1-E12
Method	BLASTN

NCBI GI	g16231
BLAST score	40
E value	3.0e-13
Match length	77
% identity	86
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145587
Seq. ID	LIB3168-061-P1-K1-F1
Method	BLASTN
NCBI GI	g4589445
BLAST score	248
E value	1.0e-137
Match length	298
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	145588
Seq. ID	LIB3168-061-P1-K1-F10
Method	BLASTN
NCBI GI	g16236
BLAST score	73
E value	2.0e-33
Match length	91
% identity	95
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145589
Seq. ID	LIB3168-061-P1-K1-F11
Method	BLASTX
NCBI GI	g2129641
BLAST score	658
E value	3.0e-69
Match length	123
% identity	97
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	145590
Seq. ID	LIB3168-061-P1-K1-F2
Method	BLASTN
NCBI GI	g166609
BLAST score	106
E value	7.0e-53
Match length	186
% identity	87
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145591
Seq. ID	LIB3168-061-P1-K1-F6

Method	BLASTN
NCBI GI	g2264311
BLAST score	42
E value	5.0e-15
Match length	93
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145592
Seq. ID	LIB3168-061-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	559
E value	1.0e-57
Match length	121
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145593
Seq. ID	LIB3168-061-P1-K1-F9
Method	BLASTX
NCBI GI	g137465
BLAST score	455
E value	1.0e-45
Match length	97
% identity	95
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	145594
Seq. ID	LIB3168-061-P1-K1-G10
Method	BLASTX
NCBI GI	g112737
BLAST score	338
E value	8.0e-32
Match length	83
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145595
Seq. ID	LIB3168-061-P1-K1-G11
Method	BLASTN
NCBI GI	g4097693
BLAST score	48
E value	1.0e-18

Match length	102
% identity	84
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	145596
Seq. ID	LIB3168-061-P1-K1-G2
Method	BLASTN
NCBI GI	g166609
BLAST score	32
E value	8.0e-09
Match length	46
% identity	91
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145597
Seq. ID	LIB3168-061-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	203
E value	3.0e-16
Match length	63
% identity	67
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145598
Seq. ID	LIB3168-061-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	386
E value	6.0e-38
Match length	72
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145599
Seq. ID	LIB3168-061-P1-K1-G6
Method	BLASTN
NCBI GI	g4097693
BLAST score	35
E value	8.0e-11
Match length	102
% identity	81
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	145600
Seq. ID	LIB3168-061-P1-K1-H1
Method	BLASTN
NCBI GI	g16236
BLAST score	56
E value	3.0e-23

Match length	80
% identity	99
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145601
Seq. ID	LIB3168-061-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	186
E value	3.0e-14
Match length	38
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145602
Seq. ID	LIB3168-061-P1-K1-H8
Method	BLASTN
NCBI GI	g3449326
BLAST score	90
E value	4.0e-43
Match length	190
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	145603
Seq. ID	LIB3168-062-P1-K1-A1
Method	BLASTX
NCBI GI	g1628583
BLAST score	504
E value	4.0e-51
Match length	94
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145604
Seq. ID	LIB3168-062-P1-K1-A10
Method	BLASTX
NCBI GI	g112682
BLAST score	430
E value	1.0e-42
Match length	108
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145605
Seq. ID	LIB3168-062-P1-K1-A11
Method	BLASTN
NCBI GI	g2160132
BLAST score	35
E value	2.0e-10
Match length	106
% identity	51
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	145606
Seq. ID	LIB3168-062-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	423
E value	1.0e-41
Match length	143
% identity	67
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145607
Seq. ID	LIB3168-062-P1-K1-A2
Method	BLASTN
NCBI GI	g3510347
BLAST score	353
E value	0.0e+00
Match length	364
% identity	61
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	145608
Seq. ID	LIB3168-062-P1-K1-A3
Method	BLASTX
NCBI GI	g2244819
BLAST score	184
E value	1.0e-13
Match length	72
% identity	54
NCBI Description	(Z97336) germin type 2 [Arabidopsis thaliana]

Seq. No.	145609
Seq. ID	LIB3168-062-P1-K1-A4
Method	BLASTX
NCBI GI	g2961373
BLAST score	238
E value	2.0e-20
Match length	86
% identity	56
NCBI Description	(AL022141) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	145610
Seq. ID	LIB3168-062-P1-K1-A5
Method	BLASTX
NCBI GI	g112739
BLAST score	440
E value	1.0e-43
Match length	124
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145611
Seq. ID	LIB3168-062-P1-K1-A6
Method	BLASTX
NCBI GI	g112737
BLAST score	544
E value	5.0e-56
Match length	116
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145612
Seq. ID	LIB3168-062-P1-K1-A8
Method	BLASTN
NCBI GI	g4512656
BLAST score	72
E value	3.0e-32
Match length	267
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	145613
Seq. ID	LIB3168-062-P1-K1-A9
Method	BLASTN
NCBI GI	g2264311
BLAST score	52
E value	8.0e-21
Match length	103
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145614
Seq. ID	LIB3168-062-P1-K1-B1
Method	BLASTX

NCBI GI g1628583
BLAST score 409
E value 6.0e-40
Match length 117
% identity 74
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 145615
Seq. ID LIB3168-062-P1-K1-B10
Method BLASTX
NCBI GI g112681
BLAST score 47
E value 2.0e-56
Match length 127
% identity 91
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 145616
Seq. ID LIB3168-062-P1-K1-B11
Method BLASTX
NCBI GI g1628583
BLAST score 188
E value 1.0e-14
Match length 36
% identity 94
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 145617
Seq. ID LIB3168-062-P1-K1-B12
Method BLASTX
NCBI GI g2586125
BLAST score 330
E value 5.0e-31
Match length 93
% identity 73
NCBI Description (U89512) b-keto acyl reductase [Arabidopsis thaliana]

Seq. No. 145618
Seq. ID LIB3168-062-P1-K1-B2
Method BLASTN
NCBI GI g1628582
BLAST score 131
E value 2.0e-67
Match length 178
% identity 55
NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No. 145619

Seq. ID	LIB3168-062-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	525
E value	1.0e-53
Match length	119
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145620
Seq. ID	LIB3168-062-P1-K1-B4
Method	BLASTN
NCBI GI	g3650026
BLAST score	157
E value	5.0e-83
Match length	273
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145621
Seq. ID	LIB3168-062-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	447
E value	1.0e-44
Match length	107
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145622
Seq. ID	LIB3168-062-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	535
E value	7.0e-55
Match length	112
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145623
Seq. ID	LIB3168-062-P1-K1-B8
Method	BLASTN
NCBI GI	g1354465
BLAST score	59
E value	1.0e-24
Match length	185
% identity	83
NCBI Description	Arabidopsis thaliana U1 snRNP 70K truncated protein mRNA,

long alternatively spliced transcript, complete cds

Seq. No.	145624
Seq. ID	LIB3168-062-P1-K1-C1
Method	BLASTX
NCBI GI	g112681
BLAST score	587
E value	7.0e-61
Match length	142
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145625
Seq. ID	LIB3168-062-P1-K1-C10
Method	BLASTX
NCBI GI	g112737
BLAST score	479
E value	2.0e-48
Match length	106
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145626
Seq. ID	LIB3168-062-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	522
E value	3.0e-53
Match length	118
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145627
Seq. ID	LIB3168-062-P1-K1-C4
Method	BLASTN
NCBI GI	g4580732
BLAST score	41
E value	6.0e-14
Match length	112
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F5J5, complete sequence

Seq. No.	145628
Seq. ID	LIB3168-062-P1-K1-C5

Method	BLASTN
NCBI GI	g2956689
BLAST score	46
E value	7.0e-17
Match length	173
% identity	77
NCBI Description	Arabidopsis thaliana mRNA for PSBY (Ycf32-related chloroplast thylakoid membrane proteins)

Seq. No.	145629
Seq. ID	LIB3168-062-P1-K1-C7
Method	BLASTN
NCBI GI	g3869066
BLAST score	213
E value	1.0e-116
Match length	328
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	145630
Seq. ID	LIB3168-062-P1-K1-C9
Method	BLASTN
NCBI GI	g2842474
BLAST score	81
E value	1.0e-37
Match length	181
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145631
Seq. ID	LIB3168-062-P1-K1-D1
Method	BLASTN
NCBI GI	g2842474
BLAST score	153
E value	2.0e-80
Match length	387
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145632
Seq. ID	LIB3168-062-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	564
E value	3.0e-58
Match length	144
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145633
Seq. ID	LIB3168-062-P1-K1-D11
Method	BLASTN

NCBI GI	g16231
BLAST score	58
E value	2.0e-24
Match length	111
% identity	85
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145634
Seq. ID	LIB3168-062-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	488
E value	3.0e-49
Match length	92
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145635
Seq. ID	LIB3168-062-P1-K1-D2
Method	BLASTX
NCBI GI	g113617
BLAST score	302
E value	2.0e-27
Match length	60
% identity	98
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68199_pir__ADMU fructose-bisphosphate aldolase (EC 4.1.2.13) - Arabidopsis thaliana >gi_16284_emb_CAA37226_ (X53058) fructose 1,6-diphosphate aldolase [Arabidopsis thaliana]

Seq. No.	145636
Seq. ID	LIB3168-062-P1-K1-D3
Method	BLASTN
NCBI GI	g3449331
BLAST score	296
E value	1.0e-166
Match length	308
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	145637
Seq. ID	LIB3168-062-P1-K1-D4
Method	BLASTX
NCBI GI	g3738315
BLAST score	387
E value	2.0e-37
Match length	105
% identity	60
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 145638

Seq. ID	LIB3168-062-P1-K1-D5
Method	BLASTX
NCBI GI	g4454010
BLAST score	372
E value	8.0e-36
Match length	89
% identity	72
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	145639
Seq. ID	LIB3168-062-P1-K1-D6
Method	BLASTX
NCBI GI	g112737
BLAST score	526
E value	7.0e-54
Match length	116
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145640
Seq. ID	LIB3168-062-P1-K1-D7
Method	BLASTN
NCBI GI	g2842474
BLAST score	80
E value	6.0e-37
Match length	284
% identity	69
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145641
Seq. ID	LIB3168-062-P1-K1-D8
Method	BLASTX
NCBI GI	g112739
BLAST score	421
E value	2.0e-41
Match length	134
% identity	63
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145642
Seq. ID	LIB3168-062-P1-K1-E1
Method	BLASTX
NCBI GI	g112682
BLAST score	572

E value	3.0e-59
Match length	126
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145643
Seq. ID	LIB3168-062-P1-K1-E11
Method	BLASTN
NCBI GI	g1628582
BLAST score	87
E value	3.0e-41
Match length	288
% identity	84
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145644
Seq. ID	LIB3168-062-P1-K1-E12
Method	BLASTX
NCBI GI	g119350
BLAST score	570
E value	7.0e-59
Match length	120
% identity	92
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	145645
Seq. ID	LIB3168-062-P1-K1-E2
Method	BLASTX
NCBI GI	g112739
BLAST score	468
E value	7.0e-47
Match length	133
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145646
Seq. ID	LIB3168-062-P1-K1-E5
Method	BLASTX
NCBI GI	g2129642

BLAST score	672
E value	8.0e-71
Match length	132
% identity	93
NCBI Description	major latex protein type 3 - Arabidopsis thaliana >gi_1107495_emb_CAA63027_ (X91961) major latex protein type3 [Arabidopsis thaliana]

Seq. No.	145647
Seq. ID	LIB3168-062-P1-K1-E6
Method	BLASTN
NCBI GI	g4314374
BLAST score	111
E value	5.0e-56
Match length	138
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145648
Seq. ID	LIB3168-062-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	527
E value	7.0e-54
Match length	102
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145649
Seq. ID	LIB3168-062-P1-K1-E8
Method	BLASTN
NCBI GI	g1628582
BLAST score	98
E value	6.0e-48
Match length	172
% identity	86
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145650
Seq. ID	LIB3168-062-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	533
E value	1.0e-54
Match length	115
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145651
Seq. ID	LIB3168-062-P1-K1-F1
Method	BLASTX
NCBI GI	g4204299
BLAST score	383
E value	2.0e-37
Match length	78
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145652
Seq. ID	LIB3168-062-P1-K1-F10
Method	BLASTX
NCBI GI	g2129659
BLAST score	292
E value	2.0e-26
Match length	92
% identity	63
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145653
Seq. ID	LIB3168-062-P1-K1-F11
Method	BLASTN
NCBI GI	g2264311
BLAST score	52
E value	1.0e-20
Match length	120
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145654
Seq. ID	LIB3168-062-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	506
E value	3.0e-51
Match length	101
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145655
Seq. ID	LIB3168-062-P1-K1-F3
Method	BLASTN
NCBI GI	g2842474
BLAST score	66
E value	8.0e-29
Match length	110
% identity	59
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145656
Seq. ID	LIB3168-062-P1-K1-F4
Method	BLASTN
NCBI GI	g2264311
BLAST score	77
E value	3.0e-35
Match length	266
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145657
Seq. ID	LIB3168-062-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	489
E value	2.0e-49
Match length	97
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145658
Seq. ID	LIB3168-062-P1-K1-F7
Method	BLASTX
NCBI GI	g112681
BLAST score	512
E value	4.0e-52
Match length	117
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145659
Seq. ID	LIB3168-062-P1-K1-G10
Method	BLASTN
NCBI GI	g4079614
BLAST score	60
E value	3.0e-25
Match length	116
% identity	84
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145660
Seq. ID	LIB3168-062-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	552
E value	9.0e-57
Match length	119
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145661
Seq. ID	LIB3168-062-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	459
E value	7.0e-46
Match length	120
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145662
Seq. ID	LIB3168-062-P1-K1-G5
Method	BLASTN
NCBI GI	g1628582
BLAST score	53
E value	6.0e-21
Match length	264
% identity	78
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145663
Seq. ID	LIB3168-062-P1-K1-G6
Method	BLASTX
NCBI GI	g112741
BLAST score	523
E value	2.0e-53
Match length	119
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145664
Seq. ID	LIB3168-062-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	48
E value	1.0e-16
Match length	74
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145665
Seq. ID	LIB3168-062-P1-K1-G8
Method	BLASTN

NCBI GI	g2842474
BLAST score	72
E value	1.0e-32
Match length	175
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145666
Seq. ID	LIB3168-062-P1-K1-G9
Method	BLASTN
NCBI GI	g4757414
BLAST score	323
E value	0.0e+00
Match length	330
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	145667
Seq. ID	LIB3168-062-P1-K1-H1
Method	BLASTX
NCBI GI	g2160151
BLAST score	436
E value	2.0e-43
Match length	90
% identity	96
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	145668
Seq. ID	LIB3168-062-P1-K1-H11
Method	BLASTX
NCBI GI	g112681
BLAST score	526
E value	6.0e-54
Match length	104
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145669
Seq. ID	LIB3168-062-P1-K1-H3
Method	BLASTX
NCBI GI	g1076366
BLAST score	585
E value	8.0e-61
Match length	111
% identity	97
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase

[Arabidopsis thaliana]

Seq. No.	145670
Seq. ID	LIB3168-062-P1-K1-H5
Method	BLASTN
NCBI GI	g4510392
BLAST score	73
E value	5.0e-33
Match length	254
% identity	78
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No.	145671
Seq. ID	LIB3168-062-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	375
E value	3.0e-36
Match length	114
% identity	69
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145672
Seq. ID	LIB3168-062-P1-K1-H7
Method	BLASTX
NCBI GI	g112737
BLAST score	242
E value	1.0e-20
Match length	82
% identity	60
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145673
Seq. ID	LIB3168-062-P1-K1-H8
Method	BLASTN
NCBI GI	g987013
BLAST score	47
E value	4.0e-18
Match length	47
% identity	100
NCBI Description	A.thaliana mRNA for oleosin (isoform; 841 bp) >gi_987015_emb_Z54165_ATOLEOSN3 A.thaliana mRNA for oleosin (isoform; 841 bp)

Seq. No.	145674
Seq. ID	LIB3168-064-P1-K1-A1
Method	BLASTX
NCBI GI	g112681

BLAST score	322
E value	5.0e-30
Match length	103
% identity	68
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145675
Seq. ID	LIB3168-064-P1-K1-A11
Method	BLASTX
NCBI GI	g112737
BLAST score	584
E value	2.0e-60
Match length	142
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145676
Seq. ID	LIB3168-064-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	515
E value	2.0e-52
Match length	137
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145677
Seq. ID	LIB3168-064-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	612
E value	8.0e-64
Match length	140
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145678
Seq. ID	LIB3168-064-P1-K1-A6
Method	BLASTN
NCBI GI	g1628582
BLAST score	94

E value	2.0e-45
Match length	230
% identity	60
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145679
Seq. ID	LIB3168-064-P1-K1-A9
Method	BLASTX
NCBI GI	g2119840
BLAST score	137
E value	1.0e-08
Match length	54
% identity	57
NCBI Description	photosystem I protein A2 - garden snapdragon chloroplast

Seq. No.	145680
Seq. ID	LIB3168-064-P1-K1-B1
Method	BLASTN
NCBI GI	g2264311
BLAST score	56
E value	7.0e-23
Match length	147
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145681
Seq. ID	LIB3168-064-P1-K1-B10
Method	BLASTN
NCBI GI	g2264311
BLAST score	51
E value	5.0e-20
Match length	121
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145682
Seq. ID	LIB3168-064-P1-K1-B11
Method	BLASTN
NCBI GI	g4097693
BLAST score	54
E value	1.0e-21
Match length	108
% identity	84
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	145683
Seq. ID	LIB3168-064-P1-K1-B2
Method	BLASTN
NCBI GI	g2605713
BLAST score	40
E value	1.0e-13
Match length	77
% identity	84

NCBI Description	Arabidopsis thaliana beta-tonoplast intrinsic protein (beta-TIP) mRNA, complete cds
Seq. No.	145684
Seq. ID	LIB3168-064-P1-K1-B4
Method	BLASTN
NCBI GI	g4757414
BLAST score	324
E value	0.0e+00
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence
Seq. No.	145685
Seq. ID	LIB3168-064-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	488
E value	2.0e-49
Match length	92
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145686
Seq. ID	LIB3168-064-P1-K1-B7
Method	BLASTN
NCBI GI	g16231
BLAST score	57
E value	2.0e-23
Match length	140
% identity	82
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4
Seq. No.	145687
Seq. ID	LIB3168-064-P1-K1-B9
Method	BLASTX
NCBI GI	g1107501
BLAST score	328
E value	1.0e-30
Match length	99
% identity	71
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]
Seq. No.	145688
Seq. ID	LIB3168-064-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	190
E value	6.0e-15

Match length	35
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145689
Seq. ID	LIB3168-064-P1-K1-C10
Method	BLASTN
NCBI GI	g1628582
BLAST score	52
E value	6.0e-21
Match length	103
% identity	84
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145690
Seq. ID	LIB3168-064-P1-K1-C11
Method	BLASTX
NCBI GI	g112737
BLAST score	547
E value	4.0e-56
Match length	139
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145691
Seq. ID	LIB3168-064-P1-K1-C12
Method	BLASTX
NCBI GI	g2781394
BLAST score	477
E value	5.0e-48
Match length	96
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	145692
Seq. ID	LIB3168-064-P1-K1-C2
Method	BLASTX
NCBI GI	g112682
BLAST score	707
E value	6.0e-75
Match length	144
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145693
Seq. ID	LIB3168-064-P1-K1-C3
Method	BLASTX
NCBI GI	g132074
BLAST score	534
E value	7.0e-55
Match length	103
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	145694
Seq. ID	LIB3168-064-P1-K1-C4
Method	BLASTN
NCBI GI	g166609
BLAST score	130
E value	5.0e-67
Match length	249
% identity	86
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145695
Seq. ID	LIB3168-064-P1-K1-C5
Method	BLASTN
NCBI GI	g3366536
BLAST score	50
E value	3.0e-19
Match length	184
% identity	83
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20, complete sequence [Arabidopsis thaliana]

Seq. No.	145696
Seq. ID	LIB3168-064-P1-K1-C7
Method	BLASTN
NCBI GI	g4454587
BLAST score	156
E value	2.0e-82
Match length	191
% identity	96
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	145697
Seq. ID	LIB3168-064-P1-K1-C8
Method	BLASTN
NCBI GI	g166609
BLAST score	124
E value	2.0e-63
Match length	269
% identity	85
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	145698
Seq. ID	LIB3168-064-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	477
E value	5.0e-48
Match length	98
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145699
Seq. ID	LIB3168-064-P1-K1-D1
Method	BLASTN
NCBI GI	g2264311
BLAST score	177
E value	4.0e-95
Match length	228
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	145700
Seq. ID	LIB3168-064-P1-K1-D10
Method	BLASTN
NCBI GI	g3047100
BLAST score	280
E value	1.0e-156
Match length	355
% identity	94
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	145701
Seq. ID	LIB3168-064-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	62
E value	2.0e-35
Match length	128
% identity	67
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145702
Seq. ID	LIB3168-064-P1-K1-D12
Method	BLASTX
NCBI GI	g461841
BLAST score	163
E value	2.0e-11
Match length	73
% identity	53
NCBI Description	CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN)

Seq. No.	145703

Seq. ID	LIB3168-064-P1-K1-D2
Method	BLASTX
NCBI GI	g112741
BLAST score	558
E value	1.0e-57
Match length	103
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145704
Seq. ID	LIB3168-064-P1-K1-D3
Method	BLASTN
NCBI GI	g4263774
BLAST score	78
E value	6.0e-36
Match length	234
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145705
Seq. ID	LIB3168-064-P1-K1-D4
Method	BLASTN
NCBI GI	g3449322
BLAST score	135
E value	5.0e-70
Match length	171
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	145706
Seq. ID	LIB3168-064-P1-K1-D5
Method	BLASTX
NCBI GI	g1170203
BLAST score	417
E value	5.0e-41
Match length	114
% identity	74
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	145707
Seq. ID	LIB3168-064-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	510
E value	6.0e-52
Match length	101
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145708
Seq. ID	LIB3168-064-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	446
E value	1.0e-44
Match length	93
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145709
Seq. ID	LIB3168-064-P1-K1-D9
Method	BLASTN
NCBI GI	g4519195
BLAST score	68
E value	9.0e-30
Match length	93
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	145710
Seq. ID	LIB3168-064-P1-K1-E10
Method	BLASTN
NCBI GI	g2564050
BLAST score	222
E value	1.0e-121
Match length	343
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	145711
Seq. ID	LIB3168-064-P1-K1-E11
Method	BLASTX
NCBI GI	g112682
BLAST score	590
E value	3.0e-61
Match length	126
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145712
Seq. ID	LIB3168-064-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	679
E value	1.0e-71

Match length	138
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145713
Seq. ID	LIB3168-064-P1-K1-E2
Method	BLASTN
NCBI GI	g4159699
BLAST score	345
E value	0.0e+00
Match length	353
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence

Seq. No.	145714
Seq. ID	LIB3168-064-P1-K1-E3
Method	BLASTN
NCBI GI	g1628582
BLAST score	99
E value	1.0e-48
Match length	174
% identity	86
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145715
Seq. ID	LIB3168-064-P1-K1-E4
Method	BLASTN
NCBI GI	g16231
BLAST score	56
E value	8.0e-23
Match length	107
% identity	84
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145716
Seq. ID	LIB3168-064-P1-K1-E5
Method	BLASTN
NCBI GI	g1628582
BLAST score	110
E value	6.0e-55
Match length	272
% identity	59
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145717
Seq. ID	LIB3168-064-P1-K1-E6
Method	BLASTN
NCBI GI	g16231

BLAST score	87
E value	2.0e-41
Match length	241
% identity	81
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145718
Seq. ID	LIB3168-064-P1-K1-E7
Method	BLASTN
NCBI GI	g2264303
BLAST score	196
E value	1.0e-106
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	145719
Seq. ID	LIB3168-064-P1-K1-E9
Method	BLASTN
NCBI GI	g395203
BLAST score	137
E value	5.0e-71
Match length	246
% identity	63
NCBI Description	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

Seq. No.	145720
Seq. ID	LIB3168-064-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	524
E value	1.0e-53
Match length	119
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145721
Seq. ID	LIB3168-064-P1-K1-F11
Method	BLASTX
NCBI GI	g112681
BLAST score	209
E value	6.0e-17
Match length	78
% identity	62
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145722
Seq. ID	LIB3168-064-P1-K1-F12

Method	BLASTX
NCBI GI	g1628583
BLAST score	271
E value	7.0e-24
Match length	60
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145723
Seq. ID	LIB3168-064-P1-K1-F9
Method	BLASTX
NCBI GI	g2497886
BLAST score	287
E value	9.0e-26
Match length	53
% identity	98
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	145724
Seq. ID	LIB3168-064-P1-K1-G10
Method	BLASTX
NCBI GI	g131143
BLAST score	583
E value	2.0e-60
Match length	153
% identity	77
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]

Seq. No.	145725
Seq. ID	LIB3168-064-P1-K1-G11
Method	BLASTX
NCBI GI	g2851508
BLAST score	481
E value	1.0e-48
Match length	101
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	145726
Seq. ID	LIB3168-064-P1-K1-G12
Method	BLASTN
NCBI GI	g4199934
BLAST score	107

E value	2.0e-53
Match length	158
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	145727
Seq. ID	LIB3168-064-P1-K1-G2
Method	BLASTN
NCBI GI	g4584519
BLAST score	35
E value	1.0e-10
Match length	76
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

Seq. No.	145728
Seq. ID	LIB3168-064-P1-K1-G5
Method	BLASTX
NCBI GI	g112682
BLAST score	360
E value	2.0e-34
Match length	92
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145729
Seq. ID	LIB3168-064-P1-K1-G6
Method	BLASTN
NCBI GI	g16231
BLAST score	85
E value	4.0e-40
Match length	160
% identity	92
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145730
Seq. ID	LIB3168-064-P1-K1-G7
Method	BLASTX
NCBI GI	g2129659
BLAST score	166
E value	4.0e-12
Match length	36
% identity	89
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145731
Seq. ID	LIB3168-064-P1-K1-G8
Method	BLASTN

NCBI GI	g16231
BLAST score	51
E value	5.0e-20
Match length	107
% identity	84
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145732
Seq. ID	LIB3168-064-P1-K1-G9
Method	BLASTN
NCBI GI	g395203
BLAST score	116
E value	2.0e-58
Match length	276
% identity	83
NCBI Description	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

Seq. No.	145733
Seq. ID	LIB3168-064-P1-K1-H1
Method	BLASTX
NCBI GI	g112741
BLAST score	187
E value	4.0e-14
Match length	68
% identity	60
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145734
Seq. ID	LIB3168-064-P1-K1-H11
Method	BLASTX
NCBI GI	g112737
BLAST score	543
E value	9.0e-56
Match length	139
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145735
Seq. ID	LIB3168-064-P1-K1-H12
Method	BLASTX
NCBI GI	g112737
BLAST score	281
E value	5.0e-25

Match length	123
% identity	50
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145736
Seq. ID	LIB3168-064-P1-K1-H3
Method	BLASTN
NCBI GI	g2842474
BLAST score	111
E value	1.0e-55
Match length	212
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145737
Seq. ID	LIB3168-064-P1-K1-H4
Method	BLASTN
NCBI GI	g4220510
BLAST score	215
E value	1.0e-117
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	145738
Seq. ID	LIB3168-064-P1-K1-H5
Method	BLASTX
NCBI GI	g112743
BLAST score	611
E value	8.0e-64
Match length	116
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145739
Seq. ID	LIB3168-064-P1-K1-H6
Method	BLASTN
NCBI GI	g2262097
BLAST score	253
E value	1.0e-140
Match length	253
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic

sequence, complete sequence

Seq. No.	145740
Seq. ID	LIB3168-064-P1-K1-H8
Method	BLASTX
NCBI GI	g3168840
BLAST score	98
E value	1.0e-03
Match length	61
% identity	80
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	145741
Seq. ID	LIB3168-065-P1-K1-A10
Method	BLASTN
NCBI GI	g3461834
BLAST score	319
E value	1.0e-179
Match length	327
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145742
Seq. ID	LIB3168-065-P1-K1-A11
Method	BLASTX
NCBI GI	g112741
BLAST score	720
E value	2.0e-76
Match length	135
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145743
Seq. ID	LIB3168-065-P1-K1-A12
Method	BLASTN
NCBI GI	g4371278
BLAST score	324
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145744
Seq. ID	LIB3168-065-P1-K1-A2
Method	BLASTN
NCBI GI	g4757407
BLAST score	186
E value	1.0e-100
Match length	362

% identity	62
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	145745
Seq. ID	LIB3168-065-P1-K1-A3
Method	BLASTN
NCBI GI	g3869069
BLAST score	395
E value	0.0e+00
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	145746
Seq. ID	LIB3168-065-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	647
E value	5.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145747
Seq. ID	LIB3168-065-P1-K1-A5
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	137
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145748
Seq. ID	LIB3168-065-P1-K1-A6
Method	BLASTX
NCBI GI	g2129657
BLAST score	398
E value	1.0e-38
Match length	109
% identity	77
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145749

Seq. ID	LIB3168-065-P1-K1-A7
Method	BLASTN
NCBI GI	g4580386
BLAST score	335
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	145750
Seq. ID	LIB3168-065-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	432
E value	9.0e-43
Match length	118
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145751
Seq. ID	LIB3168-065-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	705
E value	1.0e-74
Match length	143
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145752
Seq. ID	LIB3168-065-P1-K1-B10
Method	BLASTN
NCBI GI	g3241927
BLAST score	333
E value	0.0e+00
Match length	394
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	145753
Seq. ID	LIB3168-065-P1-K1-B11
Method	BLASTX
NCBI GI	g1170767
BLAST score	273
E value	4.0e-24
Match length	91
% identity	60
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi_626074_pir__S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi_406051 (U02280) Let1 [Schizosaccharomyces pombe]

	>gi_4106689_emb_CAA22628_ (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]
Seq. No.	145754
Seq. ID	LIB3168-065-P1-K1-B2
Method	BLASTX
NCBI GI	g4567260
BLAST score	263
E value	2.0e-23
Match length	52
% identity	98
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]
Seq. No.	145755
Seq. ID	LIB3168-065-P1-K1-B3
Method	BLASTX
NCBI GI	g21913
BLAST score	193
E value	1.0e-14
Match length	79
% identity	46
NCBI Description	(X62626) vicilin [Theobroma cacao]
Seq. No.	145756
Seq. ID	LIB3168-065-P1-K1-B4
Method	BLASTN
NCBI GI	g4159708
BLAST score	397
E value	0.0e+00
Match length	433
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence
Seq. No.	145757
Seq. ID	LIB3168-065-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	589
E value	4.0e-61
Match length	146
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145758
Seq. ID	LIB3168-065-P1-K1-B6
Method	BLASTX
NCBI GI	g112682
BLAST score	690
E value	6.0e-73
Match length	133

% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145759
Seq. ID	LIB3168-065-P1-K1-B7
Method	BLASTN
NCBI GI	g2244747
BLAST score	234
E value	1.0e-129
Match length	234
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	145760
Seq. ID	LIB3168-065-P1-K1-B8
Method	BLASTN
NCBI GI	g4262221
BLAST score	39
E value	2.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145761
Seq. ID	LIB3168-065-P1-K1-B9
Method	BLASTX
NCBI GI	g4056502
BLAST score	595
E value	7.0e-62
Match length	117
% identity	100
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	145762
Seq. ID	LIB3168-065-P1-K1-C1
Method	BLASTX
NCBI GI	g99688
BLAST score	345
E value	1.0e-32
Match length	69
% identity	99
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	145763
Seq. ID	LIB3168-065-P1-K1-C10
Method	BLASTN
NCBI GI	g3599967
BLAST score	359
E value	0.0e+00

Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

Seq. No.	145764
Seq. ID	LIB3168-065-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	585
E value	1.0e-60
Match length	111
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145765
Seq. ID	LIB3168-065-P1-K1-C12
Method	BLASTX
NCBI GI	g4204298
BLAST score	542
E value	1.0e-55
Match length	138
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145766
Seq. ID	LIB3168-065-P1-K1-C2
Method	BLASTX
NCBI GI	g4678322
BLAST score	454
E value	2.0e-45
Match length	124
% identity	79
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	145767
Seq. ID	LIB3168-065-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64
Match length	127
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145768
Seq. ID	LIB3168-065-P1-K1-C4
Method	BLASTX
NCBI GI	g112741
BLAST score	725
E value	4.0e-77
Match length	135
% identity	100

NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	145769
Seq. ID	LIB3168-065-P1-K1-C5
Method	BLASTN
NCBI GI	g3985950
BLAST score	437
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.	145770
Seq. ID	LIB3168-065-P1-K1-C6
Method	BLASTX
NCBI GI	g112682
BLAST score	613
E value	6.0e-64
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145771
Seq. ID	LIB3168-065-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	631
E value	4.0e-66
Match length	136
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145772
Seq. ID	LIB3168-065-P1-K1-C8
Method	BLASTN
NCBI GI	g4512656
BLAST score	224
E value	1.0e-123
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence
Seq. No.	145773

Seq. ID	LIB3168-065-P1-K1-C9
Method	BLASTX
NCBI GI	g112681
BLAST score	614
E value	5.0e-64
Match length	124
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145774
Seq. ID	LIB3168-065-P1-K1-D1
Method	BLASTX
NCBI GI	g112681
BLAST score	597
E value	4.0e-62
Match length	139
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145775
Seq. ID	LIB3168-065-P1-K1-D10
Method	BLASTX
NCBI GI	g112682
BLAST score	621
E value	7.0e-65
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145776
Seq. ID	LIB3168-065-P1-K1-D11
Method	BLASTX
NCBI GI	g112741
BLAST score	613
E value	6.0e-64
Match length	133
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145777
Seq. ID	LIB3168-065-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145778
Seq. ID	LIB3168-065-P1-K1-D2
Method	BLASTX
NCBI GI	g4539452
BLAST score	449
E value	1.0e-44
Match length	138
% identity	57
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	145779
Seq. ID	LIB3168-065-P1-K1-D3
Method	BLASTX
NCBI GI	g112682
BLAST score	694
E value	2.0e-73
Match length	144
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145780
Seq. ID	LIB3168-065-P1-K1-D4
Method	BLASTN
NCBI GI	g4510338
BLAST score	303
E value	1.0e-170
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	145781
Seq. ID	LIB3168-065-P1-K1-D5
Method	BLASTN
NCBI GI	g3695372
BLAST score	425
E value	0.0e+00
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana BAC F1104

Seq. No.	145782
Seq. ID	LIB3168-065-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	403
E value	2.0e-39
Match length	114
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145783
Seq. ID	LIB3168-065-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	2.0e-60
Match length	143
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145784
Seq. ID	LIB3168-065-P1-K1-D8
Method	BLASTX
NCBI GI	g2129659
BLAST score	453
E value	3.0e-45
Match length	138
% identity	72
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145785
Seq. ID	LIB3168-065-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	556
E value	4.0e-64
Match length	127
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145786
Seq. ID	LIB3168-065-P1-K1-E1
Method	BLASTX
NCBI GI	g112741
BLAST score	738
E value	1.0e-78
Match length	142
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145787
Seq. ID	LIB3168-065-P1-K1-E10
Method	BLASTX
NCBI GI	g112681
BLAST score	350
E value	3.0e-33
Match length	121
% identity	61
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145788
Seq. ID	LIB3168-065-P1-K1-E11
Method	BLASTX
NCBI GI	g2429467
BLAST score	154
E value	4.0e-10
Match length	83
% identity	36
NCBI Description	(AF025462) contains similarity to glutathione S transferases [Caenorhabditis elegans]

Seq. No.	145789
Seq. ID	LIB3168-065-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145790
Seq. ID	LIB3168-065-P1-K1-E2
Method	BLASTX
NCBI GI	g4455329
BLAST score	326
E value	3.0e-30
Match length	104
% identity	68
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	145791
Seq. ID	LIB3168-065-P1-K1-E3

Method	BLASTN
NCBI GI	g4589423
BLAST score	220
E value	1.0e-120
Match length	374
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence

Seq. No.	145792
Seq. ID	LIB3168-065-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145793
Seq. ID	LIB3168-065-P1-K1-E5
Method	BLASTN
NCBI GI	g2088638
BLAST score	294
E value	1.0e-164
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145794
Seq. ID	LIB3168-065-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145795
Seq. ID	LIB3168-065-P1-K1-E7
Method	BLASTX
NCBI GI	g112737
BLAST score	551
E value	1.0e-56
Match length	136
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145796
Seq. ID	LIB3168-065-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	610
E value	1.0e-63
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145797
Seq. ID	LIB3168-065-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	687
E value	1.0e-72
Match length	141
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145798
Seq. ID	LIB3168-065-P1-K1-F11
Method	BLASTX
NCBI GI	g112681
BLAST score	678
E value	1.0e-71
Match length	136
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145799
Seq. ID	LIB3168-065-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	717
E value	4.0e-76
Match length	139
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145800
Seq. ID	LIB3168-065-P1-K1-F2

Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145801
Seq. ID	LIB3168-065-P1-K1-F3
Method	BLASTX
NCBI GI	g226996
BLAST score	657
E value	4.0e-69
Match length	125
% identity	99
NCBI Description	petB2 gene [Pisum sativum]

Seq. No.	145802
Seq. ID	LIB3168-065-P1-K1-F4
Method	BLASTN
NCBI GI	g3150006
BLAST score	34
E value	1.0e-09
Match length	42
% identity	48
NCBI Description	CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No.	145803
Seq. ID	LIB3168-065-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145804
Seq. ID	LIB3168-065-P1-K1-F6
Method	BLASTX
NCBI GI	g1710530
BLAST score	747
E value	1.0e-79
Match length	139
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	145805

Seq. ID	LIB3168-065-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	1.0e-60
Match length	117
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145806
Seq. ID	LIB3168-065-P1-K1-F9
Method	BLASTX
NCBI GI	g112681
BLAST score	474
E value	9.0e-48
Match length	103
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145807
Seq. ID	LIB3168-065-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	523
E value	2.0e-53
Match length	110
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145808
Seq. ID	LIB3168-065-P1-K1-G11
Method	BLASTX
NCBI GI	g3461845
BLAST score	176
E value	1.0e-12
Match length	54
% identity	59
NCBI Description	(AC005315) hypothetical protein [Arabidopsis thaliana]

Seq. No.	145809
Seq. ID	LIB3168-065-P1-K1-G12
Method	BLASTN
NCBI GI	g2687440
BLAST score	61
E value	6.0e-26
Match length	93
% identity	91

NCBI Description	Tellima grandiflora large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	145810
Seq. ID	LIB3168-065-P1-K1-G2
Method	BLASTN
NCBI GI	g2264305
BLAST score	193
E value	1.0e-104
Match length	233
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	145811
Seq. ID	LIB3168-065-P1-K1-G3
Method	BLASTX
NCBI GI	g1402914
BLAST score	630
E value	6.0e-66
Match length	125
% identity	100
NCBI Description	(X98318) peroxidase [Arabidopsis thaliana]

Seq. No.	145812
Seq. ID	LIB3168-065-P1-K1-G4
Method	BLASTX
NCBI GI	g112741
BLAST score	732
E value	7.0e-78
Match length	138
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145813
Seq. ID	LIB3168-065-P1-K1-G6
Method	BLASTX
NCBI GI	g2961377
BLAST score	636
E value	1.0e-66
Match length	124
% identity	24
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	145814
Seq. ID	LIB3168-065-P1-K1-G8
Method	BLASTX
NCBI GI	g4539452
BLAST score	391
E value	6.0e-38

Match length	130
% identity	55
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	145815
Seq. ID	LIB3168-065-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	185
E value	4.0e-63
Match length	138
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145816
Seq. ID	LIB3168-065-P1-K1-H1
Method	BLASTX
NCBI GI	g1109699
BLAST score	594
E value	1.0e-61
Match length	115
% identity	99
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	145817
Seq. ID	LIB3168-065-P1-K1-H11
Method	BLASTX
NCBI GI	g2146728
BLAST score	709
E value	3.0e-75
Match length	146
% identity	92
NCBI Description	cyclin cyc1b - Arabidopsis thaliana >gi_1360646 (L27223) cyclin [Arabidopsis thaliana]

Seq. No.	145818
Seq. ID	LIB3168-065-P1-K1-H3
Method	BLASTX
NCBI GI	g112737
BLAST score	423
E value	9.0e-42
Match length	116
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145819

Seq. ID	LIB3168-065-P1-K1-H4
Method	BLASTN
NCBI GI	g4191771
BLAST score	71
E value	6.0e-32
Match length	110
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145820
Seq. ID	LIB3168-065-P1-K1-H6
Method	BLASTX
NCBI GI	g112682
BLAST score	609
E value	2.0e-63
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145821
Seq. ID	LIB3168-065-P1-K1-H7
Method	BLASTX
NCBI GI	g3452263
BLAST score	528
E value	4.0e-54
Match length	109
% identity	95
NCBI Description	(AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis thaliana]

Seq. No.	145822
Seq. ID	LIB3168-065-P1-K1-H9
Method	BLASTN
NCBI GI	g4678291
BLAST score	95
E value	1.0e-46
Match length	95
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	145823
Seq. ID	LIB3168-066-P1-K1-A1
Method	BLASTX
NCBI GI	g1628583
BLAST score	472
E value	1.0e-47
Match length	101
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145824
Seq. ID	LIB3168-066-P1-K1-A10
Method	BLASTN
NCBI GI	g3513725
BLAST score	246
E value	1.0e-136
Match length	298
% identity	78
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	145825
Seq. ID	LIB3168-066-P1-K1-A11
Method	BLASTN
NCBI GI	g2842474
BLAST score	273
E value	1.0e-152
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145826
Seq. ID	LIB3168-066-P1-K1-A2
Method	BLASTX
NCBI GI	g112681
BLAST score	464
E value	1.0e-46
Match length	101
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145827
Seq. ID	LIB3168-066-P1-K1-A3
Method	BLASTN
NCBI GI	g1628582
BLAST score	122
E value	4.0e-62
Match length	233
% identity	64
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	145828
Seq. ID	LIB3168-066-P1-K1-A4
Method	BLASTX
NCBI GI	g112681
BLAST score	618
E value	2.0e-64
Match length	142
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

	>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145829
Seq. ID	LIB3168-066-P1-K1-A5
Method	BLASTX
NCBI GI	g2583125
BLAST score	332
E value	5.0e-31
Match length	102
% identity	66
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]
Seq. No.	145830
Seq. ID	LIB3168-066-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	145831
Seq. ID	LIB3168-066-P1-K1-A7
Method	BLASTN
NCBI GI	g2335089
BLAST score	383
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	145832
Seq. ID	LIB3168-066-P1-K1-A8
Method	BLASTN
NCBI GI	g4757411
BLAST score	299
E value	1.0e-167
Match length	347
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence
Seq. No.	145833
Seq. ID	LIB3168-066-P1-K1-B10
Method	BLASTX
NCBI GI	g112681
BLAST score	471
E value	2.0e-47
Match length	129
% identity	77

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145834
Seq. ID	LIB3168-066-P1-K1-B11
Method	BLASTX
NCBI GI	g2160151
BLAST score	550
E value	1.0e-56
Match length	123
% identity	88
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	145835
Seq. ID	LIB3168-066-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	254
E value	2.0e-22
Match length	53
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145836
Seq. ID	LIB3168-066-P1-K1-B2
Method	BLASTX
NCBI GI	g2583125
BLAST score	364
E value	1.0e-34
Match length	108
% identity	67
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	145837
Seq. ID	LIB3168-066-P1-K1-B4
Method	BLASTX
NCBI GI	g2623928
BLAST score	338
E value	5.0e-32
Match length	90
% identity	72
NCBI Description	(AF031457) RNA polymerase C1 [Gossypium arboreum] >gi_2623930 (AF031458) RNA polymerase C1 [Gossypium hirsutum] >gi_2623932 (AF031459) RNA polymerase C1 [Gossypium barbadense] >gi_2623934 (AF031460) RNA polymerase C1 [Gossypium tomentosum] >gi_2623936 (AF031461) RNA polymerase C1 [Gossypium mustelinum] >gi_2623938 (AF031462) RNA polymerase C1 [Gossypium darwinii]

Seq. No. 145838

Seq. ID	LIB3168-066-P1-K1-B5
Method	BLASTX
NCBI GI	g1351837
BLAST score	144
E value	2.0e-09
Match length	79
% identity	43
NCBI Description	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II beta-carboxyltransferase chain - rape chloroplast >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase carboxyltransferase (beta subunit) [Brassica napus] >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta [Brassica napus]

Seq. No.	145839
Seq. ID	LIB3168-066-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	571
E value	5.0e-59
Match length	145
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145840
Seq. ID	LIB3168-066-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	603
E value	6.0e-63
Match length	117
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145841
Seq. ID	LIB3168-066-P1-K1-B8
Method	BLASTX
NCBI GI	g3702339
BLAST score	669
E value	1.0e-70
Match length	129
% identity	100
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	145842
Seq. ID	LIB3168-066-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	395
E value	2.0e-38
Match length	109
% identity	73

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145843
Seq. ID	LIB3168-066-P1-K1-C10
Method	BLASTX
NCBI GI	g3851640
BLAST score	155
E value	3.0e-10
Match length	106
% identity	41
NCBI Description	(AF098636) chaperone GrpE type 2 [Nicotiana tabacum]

Seq. No.	145844
Seq. ID	LIB3168-066-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	589
E value	4.0e-61
Match length	144
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145845
Seq. ID	LIB3168-066-P1-K1-C2
Method	BLASTX
NCBI GI	g112681
BLAST score	525
E value	1.0e-53
Match length	107
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145846
Seq. ID	LIB3168-066-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	323
E value	4.0e-30
Match length	82
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145847
Seq. ID	LIB3168-066-P1-K1-C4
Method	BLASTX
NCBI GI	g112737
BLAST score	639

E value	5.0e-67
Match length	130
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145848
Seq. ID	LIB3168-066-P1-K1-C5
Method	BLASTX
NCBI GI	g112681
BLAST score	549
E value	2.0e-56
Match length	140
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145849
Seq. ID	LIB3168-066-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145850
Seq. ID	LIB3168-066-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	639
E value	6.0e-67
Match length	136
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145851
Seq. ID	LIB3168-066-P1-K1-C8
Method	BLASTX
NCBI GI	g112682
BLAST score	626
E value	2.0e-65
Match length	143
% identity	83

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145852
Seq. ID	LIB3168-066-P1-K1-C9
Method	BLASTX
NCBI GI	g4262213
BLAST score	191
E value	2.0e-14
Match length	41
% identity	93
NCBI Description	(AC006161) hypothetical protein [Arabidopsis thaliana]

Seq. No.	145853
Seq. ID	LIB3168-066-P1-K1-D1
Method	BLASTX
NCBI GI	g112682
BLAST score	585
E value	1.0e-60
Match length	138
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145854
Seq. ID	LIB3168-066-P1-K1-D10
Method	BLASTX
NCBI GI	g2129657
BLAST score	323
E value	5.0e-30
Match length	97
% identity	72
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145855
Seq. ID	LIB3168-066-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	574
E value	2.0e-59
Match length	143
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145856
Seq. ID	LIB3168-066-P1-K1-D12

Method	BLASTX
NCBI GI	g3063445
BLAST score	296
E value	9.0e-27
Match length	109
% identity	55
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	145857
Seq. ID	LIB3168-066-P1-K1-D2
Method	BLASTX
NCBI GI	g112682
BLAST score	216
E value	4.0e-57
Match length	125
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145858
Seq. ID	LIB3168-066-P1-K1-D3
Method	BLASTX
NCBI GI	g585922
BLAST score	411
E value	3.0e-40
Match length	147
% identity	61
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN

Seq. No.	145859
Seq. ID	LIB3168-066-P1-K1-D4
Method	BLASTX
NCBI GI	g2129659
BLAST score	354
E value	1.0e-33
Match length	114
% identity	61
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	145860
Seq. ID	LIB3168-066-P1-K1-D5
Method	BLASTN
NCBI GI	g2842474
BLAST score	55
E value	5.0e-22
Match length	238
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	145861
Seq. ID	LIB3168-066-P1-K1-D6
Method	BLASTX

NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145862
Seq. ID	LIB3168-066-P1-K1-D7
Method	BLASTX
NCBI GI	g112681
BLAST score	644
E value	1.0e-67
Match length	126
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145863
Seq. ID	LIB3168-066-P1-K1-D8
Method	BLASTX
NCBI GI	g112681
BLAST score	511
E value	5.0e-52
Match length	131
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145864
Seq. ID	LIB3168-066-P1-K1-E10
Method	BLASTN
NCBI GI	g3985931
BLAST score	417
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	145865
Seq. ID	LIB3168-066-P1-K1-E11
Method	BLASTX
NCBI GI	g112682
BLAST score	657
E value	4.0e-69
Match length	144
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145866
Seq. ID	LIB3168-066-P1-K1-E12
Method	BLASTX
NCBI GI	g384341
BLAST score	205
E value	4.0e-16
Match length	101
% identity	43
NCBI Description	major storage protein [Theobroma cacao]

Seq. No.	145867
Seq. ID	LIB3168-066-P1-K1-E2
Method	BLASTX
NCBI GI	g122781
BLAST score	454
E value	2.0e-45
Match length	120
% identity	72
NCBI Description	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi_82210_pir__A05198 hypothetical protein 229 - common tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]

Seq. No.	145868
Seq. ID	LIB3168-066-P1-K1-E3
Method	BLASTX
NCBI GI	g4454009
BLAST score	276
E value	2.0e-24
Match length	117
% identity	55
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	145869
Seq. ID	LIB3168-066-P1-K1-E4
Method	BLASTX
NCBI GI	g112682
BLAST score	610
E value	1.0e-63
Match length	141
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145870
Seq. ID	LIB3168-066-P1-K1-E5
Method	BLASTX
NCBI GI	g2459446

BLAST score	681
E value	6.0e-72
Match length	145
% identity	90
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	145871
Seq. ID	LIB3168-066-P1-K1-E6
Method	BLASTX
NCBI GI	g4210330
BLAST score	422
E value	1.0e-41
Match length	83
% identity	100
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	145872
Seq. ID	LIB3168-066-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	565
E value	2.0e-58
Match length	141
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145873
Seq. ID	LIB3168-066-P1-K1-E8
Method	BLASTX
NCBI GI	g729486
BLAST score	183
E value	2.0e-13
Match length	102
% identity	42
NCBI Description	PRE-RRNA PROCESSING PROTEIN FHL1 >gi_626950_pir__S43738 transcription activator FHL1 - yeast (Saccharomyces cerevisiae) >gi_454255_emb_CAA82202_ (Z28348) Fhl1p [Saccharomyces cerevisiae] >gi_914975 (U32445) Pre-rRNA processing protein Fhl1 (Swiss Prot. accession number P39521) [Saccharomyces cerevisiae]

Seq. No.	145874
Seq. ID	LIB3168-066-P1-K1-F1
Method	BLASTX
NCBI GI	g2851581
BLAST score	655
E value	7.0e-69
Match length	145
% identity	88
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_2196464_emb_CAA74024_ (Y13690) DNA-dependent RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	145875
Seq. ID	LIB3168-066-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	173
E value	2.0e-12
Match length	62
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145876
Seq. ID	LIB3168-066-P1-K1-F12
Method	BLASTX
NCBI GI	g4204298
BLAST score	526
E value	9.0e-54
Match length	120
% identity	85
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145877
Seq. ID	LIB3168-066-P1-K1-F3
Method	BLASTX
NCBI GI	g112739
BLAST score	553
E value	7.0e-57
Match length	144
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145878
Seq. ID	LIB3168-066-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	8.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145879
Seq. ID	LIB3168-066-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583

BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145880
Seq. ID	LIB3168-066-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64
Match length	119
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145881
Seq. ID	LIB3168-066-P1-K1-F8
Method	BLASTX
NCBI GI	g3063693
BLAST score	252
E value	1.0e-21
Match length	45
% identity	100
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	145882
Seq. ID	LIB3168-066-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	587
E value	7.0e-61
Match length	146
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145883
Seq. ID	LIB3168-066-P1-K1-G1
Method	BLASTX
NCBI GI	g267069
BLAST score	613
E value	6.0e-64
Match length	113
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	145884
Seq. ID	LIB3168-066-P1-K1-G10

Method	BLASTX
NCBI GI	g4630748
BLAST score	58
E value	2.0e-13
Match length	46
% identity	89
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	145885
Seq. ID	LIB3168-066-P1-K1-G11
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	2.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145886
Seq. ID	LIB3168-066-P1-K1-G12
Method	BLASTX
NCBI GI	g112743
BLAST score	367
E value	3.0e-35
Match length	98
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145887
Seq. ID	LIB3168-066-P1-K1-G3
Method	BLASTX
NCBI GI	g4263525
BLAST score	571
E value	5.0e-59
Match length	133
% identity	85
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	145888
Seq. ID	LIB3168-066-P1-K1-G4
Method	BLASTN
NCBI GI	g3548797
BLAST score	380
E value	0.0e+00
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145889
Seq. ID	LIB3168-066-P1-K1-G5
Method	BLASTX
NCBI GI	g2828296
BLAST score	559
E value	1.0e-57
Match length	104
% identity	100
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	145890
Seq. ID	LIB3168-066-P1-K1-G6
Method	BLASTX
NCBI GI	g112741
BLAST score	516
E value	1.0e-52
Match length	95
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145891
Seq. ID	LIB3168-066-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145892
Seq. ID	LIB3168-066-P1-K1-G9
Method	BLASTX
NCBI GI	g4204298
BLAST score	519
E value	6.0e-53
Match length	117
% identity	85
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145893
Seq. ID	LIB3168-066-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	752
E value	3.0e-80

Match length	146
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145894
Seq. ID	LIB3168-066-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	678
E value	1.0e-71
Match length	141
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145895
Seq. ID	LIB3168-066-P1-K1-H11
Method	BLASTX
NCBI GI	g2160158
BLAST score	424
E value	8.0e-42
Match length	98
% identity	84
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	145896
Seq. ID	LIB3168-066-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	741
E value	6.0e-79
Match length	142
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145897
Seq. ID	LIB3168-066-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	606
E value	4.0e-63
Match length	147
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145898
Seq. ID	LIB3168-066-P1-K1-H3
Method	BLASTX

NCBI GI	g480450
BLAST score	446
E value	2.0e-44
Match length	101
% identity	89
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	145899
Seq. ID	LIB3168-066-P1-K1-H4
Method	BLASTX
NCBI GI	g113026
BLAST score	457
E value	9.0e-46
Match length	103
% identity	87
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	145900
Seq. ID	LIB3168-066-P1-K1-H7
Method	BLASTN
NCBI GI	g4691223
BLAST score	223
E value	1.0e-122
Match length	427
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	145901
Seq. ID	LIB3168-066-P1-K1-H8
Method	BLASTX
NCBI GI	g4510348
BLAST score	632
E value	4.0e-66
Match length	126
% identity	96
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	145902
Seq. ID	LIB3168-067-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145903
Seq. ID	LIB3168-067-P1-K1-A11
Method	BLASTX
NCBI GI	g112741
BLAST score	764
E value	2.0e-81
Match length	164
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145904
Seq. ID	LIB3168-067-P1-K1-A12
Method	BLASTX
NCBI GI	g4314378
BLAST score	837
E value	4.0e-90
Match length	160
% identity	99
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	145905
Seq. ID	LIB3168-067-P1-K1-A2
Method	BLASTN
NCBI GI	g2842474
BLAST score	47
E value	2.0e-17
Match length	146
% identity	40
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	145906
Seq. ID	LIB3168-067-P1-K1-A3
Method	BLASTX
NCBI GI	g112681
BLAST score	511
E value	3.0e-52
Match length	99
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145907
Seq. ID	LIB3168-067-P1-K1-A4
Method	BLASTX
NCBI GI	g544122
BLAST score	389

E value	2.0e-37
Match length	84
% identity	90
NCBI Description	APOCYTOCHROME F PRECURSOR >gi_629599_pir__S45661 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - turnip chloroplast >gi_441282_emb_CAA54307_ (X77011) cytochrome f [Brassica rapa]

Seq. No.	145908
Seq. ID	LIB3168-067-P1-K1-A5
Method	BLASTX
NCBI GI	g1345973
BLAST score	540
E value	5.0e-71
Match length	148
% identity	87
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	145909
Seq. ID	LIB3168-067-P1-K1-A6
Method	BLASTX
NCBI GI	g112681
BLAST score	402
E value	2.0e-39
Match length	107
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145910
Seq. ID	LIB3168-067-P1-K1-A8
Method	BLASTN
NCBI GI	g4512656
BLAST score	159
E value	3.0e-84
Match length	292
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	145911
Seq. ID	LIB3168-067-P1-K1-A9
Method	BLASTX
NCBI GI	g112741
BLAST score	840

E value	2.0e-90
Match length	157
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145912
Seq. ID	LIB3168-067-P1-K1-B1
Method	BLASTX
NCBI GI	g82051
BLAST score	212
E value	4.0e-17
Match length	92
% identity	49
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	145913
Seq. ID	LIB3168-067-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	232
E value	3.0e-85
Match length	158
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145914
Seq. ID	LIB3168-067-P1-K1-B12
Method	BLASTX
NCBI GI	g112737
BLAST score	560
E value	1.0e-57
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145915
Seq. ID	LIB3168-067-P1-K1-B2
Method	BLASTX

NCBI GI	g112682
BLAST score	741
E value	6.0e-79
Match length	146
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145916
Seq. ID	LIB3168-067-P1-K1-B4
Method	BLASTX
NCBI GI	g112681
BLAST score	872
E value	3.0e-94
Match length	176
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145917
Seq. ID	LIB3168-067-P1-K1-B5
Method	BLASTX
NCBI GI	g112681
BLAST score	619
E value	1.0e-64
Match length	124
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145918
Seq. ID	LIB3168-067-P1-K1-B6
Method	BLASTN
NCBI GI	g3492855
BLAST score	116
E value	1.0e-58
Match length	209
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	145919
Seq. ID	LIB3168-067-P1-K1-B8
Method	BLASTX
NCBI GI	g4490704
BLAST score	813
E value	3.0e-87
Match length	163

% identity	100
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	145920
Seq. ID	LIB3168-067-P1-K1-C1
Method	BLASTN
NCBI GI	g3449331
BLAST score	410
E value	0.0e+00
Match length	455
% identity	32
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	145921
Seq. ID	LIB3168-067-P1-K1-C10
Method	BLASTN
NCBI GI	g3108025
BLAST score	388
E value	0.0e+00
Match length	508
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	145922
Seq. ID	LIB3168-067-P1-K1-C11
Method	BLASTX
NCBI GI	g112682
BLAST score	795
E value	3.0e-85
Match length	152
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145923
Seq. ID	LIB3168-067-P1-K1-C12
Method	BLASTN
NCBI GI	g2924729
BLAST score	250
E value	1.0e-138
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	145924
Seq. ID	LIB3168-067-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	741
E value	7.0e-79
Match length	155

% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145925
Seq. ID	LIB3168-067-P1-K1-C3
Method	BLASTX
NCBI GI	g112682
BLAST score	793
E value	6.0e-85
Match length	164
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145926
Seq. ID	LIB3168-067-P1-K1-C5
Method	BLASTX
NCBI GI	g112739
BLAST score	357
E value	5.0e-34
Match length	109
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145927
Seq. ID	LIB3168-067-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145928
Seq. ID	LIB3168-067-P1-K1-C7
Method	BLASTX
NCBI GI	g1906830
BLAST score	731
E value	9.0e-78
Match length	143
% identity	99
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	145929
Seq. ID	LIB3168-067-P1-K1-C8
Method	BLASTX
NCBI GI	g464987
BLAST score	702
E value	3.0e-74
Match length	148
% identity	88
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	145930
Seq. ID	LIB3168-067-P1-K1-C9
Method	BLASTN
NCBI GI	g16231
BLAST score	87
E value	9.0e-42
Match length	99
% identity	97
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	145931
Seq. ID	LIB3168-067-P1-K1-D1
Method	BLASTX
NCBI GI	g4426939
BLAST score	421
E value	1.0e-41
Match length	85
% identity	99
NCBI Description	(AF118824) senescence-associated protein [Arabidopsis thaliana]

Seq. No.	145932
Seq. ID	LIB3168-067-P1-K1-D10
Method	BLASTX
NCBI GI	g112737
BLAST score	624
E value	3.0e-65
Match length	146
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145933
Seq. ID	LIB3168-067-P1-K1-D11

Method	BLASTX
NCBI GI	g4204299
BLAST score	764
E value	1.0e-81
Match length	167
% identity	89
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	145934
Seq. ID	LIB3168-067-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	638
E value	7.0e-67
Match length	144
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145935
Seq. ID	LIB3168-067-P1-K1-D3
Method	BLASTX
NCBI GI	g2129767
BLAST score	901
E value	1.0e-97
Match length	174
% identity	98
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	145936
Seq. ID	LIB3168-067-P1-K1-D4
Method	BLASTN
NCBI GI	g4757414
BLAST score	453
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	145937
Seq. ID	LIB3168-067-P1-K1-D5
Method	BLASTX
NCBI GI	g2129657
BLAST score	283
E value	4.0e-37
Match length	136
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No.	145938
Seq. ID	LIB3168-067-P1-K1-D6
Method	BLASTX
NCBI GI	g112741
BLAST score	362
E value	1.0e-34
Match length	67
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145939
Seq. ID	LIB3168-067-P1-K1-D7
Method	BLASTX
NCBI GI	g112737
BLAST score	722
E value	1.0e-76
Match length	163
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145940
Seq. ID	LIB3168-067-P1-K1-D8
Method	BLASTX
NCBI GI	g112737
BLAST score	727
E value	3.0e-77
Match length	164
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145941
Seq. ID	LIB3168-067-P1-K1-D9
Method	BLASTX
NCBI GI	g112681
BLAST score	615
E value	4.0e-64
Match length	160

% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	145942
Seq. ID	LIB3168-067-P1-K1-E1
Method	BLASTX
NCBI GI	g2702272
BLAST score	375
E value	6.0e-36
Match length	99
% identity	34
NCBI Description	(AC003033) hypothetical protein [Arabidopsis thaliana]
Seq. No.	145943
Seq. ID	LIB3168-067-P1-K1-E11
Method	BLASTN
NCBI GI	g3292807
BLAST score	280
E value	1.0e-156
Match length	470
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)
Seq. No.	145944
Seq. ID	LIB3168-067-P1-K1-E12
Method	BLASTN
NCBI GI	g4220510
BLAST score	119
E value	2.0e-60
Match length	221
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	145945
Seq. ID	LIB3168-067-P1-K1-E2
Method	BLASTX
NCBI GI	g2129657
BLAST score	423
E value	1.0e-41
Match length	120
% identity	75
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	145946
Seq. ID	LIB3168-067-P1-K1-E3
Method	BLASTX
NCBI GI	g112743
BLAST score	365

E value	6.0e-35
Match length	121
% identity	62
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	145947
Seq. ID	LIB3168-067-P1-K1-E4
Method	BLASTX
NCBI GI	g112681
BLAST score	728
E value	2.0e-77
Match length	163
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145948
Seq. ID	LIB3168-067-P1-K1-E6
Method	BLASTN
NCBI GI	g4263038
BLAST score	446
E value	0.0e+00
Match length	510
% identity	96
NCBI Description	Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	145949
Seq. ID	LIB3168-067-P1-K1-E8
Method	BLASTX
NCBI GI	g2864609
BLAST score	223
E value	3.0e-18
Match length	87
% identity	51
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	145950
Seq. ID	LIB3168-067-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	421
E value	2.0e-41
Match length	109
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145951
Seq. ID	LIB3168-067-P1-K1-F11
Method	BLASTN
NCBI GI	g3869071
BLAST score	416
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	145952
Seq. ID	LIB3168-067-P1-K1-F12
Method	BLASTX
NCBI GI	g112737
BLAST score	663
E value	1.0e-69
Match length	155
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145953
Seq. ID	LIB3168-067-P1-K1-F2
Method	BLASTX
NCBI GI	g112682
BLAST score	681
E value	8.0e-72
Match length	155
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145954
Seq. ID	LIB3168-067-P1-K1-F4
Method	BLASTN
NCBI GI	g1354467
BLAST score	145
E value	1.0e-75
Match length	153
% identity	99
NCBI Description	Arabidopsis thaliana U1 snRNP 70K protein gene, complete cds

Seq. No.	145955
Seq. ID	LIB3168-067-P1-K1-F5

Method	BLASTX
NCBI GI	g4415917
BLAST score	625
E value	9.0e-77
Match length	162
% identity	69
NCBI Description	(AC006282) putative protein containing zinc finger domain [Arabidopsis thaliana]

Seq. No.	145956
Seq. ID	LIB3168-067-P1-K1-F6
Method	BLASTX
NCBI GI	g112739
BLAST score	559
E value	2.0e-57
Match length	149
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145957
Seq. ID	LIB3168-067-P1-K1-F7
Method	BLASTX
NCBI GI	g3738257
BLAST score	486
E value	5.0e-49
Match length	112
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	145958
Seq. ID	LIB3168-067-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145959
Seq. ID	LIB3168-067-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	757
E value	1.0e-80
Match length	156
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145960
Seq. ID	LIB3168-067-P1-K1-G11
Method	BLASTX
NCBI GI	g2245032
BLAST score	213
E value	5.0e-17
Match length	95
% identity	47
NCBI Description	(Z97342) gibberellin oxidase homolog [Arabidopsis thaliana]

Seq. No.	145961
Seq. ID	LIB3168-067-P1-K1-G2
Method	BLASTX
NCBI GI	g1169476
BLAST score	633
E value	3.0e-66
Match length	121
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	145962
Seq. ID	LIB3168-067-P1-K1-G3
Method	BLASTX
NCBI GI	g112682
BLAST score	679
E value	1.0e-71
Match length	158
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145963
Seq. ID	LIB3168-067-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	558
E value	2.0e-57
Match length	118
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145964
Seq. ID	LIB3168-067-P1-K1-G6
Method	BLASTN
NCBI GI	g2894557
BLAST score	323
E value	0.0e+00

Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	145965
Seq. ID	LIB3168-067-P1-K1-G7
Method	BLASTX
NCBI GI	g119143
BLAST score	791
E value	3.0e-87
Match length	164
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	145966
Seq. ID	LIB3168-067-P1-K1-H1
Method	BLASTX
NCBI GI	g2129767
BLAST score	729
E value	2.0e-77
Match length	156
% identity	88
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	145967
Seq. ID	LIB3168-067-P1-K1-H10
Method	BLASTN
NCBI GI	g4199934
BLAST score	340
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	145968
Seq. ID	LIB3168-067-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	596
E value	7.0e-62
Match length	120
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145969
Seq. ID	LIB3168-067-P1-K1-H12
Method	BLASTX
NCBI GI	g112681
BLAST score	638
E value	8.0e-67
Match length	147
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145970
Seq. ID	LIB3168-067-P1-K1-H2
Method	BLASTX
NCBI GI	g112682
BLAST score	652
E value	2.0e-68
Match length	149
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145971
Seq. ID	LIB3168-067-P1-K1-H3
Method	BLASTX
NCBI GI	g2129657
BLAST score	430
E value	2.0e-42
Match length	119
% identity	76
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	145972
Seq. ID	LIB3168-067-P1-K1-H4
Method	BLASTX
NCBI GI	g4454043
BLAST score	347
E value	1.0e-32
Match length	145
% identity	48
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	145973
Seq. ID	LIB3168-067-P1-K1-H5
Method	BLASTN
NCBI GI	g3510345

BLAST score	295
E value	1.0e-165
Match length	359
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	145974
Seq. ID	LIB3168-067-P1-K1-H7
Method	BLASTX
NCBI GI	g4455210
BLAST score	378
E value	2.0e-36
Match length	131
% identity	66
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	145975
Seq. ID	LIB3168-067-P1-K1-H9
Method	BLASTN
NCBI GI	g3033373
BLAST score	292
E value	1.0e-163
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	145976
Seq. ID	LIB3168-068-P1-K1-A1
Method	BLASTX
NCBI GI	g544424
BLAST score	434
E value	5.0e-43
Match length	85
% identity	99
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	145977
Seq. ID	LIB3168-068-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	630
E value	5.0e-66
Match length	127
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145978
Seq. ID	LIB3168-068-P1-K1-A11
Method	BLASTX
NCBI GI	g1169476
BLAST score	636
E value	1.0e-66
Match length	124
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	145979
Seq. ID	LIB3168-068-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	652
E value	1.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145980
Seq. ID	LIB3168-068-P1-K1-A3
Method	BLASTX
NCBI GI	g112741
BLAST score	702
E value	2.0e-74
Match length	132
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145981
Seq. ID	LIB3168-068-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	603
E value	9.0e-63
Match length	117
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145982
Seq. ID	LIB3168-068-P1-K1-A5
Method	BLASTX
NCBI GI	g112682
BLAST score	551

E value	1.0e-56
Match length	115
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145983
Seq. ID	LIB3168-068-P1-K1-A6
Method	BLASTX
NCBI GI	g112681
BLAST score	604
E value	7.0e-63
Match length	139
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145984
Seq. ID	LIB3168-068-P1-K1-A7
Method	BLASTN
NCBI GI	g2337888
BLAST score	346
E value	0.0e+00
Match length	357
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	145985
Seq. ID	LIB3168-068-P1-K1-A8
Method	BLASTX
NCBI GI	g112739
BLAST score	457
E value	1.0e-45
Match length	114
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	145986
Seq. ID	LIB3168-068-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	323
E value	3.0e-30
Match length	90

% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145987
Seq. ID	LIB3168-068-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	574
E value	2.0e-59
Match length	137
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145988
Seq. ID	LIB3168-068-P1-K1-B10
Method	BLASTX
NCBI GI	g112737
BLAST score	596
E value	6.0e-62
Match length	140
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145989
Seq. ID	LIB3168-068-P1-K1-B11
Method	BLASTX
NCBI GI	g112741
BLAST score	511
E value	2.0e-56
Match length	133
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	145990
Seq. ID	LIB3168-068-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	604
E value	7.0e-63
Match length	120
% identity	97

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145991
Seq. ID	LIB3168-068-P1-K1-B2
Method	BLASTX
NCBI GI	g112681
BLAST score	548
E value	3.0e-56
Match length	147
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	145992
Seq. ID	LIB3168-068-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145993
Seq. ID	LIB3168-068-P1-K1-B4
Method	BLASTX
NCBI GI	g1079136
BLAST score	168
E value	1.0e-11
Match length	54
% identity	56
NCBI Description	RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) >gi_532788 (U13178) RNA binding protein [Drosophila melanogaster] >gi_567106 (L37083) RNA binding protein [Drosophila melanogaster]

Seq. No.	145994
Seq. ID	LIB3168-068-P1-K1-B5
Method	BLASTX
NCBI GI	g112737
BLAST score	406
E value	1.0e-39
Match length	138
% identity	62
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	145995
Seq. ID	LIB3168-068-P1-K1-B6
Method	BLASTX
NCBI GI	g112737
BLAST score	562
E value	6.0e-58
Match length	118
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145996
Seq. ID	LIB3168-068-P1-K1-B7
Method	BLASTX
NCBI GI	g112737
BLAST score	566
E value	2.0e-58
Match length	123
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	145997
Seq. ID	LIB3168-068-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	631
E value	4.0e-66
Match length	124
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145998
Seq. ID	LIB3168-068-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	584
E value	2.0e-60
Match length	147
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	145999
Seq. ID	LIB3168-068-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146000
Seq. ID	LIB3168-068-P1-K1-C10
Method	BLASTX
NCBI GI	g484640
BLAST score	169
E value	8.0e-12
Match length	31
% identity	97
NCBI Description	2S albumin, AT2S5 - Arabidopsis thaliana (fragment)

Seq. No.	146001
Seq. ID	LIB3168-068-P1-K1-C11
Method	BLASTX
NCBI GI	g112681
BLAST score	611
E value	1.0e-63
Match length	141
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146002
Seq. ID	LIB3168-068-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	9.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146003
Seq. ID	LIB3168-068-P1-K1-C4
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	142
% identity	79

NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146004
Seq. ID	LIB3168-068-P1-K1-C5
Method	BLASTX
NCBI GI	g112737
BLAST score	250
E value	2.0e-21
Match length	111
% identity	50
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146005
Seq. ID	LIB3168-068-P1-K1-C6
Method	BLASTX
NCBI GI	g112741
BLAST score	688
E value	1.0e-72
Match length	135
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146006
Seq. ID	LIB3168-068-P1-K1-C7
Method	BLASTX
NCBI GI	g112681
BLAST score	564
E value	3.0e-58
Match length	134
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146007
Seq. ID	LIB3168-068-P1-K1-C8
Method	BLASTX

NCBI GI	g1854581
BLAST score	224
E value	1.0e-18
Match length	68
% identity	66
NCBI Description	(L24120) peroxidase precursor [Linum usitatissimum]

Seq. No.	146008
Seq. ID	LIB3168-068-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	205
E value	5.0e-16
Match length	153
% identity	42
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146009
Seq. ID	LIB3168-068-P1-K1-D10
Method	BLASTX
NCBI GI	g112681
BLAST score	721
E value	1.0e-76
Match length	143
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146010
Seq. ID	LIB3168-068-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	597
E value	5.0e-62
Match length	139
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146011
Seq. ID	LIB3168-068-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	43
E value	2.0e-44
Match length	112
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146012
Seq. ID	LIB3168-068-P1-K1-D2
Method	BLASTN
NCBI GI	g4519191
BLAST score	423
E value	0.0e+00
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	146013
Seq. ID	LIB3168-068-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	604
E value	7.0e-63
Match length	140
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146014
Seq. ID	LIB3168-068-P1-K1-D5
Method	BLASTX
NCBI GI	g112682
BLAST score	627
E value	1.0e-65
Match length	138
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146015
Seq. ID	LIB3168-068-P1-K1-D6
Method	BLASTN
NCBI GI	g2182287
BLAST score	414
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	146016
Seq. ID	LIB3168-068-P1-K1-D7
Method	BLASTX
NCBI GI	g112741
BLAST score	614

E value	4.0e-64
Match length	120
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146017
Seq. ID	LIB3168-068-P1-K1-D9
Method	BLASTX
NCBI GI	g112741
BLAST score	554
E value	4.0e-57
Match length	107
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146018
Seq. ID	LIB3168-068-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146019
Seq. ID	LIB3168-068-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146020
Seq. ID	LIB3168-068-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64

Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146021
Seq. ID	LIB3168-068-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	567
E value	1.0e-58
Match length	138
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146022
Seq. ID	LIB3168-068-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	653
E value	1.0e-68
Match length	126
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146023
Seq. ID	LIB3168-068-P1-K1-E3
Method	BLASTX
NCBI GI	g112681
BLAST score	607
E value	3.0e-63
Match length	141
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146024
Seq. ID	LIB3168-068-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	597
E value	4.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146025
Seq. ID	LIB3168-068-P1-K1-E6
Method	BLASTX
NCBI GI	g112741
BLAST score	728
E value	2.0e-77
Match length	137
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146026
Seq. ID	LIB3168-068-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	578
E value	8.0e-60
Match length	119
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146027
Seq. ID	LIB3168-068-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	614
E value	5.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146028
Seq. ID	LIB3168-068-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	6.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146029
Seq. ID	LIB3168-068-P1-K1-F1
Method	BLASTX
NCBI GI	g112682

BLAST score	615
E value	4.0e-64
Match length	143
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146030
Seq. ID	LIB3168-068-P1-K1-F10
Method	BLASTX
NCBI GI	g2129657
BLAST score	293
E value	2.0e-26
Match length	120
% identity	57
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146031
Seq. ID	LIB3168-068-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	600
E value	2.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146032
Seq. ID	LIB3168-068-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146033
Seq. ID	LIB3168-068-P1-K1-F2
Method	BLASTX
NCBI GI	g112682
BLAST score	619
E value	1.0e-64
Match length	143
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146034
Seq. ID	LIB3168-068-P1-K1-F3
Method	BLASTX
NCBI GI	g2129767
BLAST score	700
E value	4.0e-74
Match length	140
% identity	94
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	146035
Seq. ID	LIB3168-068-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	402
E value	3.0e-39
Match length	128
% identity	68
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146036
Seq. ID	LIB3168-068-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146037
Seq. ID	LIB3168-068-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	543
E value	9.0e-56
Match length	118
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146038
Seq. ID	LIB3168-068-P1-K1-F8
Method	BLASTX
NCBI GI	g3834314
BLAST score	560

E value	2.0e-62
Match length	134
% identity	87
NCBI Description	(AC005679) Similar to gene pi010 glycosyltransferase gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs gb_T46079 and gb_AA394466 come from this gene. [Arabidopsis thaliana]

Seq. No.	146039
Seq. ID	LIB3168-068-P1-K1-F9
Method	BLASTX
NCBI GI	g112737
BLAST score	582
E value	3.0e-60
Match length	140
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146040
Seq. ID	LIB3168-068-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	587
E value	7.0e-61
Match length	114
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146041
Seq. ID	LIB3168-068-P1-K1-G11
Method	BLASTX
NCBI GI	g3242075
BLAST score	680
E value	8.0e-72
Match length	142
% identity	94
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	146042
Seq. ID	LIB3168-068-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	178
E value	2.0e-39
Match length	96
% identity	86

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146043
Seq. ID	LIB3168-068-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	306
E value	6.0e-28
Match length	60
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146044
Seq. ID	LIB3168-068-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	400
E value	6.0e-39
Match length	114
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146045
Seq. ID	LIB3168-068-P1-K1-G6
Method	BLASTX
NCBI GI	g3256066
BLAST score	399
E value	8.0e-39
Match length	99
% identity	83
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No.	146046
Seq. ID	LIB3168-068-P1-K1-G7
Method	BLASTN
NCBI GI	g2264310
BLAST score	285
E value	1.0e-159
Match length	420
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	146047
Seq. ID	LIB3168-068-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	5.0e-64
Match length	120
% identity	99

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146048
Seq. ID	LIB3168-068-P1-K1-G9
Method	BLASTX
NCBI GI	g112741
BLAST score	718
E value	3.0e-76
Match length	136
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146049
Seq. ID	LIB3168-068-P1-K1-H10
Method	BLASTX
NCBI GI	g112741
BLAST score	200
E value	7.0e-16
Match length	65
% identity	63
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146050
Seq. ID	LIB3168-068-P1-K1-H11
Method	BLASTX
NCBI GI	g112681
BLAST score	48
E value	1.0e-60
Match length	138
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146051
Seq. ID	LIB3168-068-P1-K1-H12
Method	BLASTX
NCBI GI	g112682
BLAST score	616
E value	3.0e-64
Match length	143

% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146052
Seq. ID	LIB3168-068-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	573
E value	3.0e-59
Match length	114
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146053
Seq. ID	LIB3168-068-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	602
E value	1.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146054
Seq. ID	LIB3168-068-P1-K1-H4
Method	BLASTX
NCBI GI	g4455351
BLAST score	348
E value	7.0e-33
Match length	118
% identity	60
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]
Seq. No.	146055
Seq. ID	LIB3168-068-P1-K1-H5
Method	BLASTN
NCBI GI	g3176701
BLAST score	424
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	146056
Seq. ID	LIB3168-068-P1-K1-H6
Method	BLASTX

NCBI GI g112682
BLAST score 577
E value 8.0e-60
Match length 124
% identity 87
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146057
Seq. ID LIB3168-068-P1-K1-H7
Method BLASTX
NCBI GI g112741
BLAST score 669
E value 2.0e-70
Match length 124
% identity 99
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 146058
Seq. ID LIB3168-068-P1-K1-H8
Method BLASTN
NCBI GI g725259
BLAST score 79
E value 4.0e-37
Match length 87
% identity 98
NCBI Description Arabidopsis thaliana oleosin mRNA, complete cds

Seq. No. 146059
Seq. ID LIB3168-068-P1-K1-H9
Method BLASTX
NCBI GI g112681
BLAST score 608
E value 2.0e-63
Match length 124
% identity 98
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146060
Seq. ID LIB3168-069-P1-K1-A1
Method BLASTX
NCBI GI g112737
BLAST score 378
E value 1.0e-36

Match length	102
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146061
Seq. ID	LIB3168-069-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146062
Seq. ID	LIB3168-069-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	204
E value	4.0e-16
Match length	54
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146063
Seq. ID	LIB3168-069-P1-K1-A12
Method	BLASTN
NCBI GI	g4539378
BLAST score	426
E value	0.0e+00
Match length	451
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	146064
Seq. ID	LIB3168-069-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	525
E value	1.0e-53
Match length	105
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146065
Seq. ID	LIB3168-069-P1-K1-A6
Method	BLASTX
NCBI GI	g4218963
BLAST score	175
E value	2.0e-12
Match length	30
% identity	100
NCBI Description	(AF093672) xyloglucan endotransglycosylase [Arabidopsis thaliana] >gi_4539300_emb_CAB39603.1_ (AL049480) putative xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis thaliana]

Seq. No.	146066
Seq. ID	LIB3168-069-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	227
E value	1.0e-18
Match length	107
% identity	50
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146067
Seq. ID	LIB3168-069-P1-K1-A8
Method	BLASTX
NCBI GI	g112741
BLAST score	498
E value	1.0e-50
Match length	98
% identity	96
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146068
Seq. ID	LIB3168-069-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	668
E value	2.0e-70
Match length	141
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146069
Seq. ID	LIB3168-069-P1-K1-B1

Method	BLASTN
NCBI GI	g4165340
BLAST score	328
E value	0.0e+00
Match length	471
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146070
Seq. ID	LIB3168-069-P1-K1-B10
Method	BLASTX
NCBI GI	g3738257
BLAST score	263
E value	2.0e-42
Match length	107
% identity	85
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	146071
Seq. ID	LIB3168-069-P1-K1-B11
Method	BLASTX
NCBI GI	g4314368
BLAST score	316
E value	4.0e-29
Match length	142
% identity	46
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146072
Seq. ID	LIB3168-069-P1-K1-B12
Method	BLASTX
NCBI GI	g3859606
BLAST score	616
E value	3.0e-64
Match length	140
% identity	86
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	146073
Seq. ID	LIB3168-069-P1-K1-B2
Method	BLASTX
NCBI GI	g112737
BLAST score	341
E value	2.0e-32
Match length	84
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146074
Seq. ID	LIB3168-069-P1-K1-B3
Method	BLASTX
NCBI GI	g2129641
BLAST score	582
E value	3.0e-60
Match length	138
% identity	86
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	146075
Seq. ID	LIB3168-069-P1-K1-B5
Method	BLASTN
NCBI GI	g3894156
BLAST score	155
E value	1.0e-81
Match length	368
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146076
Seq. ID	LIB3168-069-P1-K1-B6
Method	BLASTX
NCBI GI	g1592677
BLAST score	289
E value	6.0e-26
Match length	117
% identity	56
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No.	146077
Seq. ID	LIB3168-069-P1-K1-B9
Method	BLASTX
NCBI GI	g4375833
BLAST score	383
E value	7.0e-37
Match length	150
% identity	53
NCBI Description	(AL021713) receptor serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No.	146078
Seq. ID	LIB3168-069-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	558
E value	2.0e-57
Match length	139
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146079

Seq. ID	LIB3168-069-P1-K1-C11
Method	BLASTX
NCBI GI	g112737
BLAST score	632
E value	5.0e-66
Match length	164
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146080
Seq. ID	LIB3168-069-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146081
Seq. ID	LIB3168-069-P1-K1-C3
Method	BLASTN
NCBI GI	g2264311
BLAST score	37
E value	3.0e-12
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	146082
Seq. ID	LIB3168-069-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	314
E value	3.0e-29
Match length	84
% identity	70
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146083
Seq. ID	LIB3168-069-P1-K1-C6
Method	BLASTX
NCBI GI	g3928078
BLAST score	387
E value	2.0e-37
Match length	121

% identity	68
NCBI Description	(AC005770) putative protein kinase, calcium dependent [Arabidopsis thaliana]

Seq. No.	146084
Seq. ID	LIB3168-069-P1-K1-C7
Method	BLASTX
NCBI GI	g2651310
BLAST score	811
E value	4.0e-87
Match length	156
% identity	99
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	146085
Seq. ID	LIB3168-069-P1-K1-C8
Method	BLASTX
NCBI GI	g3548810
BLAST score	195
E value	7.0e-15
Match length	151
% identity	36
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	146086
Seq. ID	LIB3168-069-P1-K1-C9
Method	BLASTN
NCBI GI	g4757417
BLAST score	234
E value	1.0e-129
Match length	267
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	146087
Seq. ID	LIB3168-069-P1-K1-D1
Method	BLASTN
NCBI GI	g3241926
BLAST score	53
E value	4.0e-21
Match length	73
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	146088
Seq. ID	LIB3168-069-P1-K1-D10
Method	BLASTX
NCBI GI	g117238
BLAST score	414
E value	1.0e-40
Match length	124
% identity	73
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN

CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	146089
Seq. ID	LIB3168-069-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	44
E value	3.0e-45
Match length	148
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146090
Seq. ID	LIB3168-069-P1-K1-D12
Method	BLASTX
NCBI GI	g3402711
BLAST score	246
E value	7.0e-21
Match length	143
% identity	46
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	146091
Seq. ID	LIB3168-069-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	501
E value	1.0e-50
Match length	114
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146092
Seq. ID	LIB3168-069-P1-K1-D4
Method	BLASTX
NCBI GI	g1628583
BLAST score	259
E value	5.0e-23
Match length	55
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146093
Seq. ID	LIB3168-069-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	391
E value	4.0e-38
Match length	99
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146094
Seq. ID	LIB3168-069-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	450
E value	7.0e-45
Match length	112
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146095
Seq. ID	LIB3168-069-P1-K1-D7
Method	BLASTX
NCBI GI	g3023848
BLAST score	537
E value	4.0e-55
Match length	106
% identity	56
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	146096
Seq. ID	LIB3168-069-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	604
E value	9.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146097
Seq. ID	LIB3168-069-P1-K1-D9
Method	BLASTN
NCBI GI	g4512656
BLAST score	142
E value	6.0e-74

Match length	398
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146098
Seq. ID	LIB3168-069-P1-K1-E10
Method	BLASTN
NCBI GI	g2258103
BLAST score	252
E value	1.0e-139
Match length	379
% identity	91
NCBI Description	Arabidopsis thaliana chloroplast genes for trnC and rpoB, partial cds

Seq. No.	146099
Seq. ID	LIB3168-069-P1-K1-E11
Method	BLASTX
NCBI GI	g3047092
BLAST score	59
E value	8.0e-15
Match length	102
% identity	51
NCBI Description	(AF058826) No definition line found [Arabidopsis thaliana]

Seq. No.	146100
Seq. ID	LIB3168-069-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	773
E value	1.0e-82
Match length	147
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146101
Seq. ID	LIB3168-069-P1-K1-E2
Method	BLASTN
NCBI GI	g4512690
BLAST score	406
E value	0.0e+00
Match length	460
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	146102
Seq. ID	LIB3168-069-P1-K1-E3
Method	BLASTX
NCBI GI	g1335862
BLAST score	139
E value	6.0e-09

Match length	41
% identity	73
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	146103
Seq. ID	LIB3168-069-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	519
E value	8.0e-53
Match length	151
% identity	70
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146104
Seq. ID	LIB3168-069-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	284
E value	1.0e-25
Match length	60
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146105
Seq. ID	LIB3168-069-P1-K1-E8
Method	BLASTX
NCBI GI	g112681
BLAST score	619
E value	1.0e-64
Match length	124
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146106
Seq. ID	LIB3168-069-P1-K1-E9
Method	BLASTN
NCBI GI	g2264309
BLAST score	215
E value	1.0e-117
Match length	296
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	146107
Seq. ID	LIB3168-069-P1-K1-F1
Method	BLASTN
NCBI GI	g16236

BLAST score	75
E value	4.0e-34
Match length	94
% identity	96
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	146108
Seq. ID	LIB3168-069-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	634
E value	2.0e-66
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146109
Seq. ID	LIB3168-069-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	627
E value	2.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146110
Seq. ID	LIB3168-069-P1-K1-F12
Method	BLASTX
NCBI GI	g2708750
BLAST score	297
E value	6.0e-27
Match length	124
% identity	53
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	146111
Seq. ID	LIB3168-069-P1-K1-F2
Method	BLASTX
NCBI GI	g3421346
BLAST score	663
E value	1.0e-69
Match length	146
% identity	90
NCBI Description	(AJ007723) ribosomal protein S4 [Orobanche minor]

Seq. No.	146112
Seq. ID	LIB3168-069-P1-K1-F3
Method	BLASTX
NCBI GI	g2961390

BLAST score	538
E value	3.0e-60
Match length	116
% identity	96
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	146113
Seq. ID	LIB3168-069-P1-K1-F4
Method	BLASTX
NCBI GI	g112741
BLAST score	536
E value	5.0e-55
Match length	106
% identity	93
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146114
Seq. ID	LIB3168-069-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	61
E value	2.0e-52
Match length	125
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146115
Seq. ID	LIB3168-069-P1-K1-F6
Method	BLASTN
NCBI GI	g1946354
BLAST score	34
E value	7.0e-10
Match length	82
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	146116
Seq. ID	LIB3168-069-P1-K1-F9
Method	BLASTX
NCBI GI	g112681
BLAST score	419
E value	2.0e-41
Match length	118
% identity	75
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146117
Seq. ID	LIB3168-069-P1-K1-G1
Method	BLASTN
NCBI GI	g4589439
BLAST score	280
E value	1.0e-156
Match length	448
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	146118
Seq. ID	LIB3168-069-P1-K1-G10
Method	BLASTX
NCBI GI	g2129657
BLAST score	428
E value	3.0e-42
Match length	115
% identity	78
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146119
Seq. ID	LIB3168-069-P1-K1-G11
Method	BLASTX
NCBI GI	g112682
BLAST score	734
E value	5.0e-78
Match length	153
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146120
Seq. ID	LIB3168-069-P1-K1-G12
Method	BLASTX
NCBI GI	g2130159
BLAST score	162
E value	6.0e-11
Match length	78
% identity	54
NCBI Description	hypothetical protein 85 - maize chloroplast >gi_902275_emb_CAA60340_ (X86563) ORF85 [Zea mays] >gi_902296_emb_CAA60360_ (X86563) ORF85 [Zea mays]

Seq. No.	146121
Seq. ID	LIB3168-069-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583

BLAST score	191
E value	1.0e-14
Match length	48
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146122
Seq. ID	LIB3168-069-P1-K1-G3
Method	BLASTN
NCBI GI	g4512656
BLAST score	136
E value	1.0e-70
Match length	228
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146123
Seq. ID	LIB3168-069-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	334
E value	2.0e-31
Match length	94
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146124
Seq. ID	LIB3168-069-P1-K1-G6
Method	BLASTN
NCBI GI	g16472
BLAST score	273
E value	1.0e-152
Match length	309
% identity	97
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	146125
Seq. ID	LIB3168-069-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146126
Seq. ID	LIB3168-069-P1-K1-H1
Method	BLASTX
NCBI GI	g2500376

BLAST score	509
E value	1.0e-51
Match length	111
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_ (AC005508) 23552 [Arabidopsis thaliana]

Seq. No.	146127
Seq. ID	LIB3168-069-P1-K1-H10
Method	BLASTX
NCBI GI	g112739
BLAST score	66
E value	1.0e-45
Match length	137
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146128
Seq. ID	LIB3168-069-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	348
E value	3.0e-43
Match length	122
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146129
Seq. ID	LIB3168-069-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	49
E value	4.0e-60
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146130
Seq. ID	LIB3168-069-P1-K1-H2
Method	BLASTX
NCBI GI	g112682
BLAST score	638
E value	9.0e-67
Match length	172
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

	>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146131
Seq. ID	LIB3168-069-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	156
E value	2.0e-15
Match length	83
% identity	61
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146132
Seq. ID	LIB3168-069-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	561
E value	1.0e-57
Match length	157
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146133
Seq. ID	LIB3168-069-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	495
E value	4.0e-50
Match length	111
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146134
Seq. ID	LIB3168-069-P1-K1-H8
Method	BLASTX
NCBI GI	g4115943
BLAST score	770
E value	3.0e-82
Match length	148
% identity	98
NCBI Description	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]
Seq. No.	146135
Seq. ID	LIB3168-069-P1-K1-H9
Method	BLASTX
NCBI GI	g112741

BLAST score	748
E value	1.0e-79
Match length	142
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146136
Seq. ID	LIB3168-070-P1-K1-A10
Method	BLASTN
NCBI GI	g3281847
BLAST score	246
E value	1.0e-136
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	146137
Seq. ID	LIB3168-070-P1-K1-A11
Method	BLASTN
NCBI GI	g2058295
BLAST score	57
E value	3.0e-23
Match length	253
% identity	93
NCBI Description	A.thaliana chloroplast ndhG gene

Seq. No.	146138
Seq. ID	LIB3168-070-P1-K1-A12
Method	BLASTX
NCBI GI	g2961377
BLAST score	573
E value	3.0e-59
Match length	110
% identity	34
NCBI Description	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	146139
Seq. ID	LIB3168-070-P1-K1-A4
Method	BLASTX
NCBI GI	g112737
BLAST score	67
E value	3.0e-50
Match length	140
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146140
Seq. ID	LIB3168-070-P1-K1-A5
Method	BLASTN
NCBI GI	g2264307
BLAST score	98
E value	7.0e-48
Match length	198
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	146141
Seq. ID	LIB3168-070-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	1.0e-37
Match length	86
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146142
Seq. ID	LIB3168-070-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	178
E value	1.0e-13
Match length	57
% identity	68
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146143
Seq. ID	LIB3168-070-P1-K1-B4
Method	BLASTN
NCBI GI	g4512656
BLAST score	75
E value	6.0e-34
Match length	349
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146144
Seq. ID	LIB3168-070-P1-K1-B5
Method	BLASTX
NCBI GI	g3831459
BLAST score	314
E value	7.0e-29
Match length	64
% identity	98

NCBI Description	(AC005700) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	146145
Seq. ID	LIB3168-070-P1-K1-B6
Method	BLASTX
NCBI GI	g3776578
BLAST score	507
E value	2.0e-51
Match length	139
% identity	78
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	146146
Seq. ID	LIB3168-070-P1-K1-B7
Method	BLASTX
NCBI GI	g112682
BLAST score	93
E value	3.0e-14
Match length	52
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146147
Seq. ID	LIB3168-070-P1-K1-B8
Method	BLASTN
NCBI GI	g3608126
BLAST score	256
E value	1.0e-142
Match length	290
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146148
Seq. ID	LIB3168-070-P1-K1-C10
Method	BLASTX
NCBI GI	g112739
BLAST score	92
E value	5.0e-56
Match length	141
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146149
Seq. ID	LIB3168-070-P1-K1-C12
Method	BLASTX

NCBI GI	g112741
BLAST score	561
E value	7.0e-58
Match length	103
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146150
Seq. ID	LIB3168-070-P1-K1-C3
Method	BLASTN
NCBI GI	g2618602
BLAST score	382
E value	0.0e+00
Match length	436
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	146151
Seq. ID	LIB3168-070-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	494
E value	6.0e-50
Match length	129
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146152
Seq. ID	LIB3168-070-P1-K1-C7
Method	BLASTX
NCBI GI	g2129657
BLAST score	427
E value	4.0e-42
Match length	115
% identity	78
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146153
Seq. ID	LIB3168-070-P1-K1-C8
Method	BLASTX
NCBI GI	g112681
BLAST score	77
E value	4.0e-35
Match length	89
% identity	98

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146154
Seq. ID	LIB3168-070-P1-K1-C9
Method	BLASTX
NCBI GI	g112737
BLAST score	632
E value	4.0e-66
Match length	142
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	146155
Seq. ID	LIB3168-070-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	43
E value	3.0e-22
Match length	92
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146156
Seq. ID	LIB3168-070-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	394
E value	3.0e-38
Match length	97
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146157
Seq. ID	LIB3168-070-P1-K1-D2
Method	BLASTX
NCBI GI	g1072480
BLAST score	71
E value	3.0e-58
Match length	143
% identity	82
NCBI Description	cruciferin 1 precursor - rape
Seq. No.	146158

Docket No. 10020.0100

Seq. ID	LIB3168-070-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	186
E value	4.0e-14
Match length	97
% identity	73
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146159
Seq. ID	LIB3168-070-P1-K1-D6
Method	BLASTX
NCBI GI	g112739
BLAST score	105
E value	2.0e-49
Match length	139
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146160
Seq. ID	LIB3168-070-P1-K1-D9
Method	BLASTN
NCBI GI	g3510340
BLAST score	82
E value	9.0e-39
Match length	113
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	146161
Seq. ID	LIB3168-070-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	56
E value	7.0e-39
Match length	122
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146162
Seq. ID	LIB3168-070-P1-K1-E10
Method	BLASTX
NCBI GI	g112741
BLAST score	251

E value	4.0e-22
Match length	55
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146163
Seq. ID	LIB3168-070-P1-K1-E11
Method	BLASTX
NCBI GI	g3152940
BLAST score	201
E value	1.0e-15
Match length	88
% identity	49
NCBI Description	(AF065483) sorting nexin 1 [Homo sapiens]

Seq. No.	146164
Seq. ID	LIB3168-070-P1-K1-E12
Method	BLASTX
NCBI GI	g2564114
BLAST score	246
E value	5.0e-21
Match length	79
% identity	63
NCBI Description	(AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No.	146165
Seq. ID	LIB3168-070-P1-K1-E2
Method	BLASTX
NCBI GI	g4204299
BLAST score	655
E value	7.0e-69
Match length	148
% identity	87
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146166
Seq. ID	LIB3168-070-P1-K1-E3
Method	BLASTX
NCBI GI	g4204299
BLAST score	283
E value	2.0e-25
Match length	117
% identity	52
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146167
Seq. ID	LIB3168-070-P1-K1-E5
Method	BLASTX

NCBI GI	g1628583
BLAST score	651
E value	2.0e-68
Match length	138
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146168
Seq. ID	LIB3168-070-P1-K1-E7
Method	BLASTX
NCBI GI	g3834319
BLAST score	262
E value	7.0e-23
Match length	129
% identity	48
NCBI Description	(AC005679) Similar to gi_2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	146169
Seq. ID	LIB3168-070-P1-K1-E8
Method	BLASTX
NCBI GI	g4204299
BLAST score	442
E value	2.0e-46
Match length	146
% identity	76
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146170
Seq. ID	LIB3168-070-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	82
E value	2.0e-63
Match length	145
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146171
Seq. ID	LIB3168-070-P1-K1-F10
Method	BLASTN
NCBI GI	g3766106
BLAST score	282
E value	1.0e-157
Match length	442
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146172
Seq. ID	LIB3168-070-P1-K1-F3
Method	BLASTX
NCBI GI	g112682
BLAST score	83
E value	2.0e-58
Match length	146
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146173
Seq. ID	LIB3168-070-P1-K1-F5
Method	BLASTX
NCBI GI	g119350
BLAST score	56
E value	1.0e-28
Match length	76
% identity	95
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	146174
Seq. ID	LIB3168-070-P1-K1-F6
Method	BLASTX
NCBI GI	g1490554
BLAST score	231
E value	1.0e-19
Match length	71
% identity	68
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	146175
Seq. ID	LIB3168-070-P1-K1-F7
Method	BLASTX
NCBI GI	g4262250
BLAST score	460
E value	5.0e-46
Match length	96
% identity	97
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	146176
Seq. ID	LIB3168-070-P1-K1-F9
Method	BLASTX
NCBI GI	g4204299
BLAST score	95

E value	2.0e-27
Match length	74
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146177
Seq. ID	LIB3168-070-P1-K1-G10
Method	BLASTX
NCBI GI	g112739
BLAST score	227
E value	2.0e-21
Match length	95
% identity	63
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146178
Seq. ID	LIB3168-070-P1-K1-G11
Method	BLASTX
NCBI GI	g112681
BLAST score	504
E value	4.0e-51
Match length	149
% identity	71
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146179
Seq. ID	LIB3168-070-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	6.0e-38
Match length	89
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146180
Seq. ID	LIB3168-070-P1-K1-G6
Method	BLASTN
NCBI GI	g2842474
BLAST score	35
E value	1.0e-10
Match length	106
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No.	146181
Seq. ID	LIB3168-070-P1-K1-G9
Method	BLASTX
NCBI GI	g112737
BLAST score	92
E value	1.0e-64
Match length	144
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146182
Seq. ID	LIB3168-070-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	49
E value	3.0e-59
Match length	121
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146183
Seq. ID	LIB3168-070-P1-K1-H4
Method	BLASTX
NCBI GI	g1531762
BLAST score	189
E value	3.0e-14
Match length	51
% identity	73
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	146184
Seq. ID	LIB3168-070-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	113
E value	8.0e-60
Match length	119
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146185
Seq. ID	LIB3168-071-P1-K1-A1
Method	BLASTX
NCBI GI	g461838

BLAST score	82
E value	1.0e-01
Match length	69
% identity	84
NCBI Description	CRUCIFERIN PGCRURSE5 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_282895_pir__S26223 cruciferin - radish >gi_21118_emb_CAA42478_ (X59808) cruciferin [Raphanus sativus]

Seq. No.	146186
Seq. ID	LIB3168-071-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	151
E value	2.0e-10
Match length	59
% identity	54
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146187
Seq. ID	LIB3168-071-P1-K1-A11
Method	BLASTN
NCBI GI	g4589440
BLAST score	189
E value	1.0e-102
Match length	351
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	146188
Seq. ID	LIB3168-071-P1-K1-A12
Method	BLASTX
NCBI GI	g114654
BLAST score	145
E value	8.0e-13
Match length	81
% identity	58
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - common tobacco chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A ATPase III,H translocating [Nicotiana sp.] >gi_225272_prf__1211235G ATPase III [Nicotiana tabacum]

Seq. No.	146189
Seq. ID	LIB3168-071-P1-K1-A3
Method	BLASTN
NCBI GI	g2191157
BLAST score	325
E value	0.0e+00
Match length	426
% identity	94

NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	146190
Seq. ID	LIB3168-071-P1-K1-A4
Method	BLASTX
NCBI GI	g112681
BLAST score	538
E value	4.0e-55
Match length	142
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146191
Seq. ID	LIB3168-071-P1-K1-A5
Method	BLASTX
NCBI GI	g112739
BLAST score	421
E value	2.0e-41
Match length	120
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146192
Seq. ID	LIB3168-071-P1-K1-A6
Method	BLASTN
NCBI GI	g2828182
BLAST score	430
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	146193
Seq. ID	LIB3168-071-P1-K1-A8
Method	BLASTN
NCBI GI	g4115930
BLAST score	226
E value	1.0e-124
Match length	302
% identity	93
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	146194
Seq. ID	LIB3168-071-P1-K1-A9
Method	BLASTN
NCBI GI	g2842474

BLAST score	102
E value	2.0e-50
Match length	214
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146195
Seq. ID	LIB3168-071-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	432
E value	6.0e-43
Match length	92
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146196
Seq. ID	LIB3168-071-P1-K1-B11
Method	BLASTN
NCBI GI	g4678291
BLAST score	142
E value	5.0e-74
Match length	182
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	146197
Seq. ID	LIB3168-071-P1-K1-B12
Method	BLASTN
NCBI GI	g4519183
BLAST score	67
E value	1.0e-29
Match length	175
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	146198
Seq. ID	LIB3168-071-P1-K1-B3
Method	BLASTN
NCBI GI	g4589969
BLAST score	286
E value	1.0e-160
Match length	347
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	146199
Seq. ID	LIB3168-071-P1-K1-B5
Method	BLASTX
NCBI GI	g112682
BLAST score	574

E value	2.0e-59
Match length	134
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146200
Seq. ID	LIB3168-071-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	421
E value	2.0e-41
Match length	103
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146201
Seq. ID	LIB3168-071-P1-K1-B7
Method	BLASTX
NCBI GI	g4263825
BLAST score	347
E value	5.0e-33
Match length	96
% identity	67
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146202
Seq. ID	LIB3168-071-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	210
E value	6.0e-17
Match length	96
% identity	53
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146203
Seq. ID	LIB3168-071-P1-K1-C1
Method	BLASTX
NCBI GI	g4204299
BLAST score	277
E value	4.0e-25
Match length	57
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146204
Seq. ID	LIB3168-071-P1-K1-C10
Method	BLASTX

NCBI GI	g112682
BLAST score	553
E value	6.0e-57
Match length	138
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146205
Seq. ID	LIB3168-071-P1-K1-C11
Method	BLASTN
NCBI GI	g2465922
BLAST score	345
E value	0.0e+00
Match length	420
% identity	95
NCBI Description	Arabidopsis thaliana receptor-like serine/threonine kinase (RKF1) mRNA, complete cds

Seq. No.	146206
Seq. ID	LIB3168-071-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	386
E value	2.0e-37
Match length	78
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146207
Seq. ID	LIB3168-071-P1-K1-C2
Method	BLASTN
NCBI GI	g3449334
BLAST score	390
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	146208
Seq. ID	LIB3168-071-P1-K1-C3
Method	BLASTX
NCBI GI	g119143
BLAST score	605
E value	5.0e-63
Match length	120
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana]

>gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	146209
Seq. ID	LIB3168-071-P1-K1-C4
Method	BLASTX
NCBI GI	g119143
BLAST score	276
E value	4.0e-29
Match length	82
% identity	83
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	146210
Seq. ID	LIB3168-071-P1-K1-C5
Method	BLASTX
NCBI GI	g267073
BLAST score	656
E value	5.0e-69
Match length	122
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	146211
Seq. ID	LIB3168-071-P1-K1-C6
Method	BLASTX
NCBI GI	g3482929
BLAST score	245
E value	8.0e-21
Match length	66
% identity	77
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	146212
Seq. ID	LIB3168-071-P1-K1-C7
Method	BLASTX
NCBI GI	g4033349
BLAST score	529
E value	4.0e-54
Match length	111

% identity	95
NCBI Description	(AJ223496) phosphoenolpyrovate carboxylase [Brassica juncea]

Seq. No.	146213
Seq. ID	LIB3168-071-P1-K1-C8
Method	BLASTX
NCBI GI	g112682
BLAST score	563
E value	4.0e-58
Match length	128
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146214
Seq. ID	LIB3168-071-P1-K1-D1
Method	BLASTN
NCBI GI	g4079614
BLAST score	138
E value	1.0e-71
Match length	194
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146215
Seq. ID	LIB3168-071-P1-K1-D10
Method	BLASTX
NCBI GI	g1246823
BLAST score	412
E value	1.0e-40
Match length	89
% identity	80
NCBI Description	(X89865) unknown [Phoenix dactylifera]

Seq. No.	146216
Seq. ID	LIB3168-071-P1-K1-D11
Method	BLASTX
NCBI GI	g1076401
BLAST score	314
E value	7.0e-29
Match length	121
% identity	57
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Arabidopsis thaliana chloroplast (fragment) >gi_664896_emb_CAA58965_ (X84159) RNA polymerase subunit beta [Arabidopsis thaliana]

Seq. No.	146217
Seq. ID	LIB3168-071-P1-K1-D12
Method	BLASTX
NCBI GI	g112682
BLAST score	556

E value	3.0e-57
Match length	131
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146218
Seq. ID	LIB3168-071-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	681
E value	6.0e-72
Match length	142
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146219
Seq. ID	LIB3168-071-P1-K1-D3
Method	BLASTN
NCBI GI	g4582411
BLAST score	341
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	146220
Seq. ID	LIB3168-071-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	590
E value	3.0e-61
Match length	138
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146221
Seq. ID	LIB3168-071-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64
Match length	119
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146222
Seq. ID	LIB3168-071-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	658
E value	3.0e-69
Match length	128
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146223
Seq. ID	LIB3168-071-P1-K1-D7
Method	BLASTN
NCBI GI	g4586241
BLAST score	215
E value	1.0e-117
Match length	368
% identity	52
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	146224
Seq. ID	LIB3168-071-P1-K1-D8
Method	BLASTX
NCBI GI	g119150
BLAST score	719
E value	2.0e-76
Match length	137
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No.	146225
Seq. ID	LIB3168-071-P1-K1-D9
Method	BLASTN
NCBI GI	g3600062
BLAST score	318
E value	1.0e-179
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	146226
Seq. ID	LIB3168-071-P1-K1-E1
Method	BLASTN
NCBI GI	g2244870
BLAST score	116
E value	9.0e-59
Match length	214
% identity	87

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	146227
Seq. ID	LIB3168-071-P1-K1-E10
Method	BLASTN
NCBI GI	g4585952
BLAST score	368
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence
Seq. No.	146228
Seq. ID	LIB3168-071-P1-K1-E12
Method	BLASTN
NCBI GI	g441490
BLAST score	100
E value	4.0e-49
Match length	141
% identity	93
NCBI Description	S.alba chloroplast trnR gene
Seq. No.	146229
Seq. ID	LIB3168-071-P1-K1-E2
Method	BLASTX
NCBI GI	g2880057
BLAST score	657
E value	4.0e-69
Match length	140
% identity	89
NCBI Description	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
Seq. No.	146230
Seq. ID	LIB3168-071-P1-K1-E3
Method	BLASTX
NCBI GI	g3184281
BLAST score	493
E value	6.0e-50
Match length	122
% identity	80
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	146231
Seq. ID	LIB3168-071-P1-K1-E4
Method	BLASTX
NCBI GI	g1346754
BLAST score	473
E value	1.0e-47
Match length	100
% identity	90
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 >gi_421851_pir__S31086 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP2) - Arabidopsis thaliana >gi_166797 (M93409) catalytic subunit [Arabidopsis

thaliana]

Seq. No.	146232
Seq. ID	LIB3168-071-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	69
E value	3.0e-40
Match length	89
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146233
Seq. ID	LIB3168-071-P1-K1-E8
Method	BLASTN
NCBI GI	g2618603
BLAST score	122
E value	5.0e-62
Match length	278
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	146234
Seq. ID	LIB3168-071-P1-K1-E9
Method	BLASTN
NCBI GI	g3150036
BLAST score	89
E value	2.0e-42
Match length	130
% identity	93
NCBI Description	Arabidopsis thaliana Myb transcription factor homolog (ATR1) gene, complete cds, receptor-like protein kinase (RLK1) gene, partial cds

Seq. No.	146235
Seq. ID	LIB3168-071-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146236
Seq. ID	LIB3168-071-P1-K1-F10
Method	BLASTX
NCBI GI	g112743
BLAST score	681
E value	6.0e-72
Match length	137
% identity	93

NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]
Seq. No.	146237
Seq. ID	LIB3168-071-P1-K1-F11
Method	BLASTX
NCBI GI	g1592677
BLAST score	249
E value	3.0e-21
Match length	121
% identity	46
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.	146238
Seq. ID	LIB3168-071-P1-K1-F2
Method	BLASTX
NCBI GI	g4204298
BLAST score	642
E value	2.0e-67
Match length	139
% identity	89
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	146239
Seq. ID	LIB3168-071-P1-K1-F3
Method	BLASTN
NCBI GI	g4199934
BLAST score	290
E value	1.0e-162
Match length	294
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]
Seq. No.	146240
Seq. ID	LIB3168-071-P1-K1-F4
Method	BLASTN
NCBI GI	g4371278
BLAST score	81
E value	1.0e-37
Match length	193
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	146241
Seq. ID	LIB3168-071-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	564
E value	3.0e-58

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Match length	140
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146242
Seq. ID	LIB3168-071-P1-K1-G1
Method	BLASTX
NCBI GI	g2129653
BLAST score	721
E value	1.0e-76
Match length	138
% identity	100
NCBI Description	myosin heavy chain MYA2 - Arabidopsis thaliana >gi_499047_emb_CAA84066_ (Z34293) myosin [Arabidopsis thaliana]

Seq. No.	146243
Seq. ID	LIB3168-071-P1-K1-G10
Method	BLASTX
NCBI GI	g2129642
BLAST score	682
E value	5.0e-72
Match length	130
% identity	96
NCBI Description	major latex protein type 3 - Arabidopsis thaliana >gi_1107495_emb_CAA63027_ (X91961) major latex protein type3 [Arabidopsis thaliana]

Seq. No.	146244
Seq. ID	LIB3168-071-P1-K1-G11
Method	BLASTX
NCBI GI	g112681
BLAST score	563
E value	4.0e-58
Match length	133
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146245
Seq. ID	LIB3168-071-P1-K1-G2
Method	BLASTX
NCBI GI	g3894171
BLAST score	520
E value	1.0e-56
Match length	126
% identity	93
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	146246
Seq. ID	LIB3168-071-P1-K1-G4

Method	BLASTN
NCBI GI	g4691223
BLAST score	234
E value	1.0e-129
Match length	426
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	146247
Seq. ID	LIB3168-071-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	565
E value	3.0e-58
Match length	142
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146248
Seq. ID	LIB3168-071-P1-K1-G6
Method	BLASTX
NCBI GI	g2501064
BLAST score	644
E value	1.0e-67
Match length	122
% identity	96
NCBI Description	PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIGASE) (THRRS) >gi_2191162 (AF007270) Similar to threonyl-tRNA synthetase; coded for by A. thaliana cDNA R65376 [Arabidopsis thaliana]

Seq. No.	146249
Seq. ID	LIB3168-071-P1-K1-G7
Method	BLASTN
NCBI GI	g4455095
BLAST score	106
E value	2.0e-52
Match length	268
% identity	91
NCBI Description	Draba stylaris tRNA-Leu (trnL) and tRNA-Phe (trnF) genes, chloroplast genes for chloroplast RNAs, partial sequence

Seq. No.	146250
Seq. ID	LIB3168-071-P1-K1-G8
Method	BLASTX
NCBI GI	g112739
BLAST score	344
E value	2.0e-32
Match length	105
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146251
Seq. ID	LIB3168-071-P1-K1-G9
Method	BLASTN
NCBI GI	g2264316
BLAST score	67
E value	3.0e-29
Match length	423
% identity	45
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	146252
Seq. ID	LIB3168-071-P1-K1-H1
Method	BLASTN
NCBI GI	g3449331
BLAST score	35
E value	4.0e-10
Match length	422
% identity	32
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	146253
Seq. ID	LIB3168-071-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146254
Seq. ID	LIB3168-071-P1-K1-H12
Method	BLASTX
NCBI GI	g112737
BLAST score	539
E value	3.0e-55
Match length	135
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146255
Seq. ID	LIB3168-071-P1-K1-H2
Method	BLASTX

NCBI GI	g1628583
BLAST score	653
E value	1.0e-68
Match length	138
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146256
Seq. ID	LIB3168-071-P1-K1-H3
Method	BLASTX
NCBI GI	g112741
BLAST score	641
E value	3.0e-67
Match length	135
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146257
Seq. ID	LIB3168-071-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	524
E value	1.0e-53
Match length	134
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146258
Seq. ID	LIB3168-071-P1-K1-H5
Method	BLASTN
NCBI GI	g4406776
BLAST score	394
E value	0.0e+00
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146259
Seq. ID	LIB3168-071-P1-K1-H6
Method	BLASTX
NCBI GI	g112737
BLAST score	347
E value	7.0e-33
Match length	116
% identity	64
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146260
Seq. ID	LIB3168-071-P1-K1-H8
Method	BLASTX
NCBI GI	g3608135
BLAST score	290
E value	4.0e-26
Match length	82
% identity	66
NCBI Description	(AC005314) putative DNA binding factor [Arabidopsis thaliana]

Seq. No.	146261
Seq. ID	LIB3168-071-P1-K1-H9
Method	BLASTN
NCBI GI	g3242970
BLAST score	290
E value	1.0e-162
Match length	351
% identity	95
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	146262
Seq. ID	LIB3168-072-P1-K1-A1
Method	BLASTX
NCBI GI	g112737
BLAST score	650
E value	3.0e-68
Match length	151
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146263
Seq. ID	LIB3168-072-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	664
E value	5.0e-70
Match length	125
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	146264
Seq. ID	LIB3168-072-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	250
E value	5.0e-22
Match length	62
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146265
Seq. ID	LIB3168-072-P1-K1-A3
Method	BLASTX
NCBI GI	g2129538
BLAST score	241
E value	2.0e-20
Match length	50
% identity	94
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	146266
Seq. ID	LIB3168-072-P1-K1-A6
Method	BLASTX
NCBI GI	g4204299
BLAST score	537
E value	5.0e-55
Match length	105
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146267
Seq. ID	LIB3168-072-P1-K1-A7
Method	BLASTN
NCBI GI	g1906825
BLAST score	143
E value	7.0e-75
Match length	175
% identity	96
NCBI Description	A.thaliana hsp81.2 gene

Seq. No.	146268
Seq. ID	LIB3168-072-P1-K1-A9
Method	BLASTX
NCBI GI	g112743
BLAST score	481
E value	2.0e-48
Match length	148
% identity	65
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit

4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146269
Seq. ID	LIB3168-072-P1-K1-B1
Method	BLASTN
NCBI GI	g3449321
BLAST score	160
E value	1.0e-84
Match length	308
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	146270
Seq. ID	LIB3168-072-P1-K1-B11
Method	BLASTX
NCBI GI	g112682
BLAST score	618
E value	2.0e-64
Match length	144
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146271
Seq. ID	LIB3168-072-P1-K1-B12
Method	BLASTX
NCBI GI	g112737
BLAST score	554
E value	5.0e-57
Match length	124
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146272
Seq. ID	LIB3168-072-P1-K1-B3
Method	BLASTX
NCBI GI	g417383
BLAST score	397
E value	6.0e-39
Match length	89
% identity	90
NCBI Description	NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958)

nitrilase [Arabidopsis thaliana]

Seq. No.	146273
Seq. ID	LIB3168-072-P1-K1-B4
Method	BLASTX
NCBI GI	g119143
BLAST score	721
E value	1.0e-76
Match length	138
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	146274
Seq. ID	LIB3168-072-P1-K1-B5
Method	BLASTX
NCBI GI	g3335171
BLAST score	595
E value	7.0e-62
Match length	125
% identity	91
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	146275
Seq. ID	LIB3168-072-P1-K1-B6
Method	BLASTX
NCBI GI	g112743
BLAST score	667
E value	4.0e-70
Match length	166
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146276
Seq. ID	LIB3168-072-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	410
E value	2.0e-40
Match length	105
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146277
Seq. ID	LIB3168-072-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	302
E value	2.0e-27
Match length	91
% identity	67
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146278
Seq. ID	LIB3168-072-P1-K1-B9
Method	BLASTX
NCBI GI	g4490704
BLAST score	764
E value	2.0e-81
Match length	155
% identity	99
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	146279
Seq. ID	LIB3168-072-P1-K1-C1
Method	BLASTX
NCBI GI	g112737
BLAST score	724
E value	8.0e-77
Match length	164
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146280
Seq. ID	LIB3168-072-P1-K1-C11
Method	BLASTN
NCBI GI	g2341023
BLAST score	56
E value	1.0e-22
Match length	228
% identity	92
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	146281
Seq. ID	LIB3168-072-P1-K1-C12
Method	BLASTX
NCBI GI	g4204298
BLAST score	492
E value	9.0e-50

Match length 116
% identity 83
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 146282
Seq. ID LIB3168-072-P1-K1-C2
Method BLASTX
NCBI GI g4734009
BLAST score 348
E value 9.0e-33
Match length 140
% identity 50
NCBI Description (AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No. 146283
Seq. ID LIB3168-072-P1-K1-C3
Method BLASTX
NCBI GI g4432860
BLAST score 322
E value 4.0e-34
Match length 78
% identity 100
NCBI Description (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No. 146284
Seq. ID LIB3168-072-P1-K1-C4
Method BLASTX
NCBI GI g3935167
BLAST score 544
E value 1.0e-55
Match length 123
% identity 85
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]

Seq. No. 146285
Seq. ID LIB3168-072-P1-K1-C5
Method BLASTX
NCBI GI g4204299
BLAST score 827
E value 7.0e-89
Match length 176
% identity 90
NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 146286
Seq. ID LIB3168-072-P1-K1-C6
Method BLASTX
NCBI GI g1628583
BLAST score 660
E value 2.0e-69
Match length 157
% identity 82
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146287
Seq. ID	LIB3168-072-P1-K1-C8
Method	BLASTX
NCBI GI	g3850584
BLAST score	167
E value	6.0e-26
Match length	67
% identity	94
NCBI Description	(AC005278) ESTs gb_H37641 and gb_AA651422 come from this gene. [Arabidopsis thaliana]

Seq. No.	146288
Seq. ID	LIB3168-072-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	467
E value	4.0e-47
Match length	96
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146289
Seq. ID	LIB3168-072-P1-K1-D1
Method	BLASTN
NCBI GI	g4512656
BLAST score	396
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146290
Seq. ID	LIB3168-072-P1-K1-D10
Method	BLASTX
NCBI GI	g112737
BLAST score	596
E value	6.0e-62
Match length	144
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146291
Seq. ID	LIB3168-072-P1-K1-D11
Method	BLASTX
NCBI GI	g112739
BLAST score	398

E value	5.0e-49
Match length	143
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146292
Seq. ID	LIB3168-072-P1-K1-D12
Method	BLASTX
NCBI GI	g3983125
BLAST score	49
E value	7.0e-40
Match length	106
% identity	78
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	146293
Seq. ID	LIB3168-072-P1-K1-D4
Method	BLASTX
NCBI GI	g1628583
BLAST score	606
E value	5.0e-63
Match length	148
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146294
Seq. ID	LIB3168-072-P1-K1-D5
Method	BLASTN
NCBI GI	g4585952
BLAST score	256
E value	1.0e-142
Match length	371
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	146295
Seq. ID	LIB3168-072-P1-K1-D6
Method	BLASTN
NCBI GI	g2842474
BLAST score	71
E value	7.0e-32
Match length	175
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No. 146296

Seq. ID	LIB3168-072-P1-K1-D7
Method	BLASTX
NCBI GI	g112682
BLAST score	203
E value	8.0e-33
Match length	95
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146297
Seq. ID	LIB3168-072-P1-K1-D8
Method	BLASTX
NCBI GI	g112743
BLAST score	812
E value	4.0e-87
Match length	166
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146298
Seq. ID	LIB3168-072-P1-K1-D9
Method	BLASTX
NCBI GI	g112681
BLAST score	181
E value	2.0e-13
Match length	101
% identity	42
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146299
Seq. ID	LIB3168-072-P1-K1-E10
Method	BLASTX
NCBI GI	g4204298
BLAST score	607
E value	3.0e-63
Match length	151
% identity	79
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146300
Seq. ID	LIB3168-072-P1-K1-E11
Method	BLASTX

NCBI GI	g3242706
BLAST score	275
E value	3.0e-24
Match length	114
% identity	55
NCBI Description	(AC003040) cyclin-dependent kinase inhibitor protein [Arabidopsis thaliana] >gi_3550262 (AF079587) cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis thaliana]

Seq. No.	146301
Seq. ID	LIB3168-072-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	541
E value	1.0e-55
Match length	115
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146302
Seq. ID	LIB3168-072-P1-K1-E3
Method	BLASTN
NCBI GI	g3695386
BLAST score	198
E value	1.0e-107
Match length	251
% identity	94
NCBI Description	Arabidopsis thaliana BAC T2L5

Seq. No.	146303
Seq. ID	LIB3168-072-P1-K1-E4
Method	BLASTX
NCBI GI	g112682
BLAST score	810
E value	6.0e-87
Match length	173
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146304
Seq. ID	LIB3168-072-P1-K1-E5
Method	BLASTX
NCBI GI	g112737
BLAST score	515
E value	2.0e-52
Match length	117
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146305
Seq. ID	LIB3168-072-P1-K1-E6
Method	BLASTX
NCBI GI	g112681
BLAST score	199
E value	5.0e-16
Match length	45
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146306
Seq. ID	LIB3168-072-P1-K1-E7
Method	BLASTX
NCBI GI	g82051
BLAST score	290
E value	3.0e-26
Match length	113
% identity	53
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	146307
Seq. ID	LIB3168-072-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	424
E value	5.0e-42
Match length	103
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146308
Seq. ID	LIB3168-072-P1-K1-E9
Method	BLASTX
NCBI GI	g1899188
BLAST score	494
E value	7.0e-50
Match length	171
% identity	28
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	146309

Seq. ID	LIB3168-072-P1-K1-F1
Method	BLASTN
NCBI GI	g4581084
BLAST score	338
E value	0.0e+00
Match length	394
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	146310
Seq. ID	LIB3168-072-P1-K1-F10
Method	BLASTN
NCBI GI	g2182287
BLAST score	403
E value	0.0e+00
Match length	462
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	146311
Seq. ID	LIB3168-072-P1-K1-F11
Method	BLASTN
NCBI GI	g3236234
BLAST score	164
E value	2.0e-87
Match length	176
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146312
Seq. ID	LIB3168-072-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	646
E value	9.0e-68
Match length	152
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146313
Seq. ID	LIB3168-072-P1-K1-F2
Method	BLASTX
NCBI GI	g1628583
BLAST score	638
E value	7.0e-67
Match length	145
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146314

Seq. ID	LIB3168-072-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	594
E value	1.0e-61
Match length	146
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146315
Seq. ID	LIB3168-072-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	55
E value	2.0e-38
Match length	86
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146316
Seq. ID	LIB3168-072-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	545
E value	5.0e-56
Match length	113
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146317
Seq. ID	LIB3168-072-P1-K1-F7
Method	BLASTX
NCBI GI	g3193331
BLAST score	298
E value	6.0e-27
Match length	55
% identity	98
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	146318
Seq. ID	LIB3168-072-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	253
E value	2.0e-22
Match length	65
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146319
Seq. ID	LIB3168-072-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	117
E value	2.0e-65
Match length	167
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146320
Seq. ID	LIB3168-072-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	168
E value	2.0e-12
Match length	36
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146321
Seq. ID	LIB3168-072-P1-K1-G11
Method	BLASTX
NCBI GI	g112681
BLAST score	428
E value	2.0e-42
Match length	124
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146322
Seq. ID	LIB3168-072-P1-K1-G12
Method	BLASTX
NCBI GI	g112681
BLAST score	644
E value	2.0e-67
Match length	128
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146323
Seq. ID	LIB3168-072-P1-K1-G2
Method	BLASTX

NCBI GI	g3426041
BLAST score	271
E value	9.0e-24
Match length	70
% identity	64
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	146324
Seq. ID	LIB3168-072-P1-K1-G3
Method	BLASTX
NCBI GI	g112681
BLAST score	760
E value	1.0e-81
Match length	155
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146325
Seq. ID	LIB3168-072-P1-K1-G5
Method	BLASTN
NCBI GI	g1628582
BLAST score	64
E value	2.0e-27
Match length	183
% identity	85
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	146326
Seq. ID	LIB3168-072-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	606
E value	4.0e-63
Match length	145
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146327
Seq. ID	LIB3168-072-P1-K1-G9
Method	BLASTX
NCBI GI	g82232
BLAST score	399
E value	6.0e-39
Match length	121
% identity	65
NCBI Description	rpoC protein homolog - common tobacco chloroplast

Seq. No.	146328
Seq. ID	LIB3168-072-P1-K1-H1
Method	BLASTN
NCBI GI	g1877523
BLAST score	207
E value	1.0e-112
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	146329
Seq. ID	LIB3168-072-P1-K1-H10
Method	BLASTX
NCBI GI	g112737
BLAST score	571
E value	5.0e-59
Match length	137
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146330
Seq. ID	LIB3168-072-P1-K1-H11
Method	BLASTX
NCBI GI	g2246456
BLAST score	753
E value	3.0e-80
Match length	149
% identity	95
NCBI Description	(U71400) S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]

Seq. No.	146331
Seq. ID	LIB3168-072-P1-K1-H12
Method	BLASTN
NCBI GI	g3659491
BLAST score	322
E value	0.0e+00
Match length	400
% identity	94
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	146332
Seq. ID	LIB3168-072-P1-K1-H4
Method	BLASTX
NCBI GI	g112682
BLAST score	696
E value	1.0e-73
Match length	154

% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146333
Seq. ID	LIB3168-072-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	49
E value	5.0e-21
Match length	59
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146334
Seq. ID	LIB3168-073-P1-K1-A1
Method	BLASTN
NCBI GI	g4115370
BLAST score	365
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	146335
Seq. ID	LIB3168-073-P1-K1-A11
Method	BLASTX
NCBI GI	g3618320
BLAST score	345
E value	2.0e-32
Match length	93
% identity	68
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]
Seq. No.	146336
Seq. ID	LIB3168-073-P1-K1-A2
Method	BLASTX
NCBI GI	g267069
BLAST score	441
E value	6.0e-44
Match length	81
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.	146337
Seq. ID	LIB3168-073-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583

BLAST score	661
E value	1.0e-69
Match length	126
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146338
Seq. ID	LIB3168-073-P1-K1-A4
Method	BLASTN
NCBI GI	g4678340
BLAST score	433
E value	0.0e+00
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	146339
Seq. ID	LIB3168-073-P1-K1-A5
Method	BLASTN
NCBI GI	g2351066
BLAST score	339
E value	0.0e+00
Match length	428
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	146340
Seq. ID	LIB3168-073-P1-K1-A6
Method	BLASTX
NCBI GI	g2388582
BLAST score	361
E value	2.0e-34
Match length	71
% identity	100
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	146341
Seq. ID	LIB3168-073-P1-K1-A7
Method	BLASTX
NCBI GI	g398963
BLAST score	172
E value	3.0e-12
Match length	82
% identity	48
NCBI Description	4-COUMARATE--COA LIGASE 1 (4CL) >gi_100413_pir__A39827 4-coumarate--CoA ligase (EC 6.2.1.12) 1 - potato >gi_169574 (M62755) 4-coumarate--CoA ligase [Solanum tuberosum]

Seq. No.	146342
Seq. ID	LIB3168-073-P1-K1-A8
Method	BLASTX
NCBI GI	g112681

BLAST score	632
E value	3.0e-66
Match length	120
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146343
Seq. ID	LIB3168-073-P1-K1-A9
Method	BLASTX
NCBI GI	g112682
BLAST score	555
E value	9.0e-58
Match length	127
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146344
Seq. ID	LIB3168-073-P1-K1-B1
Method	BLASTN
NCBI GI	g4512656
BLAST score	117
E value	4.0e-59
Match length	303
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146345
Seq. ID	LIB3168-073-P1-K1-B11
Method	BLASTX
NCBI GI	g4193388
BLAST score	437
E value	3.0e-43
Match length	116
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	146346
Seq. ID	LIB3168-073-P1-K1-B12
Method	BLASTX
NCBI GI	g112682
BLAST score	550
E value	1.0e-56
Match length	117
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146347
Seq. ID	LIB3168-073-P1-K1-B3
Method	BLASTN
NCBI GI	g2828185
BLAST score	142
E value	5.0e-74
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	146348
Seq. ID	LIB3168-073-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	616
E value	3.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146349
Seq. ID	LIB3168-073-P1-K1-B6
Method	BLASTX
NCBI GI	g1174846
BLAST score	379
E value	2.0e-36
Match length	72
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3) >gi_1076425_pir__S43782 ubiquitin-conjugating enzyme UBC3 - Arabidopsis thaliana >gi_431262 (L19352) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	146350
Seq. ID	LIB3168-073-P1-K1-B7
Method	BLASTX
NCBI GI	g112743
BLAST score	639
E value	5.0e-67
Match length	118
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146351

Seq. ID	LIB3168-073-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	549
E value	1.0e-56
Match length	106
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146352
Seq. ID	LIB3168-073-P1-K1-B9
Method	BLASTX
NCBI GI	g3421102
BLAST score	437
E value	2.0e-43
Match length	83
% identity	99
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	146353
Seq. ID	LIB3168-073-P1-K1-C1
Method	BLASTX
NCBI GI	g112737
BLAST score	351
E value	3.0e-33
Match length	96
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146354
Seq. ID	LIB3168-073-P1-K1-C10
Method	BLASTN
NCBI GI	g2191126
BLAST score	267
E value	1.0e-148
Match length	322
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	146355
Seq. ID	LIB3168-073-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	118
E value	7.0e-06
Match length	77
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146356
Seq. ID	LIB3168-073-P1-K1-C12
Method	BLASTX
NCBI GI	g2924509
BLAST score	174
E value	2.0e-12
Match length	77
% identity	44
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	146357
Seq. ID	LIB3168-073-P1-K1-C5
Method	BLASTX
NCBI GI	g4512675
BLAST score	347
E value	9.0e-33
Match length	104
% identity	68
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	146358
Seq. ID	LIB3168-073-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	737
E value	2.0e-78
Match length	145
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146359
Seq. ID	LIB3168-073-P1-K1-C7
Method	BLASTN
NCBI GI	g3252804
BLAST score	254
E value	1.0e-141
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146360
Seq. ID	LIB3168-073-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	634
E value	2.0e-66
Match length	121
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146361
Seq. ID	LIB3168-073-P1-K1-D1
Method	BLASTX
NCBI GI	g4469003
BLAST score	413
E value	1.0e-40
Match length	102
% identity	77
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	146362
Seq. ID	LIB3168-073-P1-K1-D10
Method	BLASTX
NCBI GI	g2252866
BLAST score	201
E value	1.0e-15
Match length	52
% identity	73
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	146363
Seq. ID	LIB3168-073-P1-K1-D11
Method	BLASTX
NCBI GI	g4115918
BLAST score	222
E value	4.0e-18
Match length	50
% identity	86
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	146364
Seq. ID	LIB3168-073-P1-K1-D12
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	146365
Seq. ID	LIB3168-073-P1-K1-D2
Method	BLASTX
NCBI GI	g2129767
BLAST score	670
E value	1.0e-70
Match length	140
% identity	91
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	146366

Seq. ID	LIB3168-073-P1-K1-D5
Method	BLASTX
NCBI GI	g3193297
BLAST score	535
E value	8.0e-55
Match length	120
% identity	86
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	146367
Seq. ID	LIB3168-073-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	748
E value	9.0e-80
Match length	143
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146368
Seq. ID	LIB3168-073-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	635
E value	1.0e-66
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146369
Seq. ID	LIB3168-073-P1-K1-D9
Method	BLASTX
NCBI GI	g2232354
BLAST score	201
E value	1.0e-15
Match length	77
% identity	49
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	146370
Seq. ID	LIB3168-073-P1-K1-E10
Method	BLASTX
NCBI GI	g1363484
BLAST score	374
E value	6.0e-36
Match length	110
% identity	73
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	146371

Seq. ID	LIB3168-073-P1-K1-E11
Method	BLASTX
NCBI GI	g4063751
BLAST score	260
E value	1.0e-22
Match length	143
% identity	40
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	146372
Seq. ID	LIB3168-073-P1-K1-E12
Method	BLASTN
NCBI GI	g4589430
BLAST score	330
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	146373
Seq. ID	LIB3168-073-P1-K1-E2
Method	BLASTX
NCBI GI	g2119846
BLAST score	601
E value	2.0e-62
Match length	130
% identity	88
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	146374
Seq. ID	LIB3168-073-P1-K1-E3
Method	BLASTX
NCBI GI	g4115943
BLAST score	513
E value	2.0e-52
Match length	109
% identity	93
NCBI Description	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]

Seq. No.	146375
Seq. ID	LIB3168-073-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	109
E value	7.0e-52

Match length	113
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146376
Seq. ID	LIB3168-073-P1-K1-E6
Method	BLASTN
NCBI GI	g4581138
BLAST score	77
E value	4.0e-35
Match length	169
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	146377
Seq. ID	LIB3168-073-P1-K1-E7
Method	BLASTN
NCBI GI	g2264321
BLAST score	324
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	146378
Seq. ID	LIB3168-073-P1-K1-E8
Method	BLASTX
NCBI GI	g112743
BLAST score	525
E value	9.0e-54
Match length	113
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146379
Seq. ID	LIB3168-073-P1-K1-E9
Method	BLASTX
NCBI GI	g3413700
BLAST score	433
E value	5.0e-43
Match length	85
% identity	99
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	146380
Seq. ID	LIB3168-073-P1-K1-F1
Method	BLASTN

NCBI GI	g3449330
BLAST score	198
E value	1.0e-107
Match length	367
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	146381
Seq. ID	LIB3168-073-P1-K1-F10
Method	BLASTX
NCBI GI	g120675
BLAST score	469
E value	5.0e-47
Match length	107
% identity	84
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	146382
Seq. ID	LIB3168-073-P1-K1-F11
Method	BLASTX
NCBI GI	g4510397
BLAST score	736
E value	2.0e-78
Match length	143
% identity	99
NCBI Description	(AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No.	146383
Seq. ID	LIB3168-073-P1-K1-F12
Method	BLASTN
NCBI GI	g4371278
BLAST score	212
E value	1.0e-115
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146384
Seq. ID	LIB3168-073-P1-K1-F3
Method	BLASTN
NCBI GI	g2264307
BLAST score	126
E value	2.0e-64
Match length	316
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	146385
Seq. ID	LIB3168-073-P1-K1-F4
Method	BLASTX

NCBI GI	g1628583
BLAST score	49
E value	6.0e-23
Match length	58
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146386
Seq. ID	LIB3168-073-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	2.0e-60
Match length	136
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146387
Seq. ID	LIB3168-073-P1-K1-F6
Method	BLASTX
NCBI GI	g112682
BLAST score	617
E value	2.0e-64
Match length	124
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146388
Seq. ID	LIB3168-073-P1-K1-F7
Method	BLASTX
NCBI GI	g730129
BLAST score	707
E value	6.0e-75
Match length	140
% identity	99
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) >gi_3169310 (AF017641) nucleoside diphosphate kinase type 1 [Arabidopsis thaliana]

Seq. No.	146389
Seq. ID	LIB3168-073-P1-K1-F8
Method	BLASTX
NCBI GI	g3170525
BLAST score	400
E value	5.0e-39
Match length	99
% identity	79

NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	146390
Seq. ID	LIB3168-073-P1-K1-F9
Method	BLASTX
NCBI GI	g112681
BLAST score	504
E value	3.0e-51
Match length	121
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146391
Seq. ID	LIB3168-073-P1-K1-G1
Method	BLASTX
NCBI GI	g1169598
BLAST score	571
E value	4.0e-59
Match length	103
% identity	99
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	146392
Seq. ID	LIB3168-073-P1-K1-G10
Method	BLASTX
NCBI GI	g112682
BLAST score	686
E value	2.0e-72
Match length	141
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146393
Seq. ID	LIB3168-073-P1-K1-G12
Method	BLASTN
NCBI GI	g511598
BLAST score	338
E value	0.0e+00
Match length	374
% identity	28
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	146394
Seq. ID	LIB3168-073-P1-K1-G3
Method	BLASTN
NCBI GI	g4757414

BLAST score	412
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	146395
Seq. ID	LIB3168-073-P1-K1-G4
Method	BLASTX
NCBI GI	g112682
BLAST score	775
E value	6.0e-83
Match length	146
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146396
Seq. ID	LIB3168-073-P1-K1-G5
Method	BLASTX
NCBI GI	g112737
BLAST score	369
E value	2.0e-35
Match length	116
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146397
Seq. ID	LIB3168-073-P1-K1-G6
Method	BLASTX
NCBI GI	g131143
BLAST score	690
E value	5.0e-73
Match length	133
% identity	95
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]

Seq. No.	146398
Seq. ID	LIB3168-073-P1-K1-G7
Method	BLASTN
NCBI GI	g4585896
BLAST score	343

E value	0.0e+00
Match length	423
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F13I13 genomic sequence, complete sequence

Seq. No.	146399
Seq. ID	LIB3168-073-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	257
E value	3.0e-22
Match length	51
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146400
Seq. ID	LIB3168-073-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	573
E value	3.0e-59
Match length	109
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146401
Seq. ID	LIB3168-073-P1-K1-H12
Method	BLASTN
NCBI GI	g4519189
BLAST score	193
E value	1.0e-104
Match length	326
% identity	49
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5A21, complete sequence

Seq. No.	146402
Seq. ID	LIB3168-073-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	585
E value	1.0e-60
Match length	139
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146403
Seq. ID	LIB3168-073-P1-K1-H3

Method	BLASTX
NCBI GI	g1628583
BLAST score	608
E value	2.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146404
Seq. ID	LIB3168-073-P1-K1-H4
Method	BLASTX
NCBI GI	g112741
BLAST score	48
E value	4.0e-68
Match length	131
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146405
Seq. ID	LIB3168-073-P1-K1-H5
Method	BLASTX
NCBI GI	g112681
BLAST score	541
E value	1.0e-55
Match length	106
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146406
Seq. ID	LIB3168-073-P1-K1-H6
Method	BLASTX
NCBI GI	g595413
BLAST score	163
E value	3.0e-11
Match length	104
% identity	38
NCBI Description	(U11236) beta COP [Saccharomyces cerevisiae]

Seq. No.	146407
Seq. ID	LIB3168-073-P1-K1-H8
Method	BLASTX
NCBI GI	g2660672
BLAST score	337
E value	2.0e-31
Match length	74

% identity	89
NCBI Description	(AC002342) similar to pMS10 protein [Arabidopsis thaliana]

Seq. No.	146408
Seq. ID	LIB3168-074-P1-K1-A11
Method	BLASTX
NCBI GI	g112681
BLAST score	629
E value	9.0e-66
Match length	158
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146409
Seq. ID	LIB3168-074-P1-K1-A3
Method	BLASTX
NCBI GI	g1107501
BLAST score	420
E value	3.0e-41
Match length	139
% identity	63
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	146410
Seq. ID	LIB3168-074-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	639
E value	7.0e-67
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146411
Seq. ID	LIB3168-074-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146412
Seq. ID	LIB3168-074-P1-K1-A6
Method	BLASTX

NCBI GI	g1628583
BLAST score	393
E value	1.0e-38
Match length	78
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146413
Seq. ID	LIB3168-074-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	55
E value	1.0e-67
Match length	138
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146414
Seq. ID	LIB3168-074-P1-K1-B1
Method	BLASTX
NCBI GI	g112739
BLAST score	542
E value	1.0e-55
Match length	144
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146415
Seq. ID	LIB3168-074-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	711
E value	2.0e-75
Match length	158
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146416
Seq. ID	LIB3168-074-P1-K1-B11
Method	BLASTX
NCBI GI	g1113941
BLAST score	96
E value	3.0e-03

Match length	100
% identity	66
NCBI Description	(U40713) Pv42p [Phaseolus vulgaris]

Seq. No.	146417
Seq. ID	LIB3168-074-P1-K1-B2
Method	BLASTX
NCBI GI	g112741
BLAST score	592
E value	2.0e-61
Match length	142
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146418
Seq. ID	LIB3168-074-P1-K1-B3
Method	BLASTN
NCBI GI	g4159712
BLAST score	195
E value	1.0e-106
Match length	263
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	146419
Seq. ID	LIB3168-074-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	381
E value	1.0e-36
Match length	101
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146420
Seq. ID	LIB3168-074-P1-K1-B6
Method	BLASTN
NCBI GI	g3080430
BLAST score	272
E value	1.0e-151
Match length	496
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	146421
Seq. ID	LIB3168-074-P1-K1-B7
Method	BLASTX

NCBI GI	g4204299
BLAST score	783
E value	1.0e-83
Match length	169
% identity	90
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146422
Seq. ID	LIB3168-074-P1-K1-B8
Method	BLASTN
NCBI GI	g16231
BLAST score	55
E value	6.0e-23
Match length	67
% identity	96
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	146423
Seq. ID	LIB3168-074-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146424
Seq. ID	LIB3168-074-P1-K1-C11
Method	BLASTX
NCBI GI	g112737
BLAST score	322
E value	1.0e-29
Match length	153
% identity	49
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146425
Seq. ID	LIB3168-074-P1-K1-C12
Method	BLASTX
NCBI GI	g4204298
BLAST score	603
E value	1.0e-62
Match length	149
% identity	79
NCBI Description	(AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No.	146426
Seq. ID	LIB3168-074-P1-K1-C2
Method	BLASTX
NCBI GI	g4582468
BLAST score	722
E value	1.0e-76
Match length	146
% identity	100
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	146427
Seq. ID	LIB3168-074-P1-K1-C4
Method	BLASTN
NCBI GI	g4220645
BLAST score	165
E value	1.0e-87
Match length	380
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	146428
Seq. ID	LIB3168-074-P1-K1-C5
Method	BLASTX
NCBI GI	g112737
BLAST score	549
E value	2.0e-56
Match length	137
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146429
Seq. ID	LIB3168-074-P1-K1-C6
Method	BLASTX
NCBI GI	g112682
BLAST score	679
E value	1.0e-72
Match length	165
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146430
Seq. ID	LIB3168-074-P1-K1-C8
Method	BLASTX

NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146431
Seq. ID	LIB3168-074-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146432
Seq. ID	LIB3168-074-P1-K1-D1
Method	BLASTN
NCBI GI	g4581161
BLAST score	147
E value	6.0e-77
Match length	458
% identity	27
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	146433
Seq. ID	LIB3168-074-P1-K1-D10
Method	BLASTX
NCBI GI	g112681
BLAST score	729
E value	2.0e-77
Match length	162
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146434
Seq. ID	LIB3168-074-P1-K1-D11
Method	BLASTX
NCBI GI	g112741
BLAST score	785
E value	5.0e-84
Match length	162
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146435
Seq. ID	LIB3168-074-P1-K1-D12
Method	BLASTX
NCBI GI	g112739
BLAST score	673
E value	8.0e-71
Match length	168
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146436
Seq. ID	LIB3168-074-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146437
Seq. ID	LIB3168-074-P1-K1-D3
Method	BLASTX
NCBI GI	g4204299
BLAST score	640
E value	6.0e-67
Match length	124
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146438
Seq. ID	LIB3168-074-P1-K1-D5
Method	BLASTN
NCBI GI	g3869069
BLAST score	445
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	146439
Seq. ID	LIB3168-074-P1-K1-D6

Method	BLASTX
NCBI GI	g112741
BLAST score	862
E value	5.0e-93
Match length	160
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146440
Seq. ID	LIB3168-074-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	1.0e-63
Match length	117
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146441
Seq. ID	LIB3168-074-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	719
E value	3.0e-76
Match length	173
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146442
Seq. ID	LIB3168-074-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	626
E value	2.0e-65
Match length	167
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146443
Seq. ID	LIB3168-074-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123

% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146444
Seq. ID	LIB3168-074-P1-K1-E11
Method	BLASTN
NCBI GI	g2088638
BLAST score	468
E value	0.0e+00
Match length	484
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146445
Seq. ID	LIB3168-074-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146446
Seq. ID	LIB3168-074-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	904
E value	7.0e-98
Match length	184
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146447
Seq. ID	LIB3168-074-P1-K1-E3
Method	BLASTN
NCBI GI	g4220638
BLAST score	508
E value	0.0e+00
Match length	527
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	146448
Seq. ID	LIB3168-074-P1-K1-E4
Method	BLASTX
NCBI GI	g112739
BLAST score	321
E value	6.0e-30

Match length	83
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146449
Seq. ID	LIB3168-074-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	223
E value	5.0e-18
Match length	98
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146450
Seq. ID	LIB3168-074-P1-K1-E6
Method	BLASTX
NCBI GI	g112682
BLAST score	739
E value	2.0e-84
Match length	170
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146451
Seq. ID	LIB3168-074-P1-K1-E7
Method	BLASTX
NCBI GI	g112681
BLAST score	745
E value	3.0e-79
Match length	178
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146452
Seq. ID	LIB3168-074-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	323
E value	6.0e-30
Match length	62

% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146453
Seq. ID	LIB3168-074-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	804
E value	3.0e-86
Match length	165
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146454
Seq. ID	LIB3168-074-P1-K1-F1
Method	BLASTX
NCBI GI	g112737
BLAST score	320
E value	2.0e-29
Match length	151
% identity	49
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146455
Seq. ID	LIB3168-074-P1-K1-F11
Method	BLASTN
NCBI GI	g4691223
BLAST score	143
E value	2.0e-74
Match length	391
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	146456
Seq. ID	LIB3168-074-P1-K1-F12
Method	BLASTX
NCBI GI	g112682
BLAST score	696
E value	1.0e-73
Match length	159
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146457
Seq. ID	LIB3168-074-P1-K1-F2
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146458
Seq. ID	LIB3168-074-P1-K1-F3
Method	BLASTX
NCBI GI	g4531444
BLAST score	247
E value	6.0e-21
Match length	71
% identity	73
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	146459
Seq. ID	LIB3168-074-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	637
E value	1.0e-66
Match length	122
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146460
Seq. ID	LIB3168-074-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	673
E value	6.0e-71
Match length	154
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146461
Seq. ID	LIB3168-074-P1-K1-F6
Method	BLASTX
NCBI GI	g112737
BLAST score	549
E value	3.0e-71
Match length	163
% identity	76

NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	146462
Seq. ID	LIB3168-074-P1-K1-F7
Method	BLASTX
NCBI GI	g112739
BLAST score	676
E value	4.0e-71
Match length	170
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	146463
Seq. ID	LIB3168-074-P1-K1-F8
Method	BLASTX
NCBI GI	g1169515
BLAST score	775
E value	8.0e-83
Match length	152
% identity	97
NCBI Description	EM-LIKE PROTEIN GEA1 >gi_2119768_pir__S34819 embryonic abundant protein Em1 - Arabidopsis thaliana >gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1 protein [Arabidopsis thaliana]
Seq. No.	146464
Seq. ID	LIB3168-074-P1-K1-F9
Method	BLASTX
NCBI GI	g3335169
BLAST score	883
E value	2.0e-95
Match length	164
% identity	100
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.	146465
Seq. ID	LIB3168-074-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	675
E value	4.0e-71

Match length	158
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146466
Seq. ID	LIB3168-074-P1-K1-G10
Method	BLASTX
NCBI GI	g131289
BLAST score	69
E value	1.0e-75
Match length	171
% identity	77
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi_225285_prf__1211235W photosystem II 44kD protein [Nicotiana tabacum]

Seq. No.	146467
Seq. ID	LIB3168-074-P1-K1-G11
Method	BLASTX
NCBI GI	g119350
BLAST score	515
E value	2.0e-52
Match length	102
% identity	98
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	146468
Seq. ID	LIB3168-074-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	820
E value	4.0e-88
Match length	156
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146469
Seq. ID	LIB3168-074-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	617
E value	2.0e-64

Match length	129
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146470
Seq. ID	LIB3168-074-P1-K1-G3
Method	BLASTX
NCBI GI	g112739
BLAST score	557
E value	3.0e-57
Match length	148
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146471
Seq. ID	LIB3168-074-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	634
E value	3.0e-66
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146472
Seq. ID	LIB3168-074-P1-K1-G6
Method	BLASTX
NCBI GI	g118926
BLAST score	303
E value	1.0e-27
Match length	120
% identity	52
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	146473
Seq. ID	LIB3168-074-P1-K1-G7
Method	BLASTX
NCBI GI	g4204298
BLAST score	638
E value	8.0e-67
Match length	138
% identity	90

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146474
Seq. ID	LIB3168-074-P1-K1-G8
Method	BLASTX
NCBI GI	g3402678
BLAST score	628
E value	1.0e-65
Match length	160
% identity	79
NCBI Description	(AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	146475
Seq. ID	LIB3168-074-P1-K1-G9
Method	BLASTX
NCBI GI	g1363488
BLAST score	643
E value	2.0e-67
Match length	125
% identity	99
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	146476
Seq. ID	LIB3168-074-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	882
E value	2.0e-95
Match length	180
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146477
Seq. ID	LIB3168-074-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146478
Seq. ID	LIB3168-074-P1-K1-H12
Method	BLASTX
NCBI GI	g112682
BLAST score	530
E value	2.0e-54
Match length	102

% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146479
Seq. ID	LIB3168-074-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	631
E value	6.0e-66
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146480
Seq. ID	LIB3168-074-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146481
Seq. ID	LIB3168-074-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	255
E value	6.0e-22
Match length	136
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146482
Seq. ID	LIB3168-074-P1-K1-H8
Method	BLASTX
NCBI GI	g2129657
BLAST score	489
E value	3.0e-49
Match length	130
% identity	79
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	146483

Seq. ID	LIB3168-074-P1-K1-H9
Method	BLASTX
NCBI GI	g137465
BLAST score	778
E value	4.0e-83
Match length	157
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	146484
Seq. ID	LIB3168-075-P1-K1-A1
Method	BLASTX
NCBI GI	g112739
BLAST score	617
E value	3.0e-64
Match length	158
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146485
Seq. ID	LIB3168-075-P1-K1-A10
Method	BLASTX
NCBI GI	g112682
BLAST score	174
E value	5.0e-86
Match length	183
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146486
Seq. ID	LIB3168-075-P1-K1-A12
Method	BLASTN
NCBI GI	g3763915
BLAST score	479
E value	0.0e+00
Match length	503
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146487
Seq. ID	LIB3168-075-P1-K1-A2
Method	BLASTX

NCBI GI	g2129767
BLAST score	697
E value	1.0e-73
Match length	140
% identity	94
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	146488
Seq. ID	LIB3168-075-P1-K1-A3
Method	BLASTN
NCBI GI	g4159704
BLAST score	99
E value	6.0e-49
Match length	99
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	146489
Seq. ID	LIB3168-075-P1-K1-A4
Method	BLASTX
NCBI GI	g4204299
BLAST score	560
E value	1.0e-57
Match length	113
% identity	96
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146490
Seq. ID	LIB3168-075-P1-K1-A5
Method	BLASTX
NCBI GI	g267073
BLAST score	746
E value	2.0e-79
Match length	137
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	146491
Seq. ID	LIB3168-075-P1-K1-A6
Method	BLASTX
NCBI GI	g112743
BLAST score	713
E value	1.0e-75
Match length	148
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

	>gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]
Seq. No.	146492
Seq. ID	LIB3168-075-P1-K1-A7
Method	BLASTX
NCBI GI	g112739
BLAST score	563
E value	5.0e-58
Match length	149
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	146493
Seq. ID	LIB3168-075-P1-K1-A9
Method	BLASTX
NCBI GI	g1082359
BLAST score	174
E value	2.0e-12
Match length	68
% identity	49
NCBI Description	excision repair protein ERCC5 - human >gi_306742 (L20046) excision repair protein [Homo sapiens]
Seq. No.	146494
Seq. ID	LIB3168-075-P1-K1-B1
Method	BLASTX
NCBI GI	g112681
BLAST score	659
E value	3.0e-69
Match length	129
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146495
Seq. ID	LIB3168-075-P1-K1-B10
Method	BLASTN
NCBI GI	g1628582
BLAST score	124
E value	3.0e-63
Match length	319
% identity	58
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds
Seq. No.	146496
Seq. ID	LIB3168-075-P1-K1-B11

Method	BLASTX
NCBI GI	g129817
BLAST score	610
E value	1.0e-63
Match length	131
% identity	90
NCBI Description	BASIC PEROXIDASE E PRECURSOR >gi_81653_pir__JU0458 peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]

Seq. No.	146497
Seq. ID	LIB3168-075-P1-K1-B12
Method	BLASTX
NCBI GI	g2828281
BLAST score	482
E value	2.0e-48
Match length	171
% identity	58
NCBI Description	(AL021687) hypothetical protein [Arabidopsis thaliana] >gi_2832635_emb_CAA16764_ (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146498
Seq. ID	LIB3168-075-P1-K1-B4
Method	BLASTX
NCBI GI	g1176671
BLAST score	325
E value	5.0e-30
Match length	123
% identity	49
NCBI Description	PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 >gi_3874174_emb_CAA86666_ (Z46676) C08B11.8 [Caenorhabditis elegans]

Seq. No.	146499
Seq. ID	LIB3168-075-P1-K1-B5
Method	BLASTX
NCBI GI	g3860277
BLAST score	624
E value	4.0e-65
Match length	152
% identity	82
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	146500
Seq. ID	LIB3168-075-P1-K1-B6
Method	BLASTX
NCBI GI	g1109699
BLAST score	702
E value	3.0e-74
Match length	138
% identity	98
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	146501

Seq. ID	LIB3168-075-P1-K1-B8
Method	BLASTX
NCBI GI	g2980641
BLAST score	444
E value	4.0e-44
Match length	152
% identity	62
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	146502
Seq. ID	LIB3168-075-P1-K1-C10
Method	BLASTX
NCBI GI	g4091806
BLAST score	188
E value	3.0e-14
Match length	86
% identity	48
NCBI Description	(AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No.	146503
Seq. ID	LIB3168-075-P1-K1-C11
Method	BLASTX
NCBI GI	g112681
BLAST score	759
E value	6.0e-81
Match length	166
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146504
Seq. ID	LIB3168-075-P1-K1-C12
Method	BLASTX
NCBI GI	g4204299
BLAST score	802
E value	5.0e-86
Match length	173
% identity	90
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146505
Seq. ID	LIB3168-075-P1-K1-C2
Method	BLASTX
NCBI GI	g133916
BLAST score	605
E value	7.0e-63
Match length	124
% identity	91
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi_70857_pir__R3SP2 ribosomal protein S2 - spinach chloroplast >gi_12256_emb_CAA29343_ (X05916) rps2 protein (AA 1-236) [Spinacia oleracea]

Seq. No.	146506
Seq. ID	LIB3168-075-P1-K1-C5
Method	BLASTN
NCBI GI	g2264310
BLAST score	419
E value	0.0e+00
Match length	460
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	146507
Seq. ID	LIB3168-075-P1-K1-C6
Method	BLASTX
NCBI GI	g112682
BLAST score	766
E value	8.0e-82
Match length	160
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146508
Seq. ID	LIB3168-075-P1-K1-C7
Method	BLASTN
NCBI GI	g3449315
BLAST score	473
E value	0.0e+00
Match length	558
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	146509
Seq. ID	LIB3168-075-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146510
Seq. ID	LIB3168-075-P1-K1-C9
Method	BLASTX
NCBI GI	g82223
BLAST score	55
E value	5.0e-11
Match length	60
% identity	72
NCBI Description	hypothetical protein 70B - common tobacco chloroplast

>gi_11878_emb_CAA77391_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_1223681_emb_CAA77402_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225250_prf__1211235CJ ORF 70B [Nicotiana tabacum]

Seq. No.	146511
Seq. ID	LIB3168-075-P1-K1-D1
Method	BLASTX
NCBI GI	g2435518
BLAST score	343
E value	3.0e-32
Match length	112
% identity	68
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	146512
Seq. ID	LIB3168-075-P1-K1-D11
Method	BLASTX
NCBI GI	g2129657
BLAST score	255
E value	4.0e-30
Match length	107
% identity	74
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146513
Seq. ID	LIB3168-075-P1-K1-D12
Method	BLASTN
NCBI GI	g2104523
BLAST score	363
E value	0.0e+00
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	146514
Seq. ID	LIB3168-075-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	343
E value	1.0e-32
Match length	104
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146515
Seq. ID	LIB3168-075-P1-K1-D4
Method	BLASTX
NCBI GI	g4507311
BLAST score	215

E value	4.0e-17
Match length	103
% identity	40
NCBI Description	suppressor of Ty (S.cerevisiae) 4 homolog 1 >gi_3122873_sp_Q16550_SPT4_HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi_1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi_1401053 (U38818) SUPT4H [Homo sapiens] >gi_1401055 (U38817) SUPT4H [Homo sapiens] >gi_1401066 (U43154) Supt4h [Mus musculus] >gi_3779194 (U96809) chromatin structural protein homolog [Mus musculus]

Seq. No.	146516
Seq. ID	LIB3168-075-P1-K1-D5
Method	BLASTX
NCBI GI	g112737
BLAST score	445
E value	2.0e-44
Match length	115
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146517
Seq. ID	LIB3168-075-P1-K1-D6
Method	BLASTX
NCBI GI	g112739
BLAST score	654
E value	1.0e-68
Match length	169
% identity	76
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146518
Seq. ID	LIB3168-075-P1-K1-D9
Method	BLASTX
NCBI GI	g1903357
BLAST score	306
E value	7.0e-28
Match length	95
% identity	62
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	146519

Seq. ID	LIB3168-075-P1-K1-E10
Method	BLASTX
NCBI GI	g112681
BLAST score	455
E value	2.0e-45
Match length	140
% identity	71
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146520
Seq. ID	LIB3168-075-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	668
E value	3.0e-70
Match length	135
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146521
Seq. ID	LIB3168-075-P1-K1-E12
Method	BLASTX
NCBI GI	g4204298
BLAST score	747
E value	1.0e-79
Match length	149
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146522
Seq. ID	LIB3168-075-P1-K1-E3
Method	BLASTN
NCBI GI	g2160132
BLAST score	36
E value	2.0e-11
Match length	43
% identity	95
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	146523
Seq. ID	LIB3168-075-P1-K1-E4
Method	BLASTN
NCBI GI	g3482964
BLAST score	365
E value	0.0e+00
Match length	420
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	146524
Seq. ID	LIB3168-075-P1-K1-E5
Method	BLASTX
NCBI GI	g2529672
BLAST score	230
E value	5.0e-19
Match length	59
% identity	73
NCBI Description	(AC002535) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	146525
Seq. ID	LIB3168-075-P1-K1-E6
Method	BLASTX
NCBI GI	g1170939
BLAST score	565
E value	3.0e-58
Match length	118
% identity	90
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	146526
Seq. ID	LIB3168-075-P1-K1-E7
Method	BLASTX
NCBI GI	g132863
BLAST score	637
E value	8.0e-67
Match length	123
% identity	97
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	146527
Seq. ID	LIB3168-075-P1-K1-E8
Method	BLASTX
NCBI GI	g2154720
BLAST score	244
E value	1.0e-20
Match length	49
% identity	100
NCBI Description	(Y07648) nitrilase 1 [Arabidopsis thaliana]

Seq. No.	146528
Seq. ID	LIB3168-075-P1-K1-F10
Method	BLASTN
NCBI GI	g16181
BLAST score	40
E value	4.0e-13
Match length	279
% identity	79
NCBI Description	A.thaliana gene for tonoplast intrinsic protein

alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis thaliana tonoplast intrinsic protein (alpha-TIP) gene, complete cds

Seq. No.	146529
Seq. ID	LIB3168-075-P1-K1-F11
Method	BLASTX
NCBI GI	g112741
BLAST score	854
E value	5.0e-92
Match length	161
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146530
Seq. ID	LIB3168-075-P1-K1-F2
Method	BLASTN
NCBI GI	g3869064
BLAST score	424
E value	0.0e+00
Match length	498
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1O13, complete sequence [Arabidopsis thaliana]

Seq. No.	146531
Seq. ID	LIB3168-075-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	461
E value	2.0e-46
Match length	91
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146532
Seq. ID	LIB3168-075-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146533
Seq. ID	LIB3168-075-P1-K1-F5

Method	BLASTX
NCBI GI	g112682
BLAST score	604
E value	6.0e-63
Match length	137
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146534
Seq. ID	LIB3168-075-P1-K1-F6
Method	BLASTX
NCBI GI	g2351374
BLAST score	384
E value	4.0e-37
Match length	93
% identity	81
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No.	146535
Seq. ID	LIB3168-075-P1-K1-F7
Method	BLASTX
NCBI GI	g4337109
BLAST score	193
E value	1.0e-14
Match length	103
% identity	47
NCBI Description	(AF129756) BAT3 [Homo sapiens]

Seq. No.	146536
Seq. ID	LIB3168-075-P1-K1-F9
Method	BLASTX
NCBI GI	g112737
BLAST score	702
E value	3.0e-74
Match length	164
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146537
Seq. ID	LIB3168-075-P1-K1-G1
Method	BLASTX
NCBI GI	g2499811
BLAST score	624
E value	3.0e-65
Match length	122
% identity	98

NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	146538
Seq. ID	LIB3168-075-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	452
E value	6.0e-49
Match length	129
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146539
Seq. ID	LIB3168-075-P1-K1-G11
Method	BLASTX
NCBI GI	g4678226
BLAST score	581
E value	7.0e-61
Match length	137
% identity	93
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	146540
Seq. ID	LIB3168-075-P1-K1-G12
Method	BLASTX
NCBI GI	g112682
BLAST score	52
E value	6.0e-53
Match length	143
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146541
Seq. ID	LIB3168-075-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	667
E value	4.0e-70
Match length	161
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146542
Seq. ID	LIB3168-075-P1-K1-G4
Method	BLASTX
NCBI GI	g112739

BLAST score	435
E value	3.0e-55
Match length	141
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146543
Seq. ID	LIB3168-075-P1-K1-G5
Method	BLASTX
NCBI GI	g3292827
BLAST score	504
E value	4.0e-51
Match length	118
% identity	79
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	146544
Seq. ID	LIB3168-075-P1-K1-G6
Method	BLASTN
NCBI GI	g2342673
BLAST score	274
E value	1.0e-153
Match length	290
% identity	99
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	146545
Seq. ID	LIB3168-075-P1-K1-G7
Method	BLASTX
NCBI GI	g3924615
BLAST score	139
E value	2.0e-08
Match length	55
% identity	93
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146546
Seq. ID	LIB3168-075-P1-K1-G8
Method	BLASTX
NCBI GI	g112739
BLAST score	560
E value	2.0e-63
Match length	160
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No.	146547
Seq. ID	LIB3168-075-P1-K1-G9
Method	BLASTN
NCBI GI	g4159704
BLAST score	320
E value	1.0e-180
Match length	407
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	146548
Seq. ID	LIB3168-075-P1-K1-H10
Method	BLASTX
NCBI GI	g2245085
BLAST score	284
E value	1.0e-25
Match length	68
% identity	85
NCBI Description	(Z97343) lactate dehydrogenase [Arabidopsis thaliana]

Seq. No.	146549
Seq. ID	LIB3168-075-P1-K1-H12
Method	BLASTX
NCBI GI	g112737
BLAST score	567
E value	2.0e-58
Match length	141
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146550
Seq. ID	LIB3168-075-P1-K1-H3
Method	BLASTN
NCBI GI	g3892698
BLAST score	36
E value	2.0e-11
Match length	48
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project)

Seq. No.	146551
Seq. ID	LIB3168-075-P1-K1-H4
Method	BLASTX
NCBI GI	g112682
BLAST score	655
E value	8.0e-69
Match length	153

% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146552
Seq. ID	LIB3168-075-P1-K1-H5
Method	BLASTN
NCBI GI	g16559
BLAST score	174
E value	4.0e-93
Match length	232
% identity	95
NCBI Description	A.thaliana gene for tRNA-Ala (P-2-L)

Seq. No.	146553
Seq. ID	LIB3168-075-P1-K1-H6
Method	BLASTX
NCBI GI	g112681
BLAST score	567
E value	2.0e-58
Match length	124
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146554
Seq. ID	LIB3168-075-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	651
E value	3.0e-68
Match length	134
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146555
Seq. ID	LIB3168-075-P1-K1-H8
Method	BLASTX
NCBI GI	g112737
BLAST score	86
E value	1.0e-63
Match length	163
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	146556
Seq. ID	LIB3168-075-P1-K1-H9
Method	BLASTX
NCBI GI	g112739
BLAST score	48
E value	3.0e-49
Match length	148
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146557
Seq. ID	LIB3168-076-P1-K1-A1
Method	BLASTN
NCBI GI	g4335744
BLAST score	161
E value	3.0e-85
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146558
Seq. ID	LIB3168-076-P1-K1-A10
Method	BLASTX
NCBI GI	g2500347
BLAST score	441
E value	1.0e-43
Match length	128
% identity	71
NCBI Description	NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No.	146559
Seq. ID	LIB3168-076-P1-K1-A11
Method	BLASTN
NCBI GI	g4589428
BLAST score	433
E value	0.0e+00
Match length	491
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	146560
Seq. ID	LIB3168-076-P1-K1-A12

Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146561
Seq. ID	LIB3168-076-P1-K1-A2
Method	BLASTX
NCBI GI	g112682
BLAST score	670
E value	2.0e-70
Match length	161
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146562
Seq. ID	LIB3168-076-P1-K1-A3
Method	BLASTX
NCBI GI	g464806
BLAST score	148
E value	2.0e-09
Match length	110
% identity	32
NCBI Description	SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72) >gi_423182_pir__A40692 signal recognition particle 72K chain - dog >gi_297768_emb_CAA48014_ (X67813) signal recognition particle,72 kDa subunit [Canis familiaris]

Seq. No.	146563
Seq. ID	LIB3168-076-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	636
E value	2.0e-66
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146564
Seq. ID	LIB3168-076-P1-K1-A5
Method	BLASTN
NCBI GI	g2351067
BLAST score	355
E value	0.0e+00
Match length	429
% identity	93

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]
Seq. No.	146565
Seq. ID	LIB3168-076-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146566
Seq. ID	LIB3168-076-P1-K1-A8
Method	BLASTX
NCBI GI	g2160151
BLAST score	747
E value	2.0e-79
Match length	176
% identity	85
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]
Seq. No.	146567
Seq. ID	LIB3168-076-P1-K1-A9
Method	BLASTX
NCBI GI	g112681
BLAST score	810
E value	6.0e-87
Match length	174
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146568
Seq. ID	LIB3168-076-P1-K1-B1
Method	BLASTX
NCBI GI	g1402904
BLAST score	724
E value	7.0e-77
Match length	139
% identity	99
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]
Seq. No.	146569
Seq. ID	LIB3168-076-P1-K1-B10
Method	BLASTX
NCBI GI	g3478700
BLAST score	163
E value	8.0e-67
Match length	145

% identity	86
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	146570
Seq. ID	LIB3168-076-P1-K1-B11
Method	BLASTX
NCBI GI	g418854
BLAST score	768
E value	4.0e-82
Match length	154
% identity	18
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]

Seq. No.	146571
Seq. ID	LIB3168-076-P1-K1-B12
Method	BLASTX
NCBI GI	g2129532
BLAST score	396
E value	2.0e-38
Match length	105
% identity	73
NCBI Description	acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) - Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis thaliana]

Seq. No.	146572
Seq. ID	LIB3168-076-P1-K1-B2
Method	BLASTX
NCBI GI	g112682
BLAST score	717
E value	4.0e-76
Match length	159
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146573
Seq. ID	LIB3168-076-P1-K1-B3
Method	BLASTN
NCBI GI	g4512690
BLAST score	455
E value	0.0e+00
Match length	490
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	146574
Seq. ID	LIB3168-076-P1-K1-B4
Method	BLASTX

NCBI GI	g3367515
BLAST score	709
E value	5.0e-75
Match length	141
% identity	96
NCBI Description	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb_AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No.	146575
Seq. ID	LIB3168-076-P1-K1-B5
Method	BLASTN
NCBI GI	g3449323
BLAST score	51
E value	8.0e-20
Match length	71
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No.	146576
Seq. ID	LIB3168-076-P1-K1-B6
Method	BLASTX
NCBI GI	g112681
BLAST score	749
E value	9.0e-80
Match length	174
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146577
Seq. ID	LIB3168-076-P1-K1-B7
Method	BLASTX
NCBI GI	g4218121
BLAST score	588
E value	7.0e-61
Match length	172
% identity	67
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	146578
Seq. ID	LIB3168-076-P1-K1-B8
Method	BLASTN
NCBI GI	g3046847
BLAST score	296
E value	1.0e-165
Match length	556
% identity	75
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	146579
Seq. ID	LIB3168-076-P1-K1-B9

Method	BLASTX
NCBI GI	g2129657
BLAST score	534
E value	2.0e-54
Match length	137
% identity	81
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146580
Seq. ID	LIB3168-076-P1-K1-C1
Method	BLASTX
NCBI GI	g1817546
BLAST score	175
E value	4.0e-13
Match length	64
% identity	55
NCBI Description	(D83997) mabinlin [Capparis masaikai]

Seq. No.	146581
Seq. ID	LIB3168-076-P1-K1-C10
Method	BLASTX
NCBI GI	g112737
BLAST score	588
E value	6.0e-61
Match length	141
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146582
Seq. ID	LIB3168-076-P1-K1-C11
Method	BLASTX
NCBI GI	g112737
BLAST score	613
E value	8.0e-64
Match length	149
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146583
Seq. ID	LIB3168-076-P1-K1-C12
Method	BLASTX
NCBI GI	g112682

BLAST score	697
E value	1.0e-73
Match length	169
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146584
Seq. ID	LIB3168-076-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	760
E value	5.0e-81
Match length	159
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146585
Seq. ID	LIB3168-076-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	744
E value	4.0e-79
Match length	155
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146586
Seq. ID	LIB3168-076-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	577
E value	1.0e-59
Match length	145
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146587
Seq. ID	LIB3168-076-P1-K1-C6
Method	BLASTX
NCBI GI	g2622714
BLAST score	329
E value	2.0e-30
Match length	136
% identity	46
NCBI Description	(AE000918) phosphonopyruvate decarboxylase [Methanobacterium thermoautotrophicum]

Seq. No.	146588
Seq. ID	LIB3168-076-P1-K1-C7
Method	BLASTX
NCBI GI	g112681
BLAST score	609
E value	1.0e-63
Match length	121
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146589
Seq. ID	LIB3168-076-P1-K1-C8
Method	BLASTX
NCBI GI	g112737
BLAST score	331
E value	3.0e-31
Match length	84
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146590
Seq. ID	LIB3168-076-P1-K1-C9
Method	BLASTX
NCBI GI	g114661
BLAST score	621
E value	1.0e-64
Match length	129
% identity	91
NCBI Description	ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) >gi_67924_pir__LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast >gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit [Nicotiana tabacum] >gi_225273_prf__1211235H ATPase a [Nicotiana tabacum]

Seq. No.	146591
Seq. ID	LIB3168-076-P1-K1-D1
Method	BLASTX
NCBI GI	g112737
BLAST score	280
E value	7.0e-25
Match length	124
% identity	52
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146592
Seq. ID	LIB3168-076-P1-K1-D10
Method	BLASTN
NCBI GI	g4096078
BLAST score	38
E value	4.0e-12
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146593
Seq. ID	LIB3168-076-P1-K1-D11
Method	BLASTX
NCBI GI	g2129657
BLAST score	337
E value	5.0e-35
Match length	109
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146594
Seq. ID	LIB3168-076-P1-K1-D12
Method	BLASTN
NCBI GI	g336275
BLAST score	222
E value	1.0e-122
Match length	330
% identity	91
NCBI Description	Alnus incana chloroplast tRNA-Ala-tgc (trnA) and tRNA-Ile-gta (trnI) genes, complete cds

Seq. No.	146595
Seq. ID	LIB3168-076-P1-K1-D4
Method	BLASTN
NCBI GI	g2828182
BLAST score	533
E value	0.0e+00
Match length	552
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	146596
Seq. ID	LIB3168-076-P1-K1-D5
Method	BLASTX
NCBI GI	g112739
BLAST score	588
E value	6.0e-61
Match length	152

% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	146597
Seq. ID	LIB3168-076-P1-K1-D6
Method	BLASTX
NCBI GI	g1345973
BLAST score	638
E value	9.0e-67
Match length	137
% identity	84
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]
Seq. No.	146598
Seq. ID	LIB3168-076-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	485
E value	6.0e-49
Match length	117
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146599
Seq. ID	LIB3168-076-P1-K1-D8
Method	BLASTX
NCBI GI	g112739
BLAST score	440
E value	1.0e-64
Match length	168
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	146600
Seq. ID	LIB3168-076-P1-K1-D9

Method	BLASTX
NCBI GI	g112681
BLAST score	648
E value	6.0e-68
Match length	165
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146601
Seq. ID	LIB3168-076-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146602
Seq. ID	LIB3168-076-P1-K1-E10
Method	BLASTN
NCBI GI	g2618601
BLAST score	68
E value	7.0e-30
Match length	100
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	146603
Seq. ID	LIB3168-076-P1-K1-E11
Method	BLASTX
NCBI GI	g112681
BLAST score	639
E value	5.0e-67
Match length	125
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146604
Seq. ID	LIB3168-076-P1-K1-E12
Method	BLASTX
NCBI GI	g1351272
BLAST score	512
E value	4.0e-52
Match length	124
% identity	84

NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]
Seq. No.	146605
Seq. ID	LIB3168-076-P1-K1-E2
Method	BLASTX
NCBI GI	g4584535
BLAST score	252
E value	2.0e-21
Match length	48
% identity	98
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]
Seq. No.	146606
Seq. ID	LIB3168-076-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146607
Seq. ID	LIB3168-076-P1-K1-E4
Method	BLASTX
NCBI GI	g4204299
BLAST score	736
E value	3.0e-78
Match length	165
% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	146608
Seq. ID	LIB3168-076-P1-K1-E5
Method	BLASTX
NCBI GI	g112681
BLAST score	687
E value	2.0e-72
Match length	146
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	146609
Seq. ID	LIB3168-076-P1-K1-E6
Method	BLASTX
NCBI GI	g3176714
BLAST score	871

E value 4.0e-94
Match length 170
% identity 99
NCBI Description (AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No. 146610
Seq. ID LIB3168-076-P1-K1-E8
Method BLASTX
NCBI GI g112682
BLAST score 646
E value 5.0e-68
Match length 154
% identity 84
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146611
Seq. ID LIB3168-076-P1-K1-E9
Method BLASTN
NCBI GI g2182286
BLAST score 167
E value 5.0e-89
Match length 259
% identity 91
NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 146612
Seq. ID LIB3168-076-P1-K1-F11
Method BLASTX
NCBI GI g112739
BLAST score 500
E value 1.0e-50
Match length 142
% identity 71
NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 146613
Seq. ID LIB3168-076-P1-K1-F12
Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146614
Seq. ID	LIB3168-076-P1-K1-F2
Method	BLASTN
NCBI GI	g1707006
BLAST score	434
E value	0.0e+00
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146615
Seq. ID	LIB3168-076-P1-K1-F3
Method	BLASTX
NCBI GI	g112681
BLAST score	525
E value	3.0e-65
Match length	176
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146616
Seq. ID	LIB3168-076-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	519
E value	7.0e-53
Match length	146
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146617
Seq. ID	LIB3168-076-P1-K1-F6
Method	BLASTX
NCBI GI	g112682
BLAST score	524
E value	9.0e-75
Match length	169
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146618
Seq. ID	LIB3168-076-P1-K1-F7
Method	BLASTX
NCBI GI	g112681

BLAST score	506
E value	4.0e-52
Match length	147
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146619
Seq. ID	LIB3168-076-P1-K1-F8
Method	BLASTX
NCBI GI	g1617268
BLAST score	437
E value	5.0e-60
Match length	140
% identity	82
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	146620
Seq. ID	LIB3168-076-P1-K1-F9
Method	BLASTX
NCBI GI	g4469003
BLAST score	601
E value	8.0e-68
Match length	152
% identity	87
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	146621
Seq. ID	LIB3168-076-P1-K1-G1
Method	BLASTX
NCBI GI	g2129657
BLAST score	458
E value	1.0e-45
Match length	121
% identity	79
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146622
Seq. ID	LIB3168-076-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146623
Seq. ID	LIB3168-076-P1-K1-G2

Method	BLASTX
NCBI GI	g112681
BLAST score	596
E value	6.0e-62
Match length	138
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146624
Seq. ID	LIB3168-076-P1-K1-G3
Method	BLASTX
NCBI GI	g112682
BLAST score	607
E value	3.0e-63
Match length	142
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146625
Seq. ID	LIB3168-076-P1-K1-G4
Method	BLASTX
NCBI GI	g112682
BLAST score	737
E value	2.0e-78
Match length	163
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146626
Seq. ID	LIB3168-076-P1-K1-G5
Method	BLASTX
NCBI GI	g112739
BLAST score	516
E value	2.0e-52
Match length	139
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146627

Seq. ID	LIB3168-076-P1-K1-G6
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	7.0e-69
Match length	162
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146628
Seq. ID	LIB3168-076-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	767
E value	5.0e-82
Match length	148
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146629
Seq. ID	LIB3168-076-P1-K1-G8
Method	BLASTX
NCBI GI	g1742961
BLAST score	236
E value	4.0e-20
Match length	87
% identity	55
NCBI Description	(X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	146630
Seq. ID	LIB3168-076-P1-K1-G9
Method	BLASTX
NCBI GI	g4204299
BLAST score	688
E value	1.0e-72
Match length	135
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146631
Seq. ID	LIB3168-076-P1-K1-H1
Method	BLASTX
NCBI GI	g112741
BLAST score	545
E value	4.0e-56
Match length	101
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146632
Seq. ID	LIB3168-076-P1-K1-H10
Method	BLASTX
NCBI GI	g418854
BLAST score	654
E value	1.0e-68
Match length	136
% identity	17
NCBI Description	ubiquitin precursor - parsley >gi_288112_emb_CAA45621_ (X64344) polyubiquitin [Petroselinum crispum] >gi_288114_emb_CAA45622_ (X64345) polyubiquitin [Petroselinum crispum]

Seq. No.	146633
Seq. ID	LIB3168-076-P1-K1-H11
Method	BLASTN
NCBI GI	g3869062
BLAST score	46
E value	1.0e-16
Match length	115
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	146634
Seq. ID	LIB3168-076-P1-K1-H12
Method	BLASTX
NCBI GI	g3335169
BLAST score	656
E value	2.0e-74
Match length	144
% identity	95
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	146635
Seq. ID	LIB3168-076-P1-K1-H2
Method	BLASTN
NCBI GI	g4206762
BLAST score	243
E value	1.0e-134
Match length	363
% identity	95
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	146636
Seq. ID	LIB3168-076-P1-K1-H4
Method	BLASTN
NCBI GI	g2443899

BLAST score	298
E value	1.0e-167
Match length	475
% identity	100
NCBI Description	Arabidopsis thaliana BAC T3F12 from chromosome IV near 24 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	146637
Seq. ID	LIB3168-076-P1-K1-H5
Method	BLASTX
NCBI GI	g112737
BLAST score	572
E value	4.0e-59
Match length	140
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146638
Seq. ID	LIB3168-076-P1-K1-H6
Method	BLASTX
NCBI GI	g112737
BLAST score	399
E value	5.0e-39
Match length	105
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146639
Seq. ID	LIB3168-076-P1-K1-H7
Method	BLASTN
NCBI GI	g4159707
BLAST score	223
E value	1.0e-122
Match length	404
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	146640
Seq. ID	LIB3168-076-P1-K1-H8
Method	BLASTX
NCBI GI	g1628583
BLAST score	448
E value	2.0e-44
Match length	122

% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146641
Seq. ID	LIB3168-076-P1-K1-H9
Method	BLASTN
NCBI GI	g1497986
BLAST score	347
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana SCARECROW (SCARECROW1) gene, complete cds

Seq. No.	146642
Seq. ID	LIB3168-077-P1-K1-A1
Method	BLASTX
NCBI GI	g4204298
BLAST score	574
E value	2.0e-59
Match length	129
% identity	85
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146643
Seq. ID	LIB3168-077-P1-K1-A10
Method	BLASTX
NCBI GI	g3142289
BLAST score	420
E value	3.0e-41
Match length	123
% identity	67
NCBI Description	(AC002411) Strong similarity to beta-keto-Coa synthase gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]

Seq. No.	146644
Seq. ID	LIB3168-077-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146645
Seq. ID	LIB3168-077-P1-K1-A12
Method	BLASTX
NCBI GI	g2129639
BLAST score	697
E value	9.0e-74
Match length	136

% identity	100
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	146646
Seq. ID	LIB3168-077-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	757
E value	8.0e-81
Match length	147
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146647
Seq. ID	LIB3168-077-P1-K1-A3
Method	BLASTX
NCBI GI	g1107501
BLAST score	404
E value	2.0e-39
Match length	127
% identity	65
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	146648
Seq. ID	LIB3168-077-P1-K1-A7
Method	BLASTN
NCBI GI	g4468103
BLAST score	240
E value	1.0e-132
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	146649
Seq. ID	LIB3168-077-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	385
E value	3.0e-37
Match length	72
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146650
Seq. ID	LIB3168-077-P1-K1-B10
Method	BLASTN
NCBI GI	g2864607

BLAST score	463
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	146651
Seq. ID	LIB3168-077-P1-K1-B11
Method	BLASTX
NCBI GI	g881615
BLAST score	797
E value	2.0e-85
Match length	153
% identity	100
NCBI Description	(U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No.	146652
Seq. ID	LIB3168-077-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	593
E value	2.0e-61
Match length	113
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146653
Seq. ID	LIB3168-077-P1-K1-B6
Method	BLASTX
NCBI GI	g112741
BLAST score	691
E value	5.0e-73
Match length	132
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146654
Seq. ID	LIB3168-077-P1-K1-B7
Method	BLASTX
NCBI GI	g2492952
BLAST score	215
E value	3.0e-17
Match length	55
% identity	67
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)

>gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	146655
Seq. ID	LIB3168-077-P1-K1-B8
Method	BLASTX
NCBI GI	g115783
BLAST score	676
E value	3.0e-71
Match length	128
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	146656
Seq. ID	LIB3168-077-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146657
Seq. ID	LIB3168-077-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146658
Seq. ID	LIB3168-077-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146659
Seq. ID	LIB3168-077-P1-K1-C2
Method	BLASTX
NCBI GI	g4204260

BLAST score	257
E value	3.0e-22
Match length	59
% identity	86
NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]

Seq. No.	146660
Seq. ID	LIB3168-077-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	655
E value	8.0e-69
Match length	150
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146661
Seq. ID	LIB3168-077-P1-K1-C4
Method	BLASTN
NCBI GI	g4191760
BLAST score	221
E value	1.0e-121
Match length	425
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	146662
Seq. ID	LIB3168-077-P1-K1-C6
Method	BLASTN
NCBI GI	g3133272
BLAST score	35
E value	4.0e-10
Match length	43
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	146663
Seq. ID	LIB3168-077-P1-K1-D10
Method	BLASTX
NCBI GI	g112681
BLAST score	668
E value	2.0e-70
Match length	150
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146664

Seq. ID	LIB3168-077-P1-K1-D11
Method	BLASTN
NCBI GI	g3540210
BLAST score	350
E value	0.0e+00
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146665
Seq. ID	LIB3168-077-P1-K1-D12
Method	BLASTX
NCBI GI	g3335171
BLAST score	605
E value	6.0e-63
Match length	141
% identity	83
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	146666
Seq. ID	LIB3168-077-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146667
Seq. ID	LIB3168-077-P1-K1-D3
Method	BLASTX
NCBI GI	g112682
BLAST score	650
E value	3.0e-68
Match length	148
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146668
Seq. ID	LIB3168-077-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	816
E value	1.0e-87
Match length	155
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146669
Seq. ID	LIB3168-077-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	739
E value	1.0e-78
Match length	154
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146670
Seq. ID	LIB3168-077-P1-K1-D7
Method	BLASTX
NCBI GI	g112737
BLAST score	624
E value	3.0e-65
Match length	146
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146671
Seq. ID	LIB3168-077-P1-K1-D8
Method	BLASTX
NCBI GI	g2894562
BLAST score	216
E value	2.0e-17
Match length	39
% identity	97
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	146672
Seq. ID	LIB3168-077-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146673
Seq. ID	LIB3168-077-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	653
E value	1.0e-68

Match length	156
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146674
Seq. ID	LIB3168-077-P1-K1-E10
Method	BLASTN
NCBI GI	g166610
BLAST score	34
E value	6.0e-10
Match length	94
% identity	84
NCBI Description	A.thaliana at2S2 gene encoding albumin 2S subunit 2, complete cds

Seq. No.	146675
Seq. ID	LIB3168-077-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	62
E value	6.0e-55
Match length	119
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146676
Seq. ID	LIB3168-077-P1-K1-E12
Method	BLASTX
NCBI GI	g112682
BLAST score	662
E value	1.0e-69
Match length	146
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146677
Seq. ID	LIB3168-077-P1-K1-E2
Method	BLASTX
NCBI GI	g3337356
BLAST score	597
E value	5.0e-62
Match length	118
% identity	99
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	146678
Seq. ID	LIB3168-077-P1-K1-E3
Method	BLASTN

NCBI GI	g4691223
BLAST score	407
E value	0.0e+00
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	146679
Seq. ID	LIB3168-077-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	120
E value	7.0e-23
Match length	85
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146680
Seq. ID	LIB3168-077-P1-K1-E6
Method	BLASTN
NCBI GI	g2264321
BLAST score	328
E value	0.0e+00
Match length	472
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	146681
Seq. ID	LIB3168-077-P1-K1-E8
Method	BLASTX
NCBI GI	g3860247
BLAST score	659
E value	3.0e-69
Match length	131
% identity	92
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	146682
Seq. ID	LIB3168-077-P1-K1-E9
Method	BLASTN
NCBI GI	g166610
BLAST score	127
E value	4.0e-65
Match length	269
% identity	90
NCBI Description	A.thaliana at2S2 gene encoding albumin 2S subunit 2, complete cds

Seq. No.	146683
Seq. ID	LIB3168-077-P1-K1-F1
Method	BLASTX
NCBI GI	g112682
BLAST score	718

E value	3.0e-76
Match length	149
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146684
Seq. ID	LIB3168-077-P1-K1-F10
Method	BLASTX
NCBI GI	g136739
BLAST score	459
E value	8.0e-46
Match length	142
% identity	65
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	146685
Seq. ID	LIB3168-077-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146686
Seq. ID	LIB3168-077-P1-K1-F12
Method	BLASTX
NCBI GI	g4539005
BLAST score	348
E value	8.0e-33
Match length	149
% identity	46
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	146687
Seq. ID	LIB3168-077-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	282
E value	6.0e-36
Match length	82
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146688
Seq. ID	LIB3168-077-P1-K1-F4
Method	BLASTX
NCBI GI	g4325282
BLAST score	306
E value	7.0e-28
Match length	59
% identity	93
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	146689
Seq. ID	LIB3168-077-P1-K1-F5
Method	BLASTX
NCBI GI	g112682
BLAST score	655
E value	8.0e-69
Match length	149
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146690
Seq. ID	LIB3168-077-P1-K1-F6
Method	BLASTX
NCBI GI	g112681
BLAST score	691
E value	5.0e-73
Match length	139
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146691
Seq. ID	LIB3168-077-P1-K1-F7
Method	BLASTX
NCBI GI	g112682
BLAST score	459
E value	7.0e-46
Match length	147
% identity	65
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146692
Seq. ID	LIB3168-077-P1-K1-F8
Method	BLASTX

NCBI GI	g267073
BLAST score	638
E value	7.0e-67
Match length	117
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	146693
Seq. ID	LIB3168-077-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146694
Seq. ID	LIB3168-077-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	265
E value	3.0e-42
Match length	126
% identity	63
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146695
Seq. ID	LIB3168-077-P1-K1-G11
Method	BLASTX
NCBI GI	g2392769
BLAST score	272
E value	6.0e-24
Match length	100
% identity	50
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	146696
Seq. ID	LIB3168-077-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	9.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146697
Seq. ID	LIB3168-077-P1-K1-G2
Method	BLASTX
NCBI GI	g112681
BLAST score	737
E value	2.0e-78
Match length	139
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146698
Seq. ID	LIB3168-077-P1-K1-G3
Method	BLASTN
NCBI GI	g4584841
BLAST score	30
E value	4.0e-07
Match length	476
% identity	45
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	146699
Seq. ID	LIB3168-077-P1-K1-G4
Method	BLASTX
NCBI GI	g404690
BLAST score	219
E value	1.0e-17
Match length	89
% identity	45
NCBI Description	(L19075) cytochrome P450 [Catharanthus roseus]

Seq. No.	146700
Seq. ID	LIB3168-077-P1-K1-G5
Method	BLASTX
NCBI GI	g3157931
BLAST score	276
E value	2.0e-45
Match length	96
% identity	99
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	146701
Seq. ID	LIB3168-077-P1-K1-G7
Method	BLASTX
NCBI GI	g112741
BLAST score	771
E value	2.0e-82
Match length	144

% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146702
Seq. ID	LIB3168-077-P1-K1-G8
Method	BLASTX
NCBI GI	g136739
BLAST score	453
E value	4.0e-45
Match length	142
% identity	64
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	146703
Seq. ID	LIB3168-077-P1-K1-G9
Method	BLASTX
NCBI GI	g3747050
BLAST score	326
E value	3.0e-30
Match length	69
% identity	87
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	146704
Seq. ID	LIB3168-077-P1-K1-H1
Method	BLASTX
NCBI GI	g112682
BLAST score	615
E value	4.0e-64
Match length	138
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146705
Seq. ID	LIB3168-077-P1-K1-H11
Method	BLASTX
NCBI GI	g1170503
BLAST score	622
E value	4.0e-65
Match length	124
% identity	98
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor

eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	146706
Seq. ID	LIB3168-077-P1-K1-H12
Method	BLASTX
NCBI GI	g2605714
BLAST score	489
E value	2.0e-49
Match length	115
% identity	83
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	146707
Seq. ID	LIB3168-077-P1-K1-H2
Method	BLASTN
NCBI GI	g2114077
BLAST score	160
E value	1.0e-84
Match length	419
% identity	95
NCBI Description	Arabidopsis thaliana DNA for larger subunit of Rubisco, beta subunit of coupling factor one, partial cds

Seq. No.	146708
Seq. ID	LIB3168-077-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	523
E value	1.0e-53
Match length	102
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146709
Seq. ID	LIB3168-077-P1-K1-H6
Method	BLASTX
NCBI GI	g2129659
BLAST score	412
E value	2.0e-40
Match length	129
% identity	69
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	146710
Seq. ID	LIB3168-077-P1-K1-H7
Method	BLASTN
NCBI GI	g4220633
BLAST score	117
E value	6.0e-59
Match length	197
% identity	95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	146711
Seq. ID	LIB3168-077-P1-K1-H8
Method	BLASTX
NCBI GI	g1561730
BLAST score	153
E value	6.0e-10
Match length	58
% identity	47
NCBI Description	(U65491) Dreg-3 protein [Drosophila melanogaster]

Seq. No.	146712
Seq. ID	LIB3168-077-P1-K1-H9
Method	BLASTX
NCBI GI	g2605714
BLAST score	185
E value	1.0e-49
Match length	125
% identity	85
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	146713
Seq. ID	LIB3168-078-P1-K1-A1
Method	BLASTN
NCBI GI	g2959729
BLAST score	399
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	146714
Seq. ID	LIB3168-078-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	413
E value	2.0e-40
Match length	92
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146715
Seq. ID	LIB3168-078-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	283
E value	2.0e-25
Match length	54
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146716
Seq. ID	LIB3168-078-P1-K1-A2
Method	BLASTN
NCBI GI	g16231
BLAST score	159
E value	2.0e-84
Match length	183
% identity	97
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	146717
Seq. ID	LIB3168-078-P1-K1-A3
Method	BLASTX
NCBI GI	g112682
BLAST score	775
E value	7.0e-83
Match length	152
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146718
Seq. ID	LIB3168-078-P1-K1-A4
Method	BLASTX
NCBI GI	g112740
BLAST score	269
E value	1.0e-23
Match length	117
% identity	52
NCBI Description	NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81691_pir__A25997 napin precursor (napA) - rape >gi_167153 (J02586) prepronapin [Brassica napus] >gi_167155 (J02798) napin [Brassica napus]

Seq. No.	146719
Seq. ID	LIB3168-078-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	760
E value	4.0e-81
Match length	151
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146720
Seq. ID	LIB3168-078-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	424

E value	9.0e-42
Match length	96
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146721
Seq. ID	LIB3168-078-P1-K1-A7
Method	BLASTX
NCBI GI	g112682
BLAST score	636
E value	1.0e-66
Match length	146
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146722
Seq. ID	LIB3168-078-P1-K1-A8
Method	BLASTX
NCBI GI	g2129657
BLAST score	50
E value	5.0e-53
Match length	142
% identity	82
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146723
Seq. ID	LIB3168-078-P1-K1-A9
Method	BLASTX
NCBI GI	g112681
BLAST score	696
E value	1.0e-73
Match length	156
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146724
Seq. ID	LIB3168-078-P1-K1-B1
Method	BLASTX
NCBI GI	g2129657
BLAST score	454
E value	3.0e-45
Match length	120
% identity	79
NCBI Description	oleosin isoform - Arabidopsis thaliana

	>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]
Seq. No.	146725
Seq. ID	LIB3168-078-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	465
E value	1.0e-46
Match length	91
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146726
Seq. ID	LIB3168-078-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	522
E value	3.0e-53
Match length	112
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	146727
Seq. ID	LIB3168-078-P1-K1-B12
Method	BLASTN
NCBI GI	g2924729
BLAST score	330
E value	0.0e+00
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.	146728
Seq. ID	LIB3168-078-P1-K1-B2
Method	BLASTX
NCBI GI	g4204299
BLAST score	625
E value	2.0e-65
Match length	125
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	146729
Seq. ID	LIB3168-078-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	589
E value	4.0e-61
Match length	151

% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146730
Seq. ID	LIB3168-078-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	536
E value	6.0e-55
Match length	120
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146731
Seq. ID	LIB3168-078-P1-K1-B6
Method	BLASTX
NCBI GI	g112681
BLAST score	543
E value	1.0e-55
Match length	132
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146732
Seq. ID	LIB3168-078-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	589
E value	5.0e-61
Match length	120
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146733
Seq. ID	LIB3168-078-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	549
E value	2.0e-56
Match length	103
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146734
Seq. ID	LIB3168-078-P1-K1-B9

Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146735
Seq. ID	LIB3168-078-P1-K1-C10
Method	BLASTX
NCBI GI	g2735841
BLAST score	157
E value	1.0e-10
Match length	73
% identity	49
NCBI Description	(AF010283) No definition line found [Sorghum bicolor]

Seq. No.	146736
Seq. ID	LIB3168-078-P1-K1-C11
Method	BLASTX
NCBI GI	g4510397
BLAST score	629
E value	9.0e-66
Match length	138
% identity	87
NCBI Description	(AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No.	146737
Seq. ID	LIB3168-078-P1-K1-C12
Method	BLASTX
NCBI GI	g3184281
BLAST score	388
E value	1.0e-37
Match length	120
% identity	62
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	146738
Seq. ID	LIB3168-078-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	665
E value	5.0e-70
Match length	150
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146739
Seq. ID	LIB3168-078-P1-K1-C4
Method	BLASTX

NCBI GI	g1628583
BLAST score	573
E value	2.0e-59
Match length	117
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146740
Seq. ID	LIB3168-078-P1-K1-C5
Method	BLASTN
NCBI GI	g3402745
BLAST score	64
E value	2.0e-27
Match length	289
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	146741
Seq. ID	LIB3168-078-P1-K1-C6
Method	BLASTX
NCBI GI	g112741
BLAST score	570
E value	5.0e-59
Match length	109
% identity	96
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146742
Seq. ID	LIB3168-078-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	558
E value	2.0e-57
Match length	123
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146743
Seq. ID	LIB3168-078-P1-K1-C8
Method	BLASTX
NCBI GI	g2129767
BLAST score	631
E value	4.0e-66
Match length	130
% identity	92
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta

precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	146744
Seq. ID	LIB3168-078-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	746
E value	2.0e-79
Match length	143
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146745
Seq. ID	LIB3168-078-P1-K1-D1
Method	BLASTX
NCBI GI	g112681
BLAST score	616
E value	3.0e-64
Match length	125
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146746
Seq. ID	LIB3168-078-P1-K1-D11
Method	BLASTN
NCBI GI	g2244747
BLAST score	39
E value	6.0e-13
Match length	122
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	146747
Seq. ID	LIB3168-078-P1-K1-D12
Method	BLASTX
NCBI GI	g1173103
BLAST score	569
E value	9.0e-59
Match length	98
% identity	99
NCBI Description	RIBONUCLEASE 1 PRECURSOR >gi_561998 (U05206) ribonuclease [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease, RNS1 [Arabidopsis thaliana]

Seq. No.	146748
Seq. ID	LIB3168-078-P1-K1-D2
Method	BLASTN
NCBI GI	g1628582
BLAST score	75

E value	5.0e-34
Match length	202
% identity	91
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	146749
Seq. ID	LIB3168-078-P1-K1-D3
Method	BLASTN
NCBI GI	g2842474
BLAST score	18
E value	1.6e+00
Match length	93
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146750
Seq. ID	LIB3168-078-P1-K1-D4
Method	BLASTX
NCBI GI	g2583125
BLAST score	582
E value	2.0e-60
Match length	128
% identity	88
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	146751
Seq. ID	LIB3168-078-P1-K1-D6
Method	BLASTX
NCBI GI	g112737
BLAST score	593
E value	2.0e-61
Match length	141
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146752
Seq. ID	LIB3168-078-P1-K1-D8
Method	BLASTX
NCBI GI	g2129657
BLAST score	512
E value	4.0e-52
Match length	127
% identity	84
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146753
Seq. ID	LIB3168-078-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	630
E value	5.0e-66
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146754
Seq. ID	LIB3168-078-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	1.0e-64
Match length	123
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146755
Seq. ID	LIB3168-078-P1-K1-E11
Method	BLASTX
NCBI GI	g112741
BLAST score	645
E value	1.0e-67
Match length	119
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146756
Seq. ID	LIB3168-078-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	608
E value	3.0e-63
Match length	123
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146757
Seq. ID	LIB3168-078-P1-K1-E2
Method	BLASTX
NCBI GI	g112681
BLAST score	47

E value	4.0e-44
Match length	136
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146758
Seq. ID	LIB3168-078-P1-K1-E3
Method	BLASTX
NCBI GI	g112737
BLAST score	490
E value	3.0e-54
Match length	124
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146759
Seq. ID	LIB3168-078-P1-K1-E4
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	4.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146760
Seq. ID	LIB3168-078-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	558
E value	2.0e-59
Match length	175
% identity	67
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146761
Seq. ID	LIB3168-078-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	580
E value	5.0e-60

Match length	123
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146762
Seq. ID	LIB3168-078-P1-K1-E7
Method	BLASTX
NCBI GI	g2497543
BLAST score	184
E value	1.0e-13
Match length	59
% identity	64
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379 pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_ (Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No.	146763
Seq. ID	LIB3168-078-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	66
E value	2.0e-57
Match length	137
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146764
Seq. ID	LIB3168-078-P1-K1-E9
Method	BLASTN
NCBI GI	g4006885
BLAST score	289
E value	1.0e-161
Match length	425
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	146765
Seq. ID	LIB3168-078-P1-K1-F1
Method	BLASTX
NCBI GI	g4204299
BLAST score	481
E value	1.0e-48
Match length	99
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146766
Seq. ID	LIB3168-078-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	420

E value	3.0e-41
Match length	114
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146767
Seq. ID	LIB3168-078-P1-K1-F11
Method	BLASTX
NCBI GI	g112737
BLAST score	663
E value	1.0e-69
Match length	140
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146768
Seq. ID	LIB3168-078-P1-K1-F12
Method	BLASTX
NCBI GI	g1113941
BLAST score	97
E value	2.0e-03
Match length	77
% identity	70
NCBI Description	(U40713) Pv42p [Phaseolus vulgaris]

Seq. No.	146769
Seq. ID	LIB3168-078-P1-K1-F2
Method	BLASTX
NCBI GI	g4406773
BLAST score	397
E value	2.0e-50
Match length	137
% identity	49
NCBI Description	(AC006836) putative cell division control protein 48 [Arabidopsis thaliana]

Seq. No.	146770
Seq. ID	LIB3168-078-P1-K1-F3
Method	BLASTX
NCBI GI	g2815905
BLAST score	184
E value	8.0e-14
Match length	72
% identity	54
NCBI Description	(AF043734) Pros45 proteosome subunit homolog [Drosophila melanogaster]

Seq. No.	146771
Seq. ID	LIB3168-078-P1-K1-F6

Method	BLASTN
NCBI GI	g4191771
BLAST score	383
E value	0.0e+00
Match length	467
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146772
Seq. ID	LIB3168-078-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	506
E value	2.0e-51
Match length	107
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146773
Seq. ID	LIB3168-078-P1-K1-F8
Method	BLASTX
NCBI GI	g112681
BLAST score	549
E value	2.0e-56
Match length	129
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146774
Seq. ID	LIB3168-078-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	559
E value	9.0e-58
Match length	112
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146775
Seq. ID	LIB3168-078-P1-K1-G1
Method	BLASTX
NCBI GI	g21911
BLAST score	154
E value	4.0e-10
Match length	66
% identity	42
NCBI Description	(X62625) vicilin [Theobroma cacao]

Seq. No.	146776
Seq. ID	LIB3168-078-P1-K1-G10
Method	BLASTN
NCBI GI	g3461810
BLAST score	237
E value	1.0e-130
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146777
Seq. ID	LIB3168-078-P1-K1-G11
Method	BLASTX
NCBI GI	g112741
BLAST score	616
E value	2.0e-64
Match length	118
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146778
Seq. ID	LIB3168-078-P1-K1-G12
Method	BLASTX
NCBI GI	g3176874
BLAST score	805
E value	2.0e-86
Match length	160
% identity	96
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	146779
Seq. ID	LIB3168-078-P1-K1-G2
Method	BLASTX
NCBI GI	g4773906
BLAST score	507
E value	2.0e-51
Match length	109
% identity	89
NCBI Description	(AF074021) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	146780
Seq. ID	LIB3168-078-P1-K1-G3
Method	BLASTX
NCBI GI	g128859
BLAST score	739
E value	1.0e-78
Match length	154
% identity	88

NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT J (ORF 158) >gi_82206_pir__A05194 hypothetical protein 158 - common tobacco chloroplast >gi_11836_emb_CAA77356_ (Z00044) NADH dehydrogenase 30kD subunit [Nicotiana tabacum] >gi_225204_prf__1211235AJ ORF 158 [Nicotiana tabacum]

Seq. No.	146781
Seq. ID	LIB3168-078-P1-K1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	634
E value	2.0e-66
Match length	142
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146782
Seq. ID	LIB3168-078-P1-K1-G6
Method	BLASTX
NCBI GI	g112743
BLAST score	613
E value	6.0e-64
Match length	130
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	146783
Seq. ID	LIB3168-078-P1-K1-G8
Method	BLASTX
NCBI GI	g3980378
BLAST score	473
E value	4.0e-59
Match length	113
% identity	98
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	146784
Seq. ID	LIB3168-078-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	630
E value	6.0e-66
Match length	142
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146785
Seq. ID	LIB3168-078-P1-K1-H10
Method	BLASTN
NCBI GI	g4220510
BLAST score	171
E value	3.0e-91
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	146786
Seq. ID	LIB3168-078-P1-K1-H11
Method	BLASTX
NCBI GI	g112737
BLAST score	348
E value	5.0e-33
Match length	96
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146787
Seq. ID	LIB3168-078-P1-K1-H2
Method	BLASTX
NCBI GI	g3434971
BLAST score	305
E value	7.0e-28
Match length	102
% identity	63
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	146788
Seq. ID	LIB3168-078-P1-K1-H3
Method	BLASTX
NCBI GI	g3927831
BLAST score	630
E value	5.0e-66
Match length	124
% identity	55
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	146789
Seq. ID	LIB3168-078-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	782
E value	1.0e-83

Match length	158
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146790
Seq. ID	LIB3168-078-P1-K1-H5
Method	BLASTX
NCBI GI	g1628583
BLAST score	660
E value	2.0e-69
Match length	126
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146791
Seq. ID	LIB3168-078-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	574
E value	2.0e-59
Match length	117
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146792
Seq. ID	LIB3168-078-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	600
E value	2.0e-62
Match length	123
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146793
Seq. ID	LIB3168-078-P1-K1-H8
Method	BLASTN
NCBI GI	g4757405
BLAST score	314
E value	1.0e-176
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	146794
Seq. ID	LIB3168-078-P1-K1-H9
Method	BLASTX
NCBI GI	g112682

BLAST score	555
E value	3.0e-57
Match length	118
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146795
Seq. ID	LIB3168-079-P1-K1-A10
Method	BLASTX
NCBI GI	g112737
BLAST score	353
E value	2.0e-33
Match length	75
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146796
Seq. ID	LIB3168-079-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	597
E value	4.0e-62
Match length	122
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146797
Seq. ID	LIB3168-079-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	534
E value	1.0e-54
Match length	141
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146798
Seq. ID	LIB3168-079-P1-K1-A4
Method	BLASTX
NCBI GI	g112739
BLAST score	432

E value	1.0e-42
Match length	131
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146799
Seq. ID	LIB3168-079-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	578
E value	7.0e-60
Match length	135
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146800
Seq. ID	LIB3168-079-P1-K1-A7
Method	BLASTN
NCBI GI	g2894557
BLAST score	331
E value	0.0e+00
Match length	343
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	146801
Seq. ID	LIB3168-079-P1-K1-A8
Method	BLASTX
NCBI GI	g112681
BLAST score	574
E value	2.0e-59
Match length	134
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146802
Seq. ID	LIB3168-079-P1-K1-A9
Method	BLASTX
NCBI GI	g1402904
BLAST score	682
E value	5.0e-72
Match length	131

% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	146803
Seq. ID	LIB3168-079-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	595
E value	8.0e-62
Match length	139
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146804
Seq. ID	LIB3168-079-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	565
E value	5.0e-61
Match length	135
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146805
Seq. ID	LIB3168-079-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	597
E value	4.0e-62
Match length	114
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146806
Seq. ID	LIB3168-079-P1-K1-B12
Method	BLASTX
NCBI GI	g112681
BLAST score	511
E value	5.0e-52
Match length	144
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146807
Seq. ID	LIB3168-079-P1-K1-B2

Method	BLASTN
NCBI GI	g2842474
BLAST score	24
E value	1.0e-03
Match length	367
% identity	74
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146808
Seq. ID	LIB3168-079-P1-K1-B3
Method	BLASTN
NCBI GI	g2842474
BLAST score	39
E value	3.0e-13
Match length	98
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146809
Seq. ID	LIB3168-079-P1-K1-B4
Method	BLASTX
NCBI GI	g112737
BLAST score	526
E value	1.0e-53
Match length	134
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146810
Seq. ID	LIB3168-079-P1-K1-B5
Method	BLASTN
NCBI GI	g2760165
BLAST score	319
E value	1.0e-179
Match length	393
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	146811
Seq. ID	LIB3168-079-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	590
E value	3.0e-61
Match length	120
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146812
Seq. ID	LIB3168-079-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	736
E value	2.0e-78
Match length	147
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146813
Seq. ID	LIB3168-079-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	103
E value	5.0e-58
Match length	119
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146814
Seq. ID	LIB3168-079-P1-K1-C1
Method	BLASTX
NCBI GI	g2285885
BLAST score	682
E value	5.0e-72
Match length	147
% identity	95
NCBI Description	(D89631) sulfate transporter [Arabidopsis thaliana]

Seq. No.	146815
Seq. ID	LIB3168-079-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	585
E value	1.0e-60
Match length	111
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146816
Seq. ID	LIB3168-079-P1-K1-C11
Method	BLASTX
NCBI GI	g112682
BLAST score	684
E value	3.0e-72
Match length	141
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana
>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146817
Seq. ID	LIB3168-079-P1-K1-C12
Method	BLASTX
NCBI GI	g112682
BLAST score	621
E value	6.0e-65
Match length	130
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146818
Seq. ID	LIB3168-079-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	578
E value	6.0e-60
Match length	123
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146819
Seq. ID	LIB3168-079-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	474
E value	1.0e-47
Match length	138
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146820
Seq. ID	LIB3168-079-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	538
E value	3.0e-58
Match length	120
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146821
Seq. ID	LIB3168-079-P1-K1-C6

Method	BLASTX
NCBI GI	g3236242
BLAST score	491
E value	1.0e-49
Match length	111
% identity	91
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	146822
Seq. ID	LIB3168-079-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	681
E value	7.0e-72
Match length	146
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146823
Seq. ID	LIB3168-079-P1-K1-D1
Method	BLASTX
NCBI GI	g112741
BLAST score	175
E value	6.0e-13
Match length	69
% identity	58
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146824
Seq. ID	LIB3168-079-P1-K1-D10
Method	BLASTX
NCBI GI	g3935151
BLAST score	678
E value	1.0e-71
Match length	127
% identity	98
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	146825
Seq. ID	LIB3168-079-P1-K1-D11
Method	BLASTN
NCBI GI	g3367500
BLAST score	81
E value	3.0e-38
Match length	97
% identity	96
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	146826
Seq. ID	LIB3168-079-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	565
E value	3.0e-58
Match length	108
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146827
Seq. ID	LIB3168-079-P1-K1-D2
Method	BLASTN
NCBI GI	g58298
BLAST score	47
E value	9.0e-18
Match length	96
% identity	84
NCBI Description	Synthetic DNA for A.thaliana ats1A leader spliced to B.thuringiensis CryIA(c)

Seq. No.	146828
Seq. ID	LIB3168-079-P1-K1-D3
Method	BLASTX
NCBI GI	g484640
BLAST score	169
E value	5.0e-12
Match length	31
% identity	97
NCBI Description	2S albumin, AT2S5 - Arabidopsis thaliana (fragment)

Seq. No.	146829
Seq. ID	LIB3168-079-P1-K1-D4
Method	BLASTX
NCBI GI	g1628583
BLAST score	88
E value	4.0e-42
Match length	106
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146830
Seq. ID	LIB3168-079-P1-K1-D5
Method	BLASTX
NCBI GI	g112741
BLAST score	539
E value	2.0e-55
Match length	101
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146831
Seq. ID	LIB3168-079-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	165
E value	5.0e-12
Match length	35
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146832
Seq. ID	LIB3168-079-P1-K1-D7
Method	BLASTX
NCBI GI	g477819
BLAST score	216
E value	9.0e-18
Match length	55
% identity	76
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	146833
Seq. ID	LIB3168-079-P1-K1-D8
Method	BLASTX
NCBI GI	g112681
BLAST score	565
E value	2.0e-58
Match length	122
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146834
Seq. ID	LIB3168-079-P1-K1-D9
Method	BLASTX
NCBI GI	g112682
BLAST score	625
E value	2.0e-65
Match length	143
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	146835
Seq. ID	LIB3168-079-P1-K1-E10
Method	BLASTX
NCBI GI	g3873913
BLAST score	183
E value	1.0e-13
Match length	114
% identity	37
NCBI Description	(Z71258) similar to Flavin-binding monooxygenase-like [Caenorhabditis elegans]

Seq. No.	146836
Seq. ID	LIB3168-079-P1-K1-E11
Method	BLASTX
NCBI GI	g135858
BLAST score	292
E value	2.0e-26
Match length	57
% identity	100
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha - Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

Seq. No.	146837
Seq. ID	LIB3168-079-P1-K1-E2
Method	BLASTN
NCBI GI	g1628582
BLAST score	29
E value	1.0e-06
Match length	282
% identity	60
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	146838
Seq. ID	LIB3168-079-P1-K1-E3
Method	BLASTN
NCBI GI	g557693
BLAST score	264
E value	1.0e-147
Match length	316
% identity	96
NCBI Description	Arabidopsis thaliana Columbia GTP binding protein beta subunit (AGB1) mRNA, complete cds

Seq. No.	146839
Seq. ID	LIB3168-079-P1-K1-E5
Method	BLASTX
NCBI GI	g82051
BLAST score	130
E value	3.0e-26

Match length	120
% identity	47
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	146840
Seq. ID	LIB3168-079-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	497
E value	2.0e-50
Match length	137
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146841
Seq. ID	LIB3168-079-P1-K1-E7
Method	BLASTN
NCBI GI	g4539378
BLAST score	234
E value	1.0e-129
Match length	445
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	146842
Seq. ID	LIB3168-079-P1-K1-F1
Method	BLASTX
NCBI GI	g112737
BLAST score	363
E value	9.0e-40
Match length	108
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146843
Seq. ID	LIB3168-079-P1-K1-F10
Method	BLASTX
NCBI GI	g1669387
BLAST score	605
E value	5.0e-63
Match length	119
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	146844

Seq. ID	LIB3168-079-P1-K1-F2
Method	BLASTX
NCBI GI	g1628583
BLAST score	365
E value	8.0e-35
Match length	138
% identity	58
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146845
Seq. ID	LIB3168-079-P1-K1-F4
Method	BLASTN
NCBI GI	g2842474
BLAST score	133
E value	1.0e-68
Match length	314
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146846
Seq. ID	LIB3168-079-P1-K1-F5
Method	BLASTN
NCBI GI	g166611
BLAST score	77
E value	3.0e-35
Match length	253
% identity	83
NCBI Description	A.thaliana at2S3 gene encoding albumin 2S subunit 3, complete cds

Seq. No.	146847
Seq. ID	LIB3168-079-P1-K1-F6
Method	BLASTX
NCBI GI	g112682
BLAST score	533
E value	1.0e-54
Match length	103
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146848
Seq. ID	LIB3168-079-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	523
E value	2.0e-53
Match length	121
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146849
Seq. ID	LIB3168-079-P1-K1-F8
Method	BLASTX
NCBI GI	g2961542
BLAST score	636
E value	1.0e-66
Match length	116
% identity	98
NCBI Description	(AF050463) zinc finger transcription factor [Arabidopsis thaliana]

Seq. No.	146850
Seq. ID	LIB3168-079-P1-K1-F9
Method	BLASTX
NCBI GI	g4204298
BLAST score	529
E value	4.0e-54
Match length	101
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146851
Seq. ID	LIB3168-079-P1-K1-G11
Method	BLASTX
NCBI GI	g4204299
BLAST score	53
E value	1.0e-48
Match length	110
% identity	89
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146852
Seq. ID	LIB3168-079-P1-K1-G3
Method	BLASTX
NCBI GI	g1070654
BLAST score	208
E value	4.0e-26
Match length	91
% identity	70
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	146853
Seq. ID	LIB3168-079-P1-K1-G4
Method	BLASTX
NCBI GI	g4337025
BLAST score	561
E value	7.0e-58
Match length	133
% identity	85
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	146854
Seq. ID	LIB3168-079-P1-K1-G6

Method	BLASTX
NCBI GI	g1076416
BLAST score	161
E value	1.0e-11
Match length	59
% identity	63
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]

Seq. No.	146855
Seq. ID	LIB3168-079-P1-K1-G7
Method	BLASTX
NCBI GI	g2781345
BLAST score	206
E value	3.0e-16
Match length	97
% identity	49
NCBI Description	(AC003113) F24O1.2 [Arabidopsis thaliana]

Seq. No.	146856
Seq. ID	LIB3168-079-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	415
E value	7.0e-41
Match length	91
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146857
Seq. ID	LIB3168-079-P1-K1-H10
Method	BLASTX
NCBI GI	g2708741
BLAST score	579
E value	5.0e-60
Match length	113
% identity	99
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146858
Seq. ID	LIB3168-079-P1-K1-H11
Method	BLASTX
NCBI GI	g3808062
BLAST score	155
E value	3.0e-10
Match length	64
% identity	45
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	146859

Seq. ID	LIB3168-079-P1-K1-H12
Method	BLASTX
NCBI GI	g2062164
BLAST score	418
E value	4.0e-41
Match length	136
% identity	31
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	146860
Seq. ID	LIB3168-079-P1-K1-H3
Method	BLASTN
NCBI GI	g16236
BLAST score	69
E value	2.0e-30
Match length	162
% identity	86
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	146861
Seq. ID	LIB3168-079-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	525
E value	1.0e-53
Match length	100
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146862
Seq. ID	LIB3168-079-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	385
E value	2.0e-37
Match length	113
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146863
Seq. ID	LIB3168-079-P1-K1-H7
Method	BLASTX
NCBI GI	g1592677
BLAST score	239
E value	4.0e-20
Match length	122
% identity	44
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No. 146864

Seq. ID	LIB3168-079-P1-K1-H8
Method	BLASTX
NCBI GI	g2984196
BLAST score	207
E value	2.0e-16
Match length	110
% identity	39
NCBI Description	(AE000764) ribosomal protein L11 [Aquifex aeolicus]

Seq. No.	146865
Seq. ID	LIB3168-080-P1-K1-A1
Method	BLASTX
NCBI GI	g2914700
BLAST score	391
E value	5.0e-38
Match length	99
% identity	82
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	146866
Seq. ID	LIB3168-080-P1-K1-A10
Method	BLASTX
NCBI GI	g2654208
BLAST score	460
E value	4.0e-46
Match length	120
% identity	80
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	146867
Seq. ID	LIB3168-080-P1-K1-A11
Method	BLASTX
NCBI GI	g112737
BLAST score	559
E value	1.0e-57
Match length	119
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146868
Seq. ID	LIB3168-080-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	657
E value	4.0e-69
Match length	128
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146869
Seq. ID	LIB3168-080-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	247
E value	1.0e-32
Match length	91
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146870
Seq. ID	LIB3168-080-P1-K1-A6
Method	BLASTX
NCBI GI	g112681
BLAST score	526
E value	9.0e-54
Match length	133
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146871
Seq. ID	LIB3168-080-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	697
E value	8.0e-74
Match length	140
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146872
Seq. ID	LIB3168-080-P1-K1-B10
Method	BLASTX
NCBI GI	g4585882
BLAST score	474
E value	1.0e-47
Match length	99
% identity	91
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	146873
Seq. ID	LIB3168-080-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	543

E value	9.0e-56
Match length	113
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146874
Seq. ID	LIB3168-080-P1-K1-B2
Method	BLASTN
NCBI GI	g395200
BLAST score	66
E value	4.0e-29
Match length	118
% identity	88
NCBI Description	A.thaliana 2S albumin gene isoforms 3 and 4, complete CDS's

Seq. No.	146875
Seq. ID	LIB3168-080-P1-K1-B4
Method	BLASTN
NCBI GI	g4454022
BLAST score	309
E value	1.0e-173
Match length	383
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	146876
Seq. ID	LIB3168-080-P1-K1-B5
Method	BLASTX
NCBI GI	g112737
BLAST score	491
E value	9.0e-50
Match length	110
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146877
Seq. ID	LIB3168-080-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	338
E value	6.0e-32
Match length	72
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146878

Seq. ID	LIB3168-080-P1-K1-B7
Method	BLASTX
NCBI GI	g2129657
BLAST score	202
E value	7.0e-16
Match length	59
% identity	69
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146879
Seq. ID	LIB3168-080-P1-K1-B8
Method	BLASTN
NCBI GI	g4756963
BLAST score	40
E value	2.0e-13
Match length	94
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	146880
Seq. ID	LIB3168-080-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	312
E value	4.0e-29
Match length	76
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146881
Seq. ID	LIB3168-080-P1-K1-C10
Method	BLASTX
NCBI GI	g3193297
BLAST score	580
E value	4.0e-60
Match length	126
% identity	87
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	146882
Seq. ID	LIB3168-080-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	614
E value	3.0e-64
Match length	124
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146883
Seq. ID	LIB3168-080-P1-K1-C12
Method	BLASTX
NCBI GI	g1170191
BLAST score	523
E value	2.0e-53
Match length	115
% identity	92
NCBI Description	HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535 homeodomain-containing protein - rape >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing protein [Brassica napus] >gi_1090522_prf__2019252A homeobox protein [Brassica napus]

Seq. No.	146884
Seq. ID	LIB3168-080-P1-K1-C4
Method	BLASTX
NCBI GI	g112682
BLAST score	576
E value	1.0e-59
Match length	132
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146885
Seq. ID	LIB3168-080-P1-K1-C6
Method	BLASTX
NCBI GI	g112681
BLAST score	94
E value	3.0e-54
Match length	115
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146886
Seq. ID	LIB3168-080-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	203
E value	1.0e-16
Match length	56
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146887
Seq. ID	LIB3168-080-P1-K1-C8

Method	BLASTX
NCBI GI	g1628583
BLAST score	536
E value	5.0e-55
Match length	103
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146888
Seq. ID	LIB3168-080-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	70
E value	1.0e-50
Match length	119
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146889
Seq. ID	LIB3168-080-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	498
E value	1.0e-50
Match length	104
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146890
Seq. ID	LIB3168-080-P1-K1-D11
Method	BLASTX
NCBI GI	g4704730
BLAST score	43
E value	4.0e-22
Match length	91
% identity	69
NCBI Description	(AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]

Seq. No.	146891
Seq. ID	LIB3168-080-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	491
E value	1.0e-49
Match length	107
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146892
Seq. ID	LIB3168-080-P1-K1-D2
Method	BLASTX
NCBI GI	g112681
BLAST score	210
E value	5.0e-17
Match length	72
% identity	58
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146893
Seq. ID	LIB3168-080-P1-K1-D4
Method	BLASTX
NCBI GI	g112682
BLAST score	622
E value	5.0e-65
Match length	137
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146894
Seq. ID	LIB3168-080-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	335
E value	1.0e-31
Match length	83
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146895
Seq. ID	LIB3168-080-P1-K1-D7
Method	BLASTN
NCBI GI	g3250673
BLAST score	54
E value	1.0e-21
Match length	289
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	146896
Seq. ID	LIB3168-080-P1-K1-D8
Method	BLASTX
NCBI GI	g2688544
BLAST score	169

E value	5.0e-12
Match length	89
% identity	36
NCBI Description	(AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) [Borrelia burgdorferi]

Seq. No.	146897
Seq. ID	LIB3168-080-P1-K1-D9
Method	BLASTN
NCBI GI	g4753645
BLAST score	94
E value	8.0e-46
Match length	139
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	146898
Seq. ID	LIB3168-080-P1-K1-E1
Method	BLASTN
NCBI GI	g1877523
BLAST score	249
E value	1.0e-138
Match length	253
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	146899
Seq. ID	LIB3168-080-P1-K1-E10
Method	BLASTX
NCBI GI	g112681
BLAST score	495
E value	3.0e-50
Match length	94
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146900
Seq. ID	LIB3168-080-P1-K1-E11
Method	BLASTN
NCBI GI	g18058
BLAST score	45
E value	3.0e-16
Match length	157
% identity	88
NCBI Description	Citrus limon cistron for 26S ribosomal RNA

Seq. No.	146901
Seq. ID	LIB3168-080-P1-K1-E12
Method	BLASTX
NCBI GI	g112681

BLAST score	304
E value	5.0e-28
Match length	72
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146902
Seq. ID	LIB3168-080-P1-K1-E2
Method	BLASTN
NCBI GI	g4510392
BLAST score	48
E value	2.0e-18
Match length	133
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No.	146903
Seq. ID	LIB3168-080-P1-K1-E4
Method	BLASTX
NCBI GI	g267073
BLAST score	470
E value	2.0e-47
Match length	88
% identity	98
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	146904
Seq. ID	LIB3168-080-P1-K1-E5
Method	BLASTN
NCBI GI	g4572664
BLAST score	101
E value	9.0e-50
Match length	149
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	146905
Seq. ID	LIB3168-080-P1-K1-E7
Method	BLASTX
NCBI GI	g112681
BLAST score	192
E value	8.0e-15
Match length	49
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	146906
Seq. ID	LIB3168-080-P1-K1-E8
Method	BLASTX
NCBI GI	g112681
BLAST score	258
E value	4.0e-23
Match length	110
% identity	63
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146907
Seq. ID	LIB3168-080-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	295
E value	2.0e-28
Match length	95
% identity	71
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146908
Seq. ID	LIB3168-080-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	420
E value	1.0e-41
Match length	84
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146909
Seq. ID	LIB3168-080-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	476
E value	4.0e-48
Match length	97
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146910
Seq. ID	LIB3168-080-P1-K1-F2
Method	BLASTX

NCBI GI	g112741
BLAST score	491
E value	9.0e-50
Match length	94
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146911
Seq. ID	LIB3168-080-P1-K1-F3
Method	BLASTX
NCBI GI	g112682
BLAST score	152
E value	4.0e-10
Match length	83
% identity	47
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146912
Seq. ID	LIB3168-080-P1-K1-F4
Method	BLASTX
NCBI GI	g2244750
BLAST score	46
E value	2.0e-13
Match length	48
% identity	88
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	146913
Seq. ID	LIB3168-080-P1-K1-F5
Method	BLASTX
NCBI GI	g112737
BLAST score	56
E value	4.0e-23
Match length	125
% identity	56
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146914
Seq. ID	LIB3168-080-P1-K1-F6

Method	BLASTX
NCBI GI	g112681
BLAST score	506
E value	2.0e-51
Match length	109
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146915
Seq. ID	LIB3168-080-P1-K1-F7
Method	BLASTX
NCBI GI	g112681
BLAST score	508
E value	8.0e-52
Match length	102
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146916
Seq. ID	LIB3168-080-P1-K1-F8
Method	BLASTN
NCBI GI	g1628582
BLAST score	37
E value	1.0e-11
Match length	113
% identity	88
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	146917
Seq. ID	LIB3168-080-P1-K1-G10
Method	BLASTX
NCBI GI	g112737
BLAST score	322
E value	3.0e-30
Match length	84
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146918
Seq. ID	LIB3168-080-P1-K1-G11
Method	BLASTN
NCBI GI	g4691223

BLAST score	376
E value	0.0e+00
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	146919
Seq. ID	LIB3168-080-P1-K1-G3
Method	BLASTX
NCBI GI	g112739
BLAST score	195
E value	4.0e-15
Match length	84
% identity	55
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146920
Seq. ID	LIB3168-080-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	553
E value	5.0e-57
Match length	111
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146921
Seq. ID	LIB3168-080-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	301
E value	8.0e-38
Match length	95
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146922
Seq. ID	LIB3168-080-P1-K1-G7
Method	BLASTX
NCBI GI	g112741
BLAST score	643
E value	2.0e-67
Match length	122
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146923
Seq. ID	LIB3168-080-P1-K1-G8
Method	BLASTX
NCBI GI	g112681
BLAST score	536
E value	6.0e-55
Match length	132
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146924
Seq. ID	LIB3168-080-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	545
E value	5.0e-56
Match length	129
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146925
Seq. ID	LIB3168-080-P1-K1-H1
Method	BLASTN
NCBI GI	g4097693
BLAST score	37
E value	6.0e-12
Match length	109
% identity	83
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	146926
Seq. ID	LIB3168-080-P1-K1-H3
Method	BLASTN
NCBI GI	g4469002
BLAST score	61
E value	8.0e-26
Match length	164
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No. 146927

Seq. ID	LIB3168-080-P1-K1-H4
Method	BLASTX
NCBI GI	g2129657
BLAST score	189
E value	3.0e-14
Match length	84
% identity	54
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146928
Seq. ID	LIB3168-080-P1-K1-H5
Method	BLASTN
NCBI GI	g16231
BLAST score	37
E value	6.0e-12
Match length	117
% identity	82
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	146929
Seq. ID	LIB3168-080-P1-K1-H6
Method	BLASTX
NCBI GI	g112737
BLAST score	187
E value	1.0e-14
Match length	53
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146930
Seq. ID	LIB3168-080-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	497
E value	2.0e-50
Match length	111
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146931
Seq. ID	LIB3168-080-P1-K1-H9
Method	BLASTN
NCBI GI	g4006885
BLAST score	269

E value	1.0e-150
Match length	330
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	146932
Seq. ID	LIB3168-082-P1-K1-A1
Method	BLASTX
NCBI GI	g112681
BLAST score	54
E value	1.0e-77
Match length	147
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146933
Seq. ID	LIB3168-082-P1-K1-A10
Method	BLASTN
NCBI GI	g2275194
BLAST score	389
E value	0.0e+00
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146934
Seq. ID	LIB3168-082-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	614
E value	4.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146935
Seq. ID	LIB3168-082-P1-K1-A2
Method	BLASTX
NCBI GI	g112737
BLAST score	581
E value	4.0e-60
Match length	122
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	146936
Seq. ID	LIB3168-082-P1-K1-A3
Method	BLASTX
NCBI GI	g3023190
BLAST score	393
E value	4.0e-38
Match length	84
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685) 14-3-3 protein [Solanum tuberosum]

Seq. No.	146937
Seq. ID	LIB3168-082-P1-K1-A4
Method	BLASTX
NCBI GI	g112682
BLAST score	659
E value	2.0e-69
Match length	138
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146938
Seq. ID	LIB3168-082-P1-K1-A8
Method	BLASTX
NCBI GI	g3367576
BLAST score	594
E value	1.0e-61
Match length	130
% identity	81
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	146939
Seq. ID	LIB3168-082-P1-K1-A9
Method	BLASTX
NCBI GI	g2252634
BLAST score	217
E value	2.0e-17
Match length	82
% identity	55
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146940
Seq. ID	LIB3168-082-P1-K1-B10
Method	BLASTX
NCBI GI	g4678226
BLAST score	561
E value	6.0e-58
Match length	131
% identity	89
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	146941
Seq. ID	LIB3168-082-P1-K1-B11
Method	BLASTN
NCBI GI	g1402874
BLAST score	91
E value	1.0e-43
Match length	119
% identity	95
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	146942
Seq. ID	LIB3168-082-P1-K1-B12
Method	BLASTN
NCBI GI	g2842474
BLAST score	126
E value	6.0e-65
Match length	130
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	146943
Seq. ID	LIB3168-082-P1-K1-B2
Method	BLASTX
NCBI GI	g3152581
BLAST score	519
E value	6.0e-53
Match length	115
% identity	88
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	146944
Seq. ID	LIB3168-082-P1-K1-B4
Method	BLASTN
NCBI GI	g4589434
BLAST score	306
E value	1.0e-172
Match length	446
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	146945
Seq. ID	LIB3168-082-P1-K1-B5
Method	BLASTN
NCBI GI	g2262155
BLAST score	85
E value	6.0e-40
Match length	335
% identity	87
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No. 146946

Seq. ID	LIB3168-082-P1-K1-B6
Method	BLASTX
NCBI GI	g4165488
BLAST score	622
E value	5.0e-65
Match length	117
% identity	98
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No.	146947
Seq. ID	LIB3168-082-P1-K1-B7
Method	BLASTN
NCBI GI	g4159705
BLAST score	393
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	146948
Seq. ID	LIB3168-082-P1-K1-B8
Method	BLASTX
NCBI GI	g112737
BLAST score	43
E value	3.0e-36
Match length	121
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146949
Seq. ID	LIB3168-082-P1-K1-B9
Method	BLASTX
NCBI GI	g112681
BLAST score	625
E value	2.0e-65
Match length	142
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146950
Seq. ID	LIB3168-082-P1-K1-C1
Method	BLASTX
NCBI GI	g3212869
BLAST score	592
E value	2.0e-61
Match length	123

% identity	87
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	146951
Seq. ID	LIB3168-082-P1-K1-C11
Method	BLASTN
NCBI GI	g2264321
BLAST score	141
E value	2.0e-73
Match length	386
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	146952
Seq. ID	LIB3168-082-P1-K1-C12
Method	BLASTX
NCBI GI	g3482913
BLAST score	230
E value	5.0e-19
Match length	119
% identity	35
NCBI Description	(AC003970) Similar to MtN21, gi_2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No.	146953
Seq. ID	LIB3168-082-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146954
Seq. ID	LIB3168-082-P1-K1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	514
E value	3.0e-52
Match length	111
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146955
Seq. ID	LIB3168-082-P1-K1-C4
Method	BLASTN
NCBI GI	g4678266
BLAST score	189
E value	1.0e-102
Match length	416
% identity	95

NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	146956
Seq. ID	LIB3168-082-P1-K1-C5
Method	BLASTX
NCBI GI	g112739
BLAST score	516
E value	1.0e-52
Match length	139
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146957
Seq. ID	LIB3168-082-P1-K1-C7
Method	BLASTX
NCBI GI	g112741
BLAST score	606
E value	3.0e-63
Match length	113
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146958
Seq. ID	LIB3168-082-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	6.0e-57
Match length	120
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146959
Seq. ID	LIB3168-082-P1-K1-D1
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	5.0e-62
Match length	139
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana

>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146960
Seq. ID	LIB3168-082-P1-K1-D10
Method	BLASTN
NCBI GI	g3335170
BLAST score	111
E value	1.0e-55
Match length	278
% identity	95
NCBI Description	Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No.	146961
Seq. ID	LIB3168-082-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	119
E value	4.0e-06
Match length	104
% identity	52
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146962
Seq. ID	LIB3168-082-P1-K1-D3
Method	BLASTX
NCBI GI	g112682
BLAST score	621
E value	7.0e-65
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146963
Seq. ID	LIB3168-082-P1-K1-D4
Method	BLASTX
NCBI GI	g129817
BLAST score	417
E value	6.0e-41
Match length	113
% identity	80
NCBI Description	BASIC PEROXIDASE E PRECURSOR >gi_81653_pir__JU0458 peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]

Seq. No.	146964
Seq. ID	LIB3168-082-P1-K1-D5

Method	BLASTX
NCBI GI	g112681
BLAST score	623
E value	4.0e-65
Match length	132
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146965
Seq. ID	LIB3168-082-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	478
E value	2.0e-48
Match length	95
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146966
Seq. ID	LIB3168-082-P1-K1-D7
Method	BLASTN
NCBI GI	g2264314
BLAST score	419
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	146967
Seq. ID	LIB3168-082-P1-K1-D8
Method	BLASTX
NCBI GI	g899608
BLAST score	587
E value	5.0e-61
Match length	120
% identity	21
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	146968
Seq. ID	LIB3168-082-P1-K1-D9
Method	BLASTN
NCBI GI	g2264306
BLAST score	50
E value	4.0e-19
Match length	54
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No. 146969

Seq. ID	LIB3168-082-P1-K1-E1
Method	BLASTX
NCBI GI	g2129657
BLAST score	398
E value	1.0e-38
Match length	109
% identity	77
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146970
Seq. ID	LIB3168-082-P1-K1-E10
Method	BLASTX
NCBI GI	g112741
BLAST score	717
E value	4.0e-76
Match length	135
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146971
Seq. ID	LIB3168-082-P1-K1-E11
Method	BLASTX
NCBI GI	g112681
BLAST score	499
E value	1.0e-50
Match length	120
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146972
Seq. ID	LIB3168-082-P1-K1-E12
Method	BLASTN
NCBI GI	g4512656
BLAST score	422
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	146973
Seq. ID	LIB3168-082-P1-K1-E2
Method	BLASTX
NCBI GI	g1628583

BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146974
Seq. ID	LIB3168-082-P1-K1-E3
Method	BLASTX
NCBI GI	g2501296
BLAST score	248
E value	4.0e-21
Match length	115
% identity	41
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]

Seq. No.	146975
Seq. ID	LIB3168-082-P1-K1-E4
Method	BLASTX
NCBI GI	g4581146
BLAST score	309
E value	9.0e-29
Match length	64
% identity	98
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	146976
Seq. ID	LIB3168-082-P1-K1-E5
Method	BLASTX
NCBI GI	g4454050
BLAST score	161
E value	6.0e-11
Match length	40
% identity	72
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	146977
Seq. ID	LIB3168-082-P1-K1-E7
Method	BLASTX
NCBI GI	g112737
BLAST score	566
E value	2.0e-58
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	146978

Seq. ID	LIB3168-082-P1-K1-E8
Method	BLASTX
NCBI GI	g112682
BLAST score	650
E value	3.0e-68
Match length	137
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146979
Seq. ID	LIB3168-082-P1-K1-E9
Method	BLASTX
NCBI GI	g2129657
BLAST score	433
E value	8.0e-43
Match length	116
% identity	78
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	146980
Seq. ID	LIB3168-082-P1-K1-F1
Method	BLASTN
NCBI GI	g4191771
BLAST score	411
E value	0.0e+00
Match length	435
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	146981
Seq. ID	LIB3168-082-P1-K1-F10
Method	BLASTX
NCBI GI	g4204299
BLAST score	674
E value	4.0e-71
Match length	132
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	146982
Seq. ID	LIB3168-082-P1-K1-F11
Method	BLASTX
NCBI GI	g3023516
BLAST score	492
E value	6.0e-50
Match length	112
% identity	85
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR

(DXP SYNTHASE) >gi_1399261 (U27099) DEF [Arabidopsis thaliana]

Seq. No.	146983
Seq. ID	LIB3168-082-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146984
Seq. ID	LIB3168-082-P1-K1-F2
Method	BLASTX
NCBI GI	g112681
BLAST score	739
E value	1.0e-78
Match length	145
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146985
Seq. ID	LIB3168-082-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	651
E value	2.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146986
Seq. ID	LIB3168-082-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	567
E value	1.0e-58
Match length	141
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146987
Seq. ID	LIB3168-082-P1-K1-F7
Method	BLASTX
NCBI GI	g2921158

BLAST score	708
E value	4.0e-75
Match length	144
% identity	99
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	146988
Seq. ID	LIB3168-082-P1-K1-F8
Method	BLASTX
NCBI GI	g112739
BLAST score	468
E value	6.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	146989
Seq. ID	LIB3168-082-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146990
Seq. ID	LIB3168-082-P1-K1-G10
Method	BLASTX
NCBI GI	g2253579
BLAST score	159
E value	8.0e-11
Match length	119
% identity	42
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	146991
Seq. ID	LIB3168-082-P1-K1-G11
Method	BLASTX
NCBI GI	g1350634
BLAST score	395
E value	2.0e-38
Match length	76
% identity	99
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L23 >gi_12213_emb_CAA46567_ (X65615) ribosomal protein L23 [Sinapis alba]

Seq. No.	146992

Seq. ID	LIB3168-082-P1-K1-G12
Method	BLASTX
NCBI GI	g2924779
BLAST score	658
E value	3.0e-69
Match length	130
% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	146993
Seq. ID	LIB3168-082-P1-K1-G2
Method	BLASTX
NCBI GI	g3600030
BLAST score	521
E value	4.0e-53
Match length	118
% identity	88
NCBI Description	(AF080119) contains similarity to ankyrin repeats (Pfam: ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis thaliana]

Seq. No.	146994
Seq. ID	LIB3168-082-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	146995
Seq. ID	LIB3168-082-P1-K1-G4
Method	BLASTX
NCBI GI	g112741
BLAST score	604
E value	6.0e-63
Match length	117
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	146996
Seq. ID	LIB3168-082-P1-K1-G5
Method	BLASTX
NCBI GI	g112681

BLAST score	604
E value	7.0e-63
Match length	139
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146997
Seq. ID	LIB3168-082-P1-K1-G6
Method	BLASTX
NCBI GI	g112682
BLAST score	614
E value	5.0e-64
Match length	142
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146998
Seq. ID	LIB3168-082-P1-K1-G7
Method	BLASTX
NCBI GI	g112681
BLAST score	547
E value	3.0e-56
Match length	126
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	146999
Seq. ID	LIB3168-082-P1-K1-G8
Method	BLASTX
NCBI GI	g4220514
BLAST score	307
E value	5.0e-28
Match length	74
% identity	73
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	147000
Seq. ID	LIB3168-082-P1-K1-G9
Method	BLASTX
NCBI GI	g2129657
BLAST score	315
E value	5.0e-29
Match length	93
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147001
Seq. ID	LIB3168-082-P1-K1-H10
Method	BLASTX
NCBI GI	g2160151
BLAST score	629
E value	8.0e-66
Match length	136
% identity	89
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	147002
Seq. ID	LIB3168-082-P1-K1-H12
Method	BLASTX
NCBI GI	g4204298
BLAST score	452
E value	3.0e-45
Match length	115
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147003
Seq. ID	LIB3168-082-P1-K1-H2
Method	BLASTX
NCBI GI	g2961378
BLAST score	565
E value	3.0e-58
Match length	135
% identity	55
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	147004
Seq. ID	LIB3168-082-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147005
Seq. ID	LIB3168-082-P1-K1-H4
Method	BLASTX
NCBI GI	g112737
BLAST score	599
E value	3.0e-62
Match length	141
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147006
Seq. ID	LIB3168-082-P1-K1-H5
Method	BLASTX
NCBI GI	g585536
BLAST score	584
E value	1.0e-60
Match length	105
% identity	100
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	147007
Seq. ID	LIB3168-082-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	4.0e-56
Match length	110
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147008
Seq. ID	LIB3168-082-P1-K1-H7
Method	BLASTX
NCBI GI	g112681
BLAST score	643
E value	2.0e-67
Match length	132
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147009
Seq. ID	LIB3168-082-P1-K1-H8
Method	BLASTX
NCBI GI	g266693
BLAST score	423
E value	9.0e-42
Match length	106
% identity	82
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin

[Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	147010
Seq. ID	LIB3168-082-P1-K1-H9
Method	BLASTX
NCBI GI	g4539335
BLAST score	152
E value	6.0e-10
Match length	93
% identity	41
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	147011
Seq. ID	LIB3168-083-P1-K1-A1
Method	BLASTX
NCBI GI	g112739
BLAST score	345
E value	1.0e-32
Match length	109
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147012
Seq. ID	LIB3168-083-P1-K1-A11
Method	BLASTX
NCBI GI	g112737
BLAST score	251
E value	2.0e-21
Match length	115
% identity	48
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147013
Seq. ID	LIB3168-083-P1-K1-A2
Method	BLASTX
NCBI GI	g4204299
BLAST score	105
E value	8.0e-64
Match length	127
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 147014

Seq. ID	LIB3168-083-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	386
E value	1.0e-46
Match length	119
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147015
Seq. ID	LIB3168-083-P1-K1-A7
Method	BLASTN
NCBI GI	g3236234
BLAST score	362
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147016
Seq. ID	LIB3168-083-P1-K1-A9
Method	BLASTX
NCBI GI	g112682
BLAST score	571
E value	5.0e-59
Match length	137
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147017
Seq. ID	LIB3168-083-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	390
E value	9.0e-38
Match length	97
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147018
Seq. ID	LIB3168-083-P1-K1-B11
Method	BLASTX
NCBI GI	g112741
BLAST score	708
E value	4.0e-75
Match length	133
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147019
Seq. ID	LIB3168-083-P1-K1-B2
Method	BLASTX
NCBI GI	g112682
BLAST score	609
E value	2.0e-63
Match length	126
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147020
Seq. ID	LIB3168-083-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	342
E value	1.0e-32
Match length	77
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147021
Seq. ID	LIB3168-083-P1-K1-B7
Method	BLASTN
NCBI GI	g21157
BLAST score	110
E value	4.0e-55
Match length	170
% identity	92
NCBI Description	S.alba 18S, 5.8S & 25S rRNA genes

Seq. No.	147022
Seq. ID	LIB3168-083-P1-K1-B9
Method	BLASTX
NCBI GI	g4584542
BLAST score	42
E value	1.0e-60
Match length	128
% identity	97
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	147023
Seq. ID	LIB3168-083-P1-K1-C10
Method	BLASTN
NCBI GI	g4079614

BLAST score 102
E value 5.0e-50
Match length 332
% identity 92
NCBI Description Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 147024
Seq. ID LIB3168-083-P1-K1-C11
Method BLASTX
NCBI GI g112737
BLAST score 598
E value 4.0e-62
Match length 146
% identity 79
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 147025
Seq. ID LIB3168-083-P1-K1-C2
Method BLASTX
NCBI GI g1628583
BLAST score 90
E value 9.0e-73
Match length 145
% identity 97
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147026
Seq. ID LIB3168-083-P1-K1-C5
Method BLASTX
NCBI GI g99688
BLAST score 460
E value 3.0e-46
Match length 99
% identity 90
NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No. 147027
Seq. ID LIB3168-083-P1-K1-C6
Method BLASTX
NCBI GI g112737
BLAST score 389
E value 1.0e-37
Match length 135
% identity 59
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147028
Seq. ID	LIB3168-083-P1-K1-C8
Method	BLASTN
NCBI GI	g2760171
BLAST score	37
E value	2.0e-11
Match length	104
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]

Seq. No.	147029
Seq. ID	LIB3168-083-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	537
E value	5.0e-55
Match length	120
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147030
Seq. ID	LIB3168-083-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	612
E value	9.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147031
Seq. ID	LIB3168-083-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	438
E value	6.0e-69
Match length	146
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147032
Seq. ID	LIB3168-083-P1-K1-D11
Method	BLASTX
NCBI GI	g112737

BLAST score	597
E value	5.0e-62
Match length	145
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147033
Seq. ID	LIB3168-083-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	392
E value	4.0e-38
Match length	87
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147034
Seq. ID	LIB3168-083-P1-K1-D2
Method	BLASTX
NCBI GI	g2454182
BLAST score	407
E value	9.0e-40
Match length	116
% identity	71
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	147035
Seq. ID	LIB3168-083-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	547
E value	3.0e-56
Match length	111
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147036
Seq. ID	LIB3168-083-P1-K1-D6
Method	BLASTX
NCBI GI	g112682
BLAST score	549
E value	2.0e-56

Match length	142
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147037
Seq. ID	LIB3168-083-P1-K1-D7
Method	BLASTX
NCBI GI	g2894568
BLAST score	503
E value	5.0e-51
Match length	145
% identity	71
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	147038
Seq. ID	LIB3168-083-P1-K1-D9
Method	BLASTN
NCBI GI	g166609
BLAST score	147
E value	7.0e-77
Match length	415
% identity	91
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	147039
Seq. ID	LIB3168-083-P1-K1-E1
Method	BLASTN
NCBI GI	g4587582
BLAST score	87
E value	3.0e-41
Match length	261
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	147040
Seq. ID	LIB3168-083-P1-K1-E10
Method	BLASTN
NCBI GI	g4206762
BLAST score	235
E value	1.0e-129
Match length	363
% identity	95
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	147041
Seq. ID	LIB3168-083-P1-K1-E11
Method	BLASTX
NCBI GI	g3687228
BLAST score	632
E value	4.0e-66

Match length	129
% identity	95
NCBI Description	(AC005169) putative malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	147042
Seq. ID	LIB3168-083-P1-K1-E12
Method	BLASTN
NCBI GI	g3299824
BLAST score	367
E value	0.0e+00
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	147043
Seq. ID	LIB3168-083-P1-K1-E2
Method	BLASTX
NCBI GI	g112737
BLAST score	597
E value	5.0e-62
Match length	138
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147044
Seq. ID	LIB3168-083-P1-K1-E4
Method	BLASTX
NCBI GI	g132866
BLAST score	441
E value	9.0e-44
Match length	91
% identity	93
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2 ribosomal protein L2 - common tobacco chloroplast >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_225238_prf__1211235BW ribosomal protein L2 [Nicotiana tabacum]

Seq. No.	147045
Seq. ID	LIB3168-083-P1-K1-E6
Method	BLASTX
NCBI GI	g2129657
BLAST score	362
E value	2.0e-34
Match length	103
% identity	76
NCBI Description	oleosin isoform - Arabidopsis thaliana

>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147046
Seq. ID	LIB3168-083-P1-K1-E7
Method	BLASTX
NCBI GI	g2129767
BLAST score	608
E value	2.0e-63
Match length	122
% identity	93
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	147047
Seq. ID	LIB3168-083-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	574
E value	2.0e-59
Match length	113
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147048
Seq. ID	LIB3168-083-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	125
E value	3.0e-26
Match length	71
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147049
Seq. ID	LIB3168-083-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	376
E value	1.0e-36
Match length	80
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147050
Seq. ID	LIB3168-083-P1-K1-F12
Method	BLASTX
NCBI GI	g3242706
BLAST score	314

E value	8.0e-32
Match length	124
% identity	64
NCBI Description	(AC003040) cyclin-dependent kinase inhibitor protein [Arabidopsis thaliana] >gi_3550262 (AF079587) cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis thaliana]

Seq. No.	147051
Seq. ID	LIB3168-083-P1-K1-F2
Method	BLASTX
NCBI GI	g2160151
BLAST score	550
E value	2.0e-56
Match length	129
% identity	84
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	147052
Seq. ID	LIB3168-083-P1-K1-F3
Method	BLASTN
NCBI GI	g2924257
BLAST score	28
E value	7.0e-06
Match length	143
% identity	90
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	147053
Seq. ID	LIB3168-083-P1-K1-F4
Method	BLASTX
NCBI GI	g112682
BLAST score	142
E value	7.0e-09
Match length	95
% identity	58
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147054
Seq. ID	LIB3168-083-P1-K1-F5
Method	BLASTN
NCBI GI	g3695372
BLAST score	65
E value	2.0e-28
Match length	153
% identity	86
NCBI Description	Arabidopsis thaliana BAC F1104

Seq. No.	147055
Seq. ID	LIB3168-083-P1-K1-F6
Method	BLASTX
NCBI GI	g4510397

BLAST score 119
E value 6.0e-14
Match length 61
% identity 72
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No. 147056
Seq. ID LIB3168-083-P1-K1-F7
Method BLASTX
NCBI GI g112682
BLAST score 44
E value 1.0e-46
Match length 116
% identity 84
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 147057
Seq. ID LIB3168-083-P1-K1-F9
Method BLASTN
NCBI GI g4220640
BLAST score 133
E value 1.0e-68
Match length 280
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 147058
Seq. ID LIB3168-083-P1-K1-G10
Method BLASTX
NCBI GI g4580461
BLAST score 503
E value 5.0e-51
Match length 111
% identity 92
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 147059
Seq. ID LIB3168-083-P1-K1-G11
Method BLASTX
NCBI GI g1628583
BLAST score 496
E value 3.0e-50
Match length 126
% identity 75
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147060
Seq. ID LIB3168-083-P1-K1-G12
Method BLASTX
NCBI GI g1628583

BLAST score	74
E value	3.0e-60
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147061
Seq. ID	LIB3168-083-P1-K1-G2
Method	BLASTX
NCBI GI	g4336436
BLAST score	528
E value	6.0e-54
Match length	149
% identity	70
NCBI Description	(AF092432) protein phosphatase type 2C [Lotus japonicus]

Seq. No.	147062
Seq. ID	LIB3168-083-P1-K1-G3
Method	BLASTX
NCBI GI	g2832777
BLAST score	276
E value	2.0e-24
Match length	114
% identity	43
NCBI Description	(AL021086) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /match=(desc:; /match=(desc:; EST embl_AA735498_AA735498 comes from the 5' UTR [Drosophila melanogaster]

Seq. No.	147063
Seq. ID	LIB3168-083-P1-K1-G5
Method	BLASTN
NCBI GI	g3406756
BLAST score	43
E value	5.0e-15
Match length	104
% identity	86
NCBI Description	Arabidopsis thaliana rac-like GTP binding protein Arac6 (Arac6) mRNA, complete cds

Seq. No.	147064
Seq. ID	LIB3168-083-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	82
E value	2.0e-54
Match length	119
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147065
Seq. ID	LIB3168-083-P1-K1-G7
Method	BLASTX

NCBI GI	g112741
BLAST score	255
E value	3.0e-22
Match length	65
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147066
Seq. ID	LIB3168-083-P1-K1-H1
Method	BLASTX
NCBI GI	g1750376
BLAST score	56
E value	2.0e-58
Match length	138
% identity	62
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	147067
Seq. ID	LIB3168-083-P1-K1-H10
Method	BLASTN
NCBI GI	g3659908
BLAST score	131
E value	2.0e-67
Match length	263
% identity	100
NCBI Description	Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds

Seq. No.	147068
Seq. ID	LIB3168-083-P1-K1-H12
Method	BLASTN
NCBI GI	g4159712
BLAST score	308
E value	1.0e-173
Match length	324
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	147069
Seq. ID	LIB3168-083-P1-K1-H2
Method	BLASTX
NCBI GI	g112743
BLAST score	669
E value	2.0e-70
Match length	143
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -

	Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]
Seq. No.	147070
Seq. ID	LIB3168-083-P1-K1-H3
Method	BLASTN
NCBI GI	g4100059
BLAST score	380
E value	0.0e+00
Match length	396
% identity	50
NCBI Description	Arabidopsis thaliana AthlecRK4 pseudogene, complete sequence, receptor lectin kinase 3 (AthlecRK3) gene, complete cds, and AthlecRK2 pseudogene, complete sequence
Seq. No.	147071
Seq. ID	LIB3168-083-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	130
E value	4.0e-71
Match length	146
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	147072
Seq. ID	LIB3168-083-P1-K1-H5
Method	BLASTX
NCBI GI	g112741
BLAST score	598
E value	3.0e-62
Match length	129
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	147073
Seq. ID	LIB3168-083-P1-K1-H7
Method	BLASTX
NCBI GI	g2961378
BLAST score	45
E value	6.0e-41
Match length	139
% identity	43
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]
Seq. No.	147074

Seq. ID	LIB3168-083-P1-K1-H9
Method	BLASTX
NCBI GI	g112739
BLAST score	467
E value	8.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147075
Seq. ID	LIB3168-084-P1-K1-A1
Method	BLASTX
NCBI GI	g4193388
BLAST score	475
E value	9.0e-48
Match length	117
% identity	79
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	147076
Seq. ID	LIB3168-084-P1-K1-A10
Method	BLASTX
NCBI GI	g2244897
BLAST score	719
E value	2.0e-76
Match length	142
% identity	99
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147077
Seq. ID	LIB3168-084-P1-K1-A11
Method	BLASTN
NCBI GI	g16472
BLAST score	416
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	147078
Seq. ID	LIB3168-084-P1-K1-A12
Method	BLASTX
NCBI GI	g3273743
BLAST score	620
E value	9.0e-65
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	147079
Seq. ID	LIB3168-084-P1-K1-A2
Method	BLASTN
NCBI GI	g4512656
BLAST score	143
E value	1.0e-74
Match length	350
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	147080
Seq. ID	LIB3168-084-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	9.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147081
Seq. ID	LIB3168-084-P1-K1-A4
Method	BLASTX
NCBI GI	g112682
BLAST score	46
E value	1.0e-27
Match length	77
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147082
Seq. ID	LIB3168-084-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147083
Seq. ID	LIB3168-084-P1-K1-A6
Method	BLASTX
NCBI GI	g2661422
BLAST score	580
E value	4.0e-60
Match length	119

% identity	93
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	147084
Seq. ID	LIB3168-084-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	573
E value	3.0e-59
Match length	144
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147085
Seq. ID	LIB3168-084-P1-K1-A8
Method	BLASTX
NCBI GI	g112681
BLAST score	545
E value	6.0e-56
Match length	144
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147086
Seq. ID	LIB3168-084-P1-K1-A9
Method	BLASTN
NCBI GI	g511598
BLAST score	346
E value	0.0e+00
Match length	390
% identity	32
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	147087
Seq. ID	LIB3168-084-P1-K1-B1
Method	BLASTX
NCBI GI	g112682
BLAST score	582
E value	2.0e-60
Match length	126
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147088
Seq. ID	LIB3168-084-P1-K1-B10
Method	BLASTX
NCBI GI	g2605714
BLAST score	514
E value	2.0e-52
Match length	122
% identity	84
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	147089
Seq. ID	LIB3168-084-P1-K1-B11
Method	BLASTX
NCBI GI	g4204299
BLAST score	685
E value	2.0e-72
Match length	134
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147090
Seq. ID	LIB3168-084-P1-K1-B12
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	3.0e-52
Match length	98
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	147091
Seq. ID	LIB3168-084-P1-K1-B2
Method	BLASTX
NCBI GI	g3660465
BLAST score	542
E value	8.0e-56
Match length	110
% identity	98
NCBI Description	(AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana]

Seq. No.	147092
Seq. ID	LIB3168-084-P1-K1-B3
Method	BLASTX
NCBI GI	g3328490
BLAST score	156
E value	3.0e-10
Match length	86
% identity	47
NCBI Description	(AE001283) tRNA Pseudouridine Synthase [Chlamydia trachomatis]

Seq. No.	147093
Seq. ID	LIB3168-084-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	689
E value	7.0e-73
Match length	144
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147094
Seq. ID	LIB3168-084-P1-K1-B5
Method	BLASTX
NCBI GI	g2459446
BLAST score	589
E value	4.0e-61
Match length	132
% identity	88
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	147095
Seq. ID	LIB3168-084-P1-K1-B7
Method	BLASTX
NCBI GI	g2708747
BLAST score	500
E value	8.0e-51
Match length	97
% identity	99
NCBI Description	(AC003952) putative glycine-rich, zinc-finger DNA-binding protein [Arabidopsis thaliana]

Seq. No.	147096
Seq. ID	LIB3168-084-P1-K1-B8
Method	BLASTX
NCBI GI	g112681
BLAST score	469
E value	4.0e-47
Match length	138
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147097
Seq. ID	LIB3168-084-P1-K1-C1
Method	BLASTX
NCBI GI	g112682
BLAST score	655
E value	6.0e-69
Match length	133
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

	cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	147098
Seq. ID	LIB3168-084-P1-K1-C10
Method	BLASTX
NCBI GI	g1526424
BLAST score	579
E value	6.0e-60
Match length	129
% identity	46
NCBI Description	(D64140) LEA protein in group 3 [Arabidopsis thaliana]
Seq. No.	147099
Seq. ID	LIB3168-084-P1-K1-C11
Method	BLASTX
NCBI GI	g112743
BLAST score	632
E value	4.0e-66
Match length	133
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]
Seq. No.	147100
Seq. ID	LIB3168-084-P1-K1-C12
Method	BLASTX
NCBI GI	g112682
BLAST score	595
E value	7.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	147101
Seq. ID	LIB3168-084-P1-K1-C2
Method	BLASTX
NCBI GI	g2252866
BLAST score	279
E value	9.0e-25
Match length	59
% identity	93
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]
Seq. No.	147102

Seq. ID LIB3168-084-P1-K1-C3
Method BLASTX
NCBI GI g1109699
BLAST score 609
E value 2.0e-63
Match length 118
% identity 99
NCBI Description (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No. 147103
Seq. ID LIB3168-084-P1-K1-C4
Method BLASTX
NCBI GI g1871192
BLAST score 155
E value 3.0e-10
Match length 59
% identity 54
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

Seq. No. 147104
Seq. ID LIB3168-084-P1-K1-C5
Method BLASTX
NCBI GI g112682
BLAST score 609
E value 2.0e-63
Match length 140
% identity 82
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 147105
Seq. ID LIB3168-084-P1-K1-C6
Method BLASTX
NCBI GI g1628583
BLAST score 319
E value 2.0e-29
Match length 76
% identity 97
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147106
Seq. ID LIB3168-084-P1-K1-C7
Method BLASTX
NCBI GI g1429207
BLAST score 636
E value 1.0e-66
Match length 123
% identity 69
NCBI Description (X99224) annexin [Arabidopsis thaliana]

Seq. No. 147107

Seq. ID	LIB3168-084-P1-K1-C8
Method	BLASTX
NCBI GI	g4584110
BLAST score	299
E value	4.0e-27
Match length	111
% identity	53
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	147108
Seq. ID	LIB3168-084-P1-K1-C9
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61
Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147109
Seq. ID	LIB3168-084-P1-K1-D1
Method	BLASTX
NCBI GI	g112681
BLAST score	753
E value	2.0e-80
Match length	143
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147110
Seq. ID	LIB3168-084-P1-K1-D10
Method	BLASTN
NCBI GI	g4159709
BLAST score	361
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	147111
Seq. ID	LIB3168-084-P1-K1-D11
Method	BLASTX
NCBI GI	g133959
BLAST score	263
E value	6.0e-23
Match length	56
% identity	91
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_81526_pir__A30833

ribosomal protein S4 - spinach chloroplast >gi_343377 (M16878) ribosomal protein S4 [Spinacia oleracea] >gi_225464_prf__1303355A ribosomal protein S4 [Spinacia oleracea]

Seq. No.	147112
Seq. ID	LIB3168-084-P1-K1-D12
Method	BLASTN
NCBI GI	g3449326
BLAST score	88
E value	1.0e-41
Match length	315
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	147113
Seq. ID	LIB3168-084-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	267
E value	2.0e-23
Match length	65
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147114
Seq. ID	LIB3168-084-P1-K1-D3
Method	BLASTX
NCBI GI	g2911042
BLAST score	535
E value	7.0e-55
Match length	111
% identity	99
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	147115
Seq. ID	LIB3168-084-P1-K1-D4
Method	BLASTN
NCBI GI	g3228389
BLAST score	387
E value	0.0e+00
Match length	395
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	147116
Seq. ID	LIB3168-084-P1-K1-D5
Method	BLASTX
NCBI GI	g2446981
BLAST score	626
E value	2.0e-65
Match length	120

% identity	100
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]

Seq. No.	147117
Seq. ID	LIB3168-084-P1-K1-D6
Method	BLASTX
NCBI GI	g3434975
BLAST score	142
E value	1.0e-08
Match length	31
% identity	77
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	147118
Seq. ID	LIB3168-084-P1-K1-D7
Method	BLASTX
NCBI GI	g3335169
BLAST score	685
E value	2.0e-72
Match length	128
% identity	99
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147119
Seq. ID	LIB3168-084-P1-K1-D8
Method	BLASTX
NCBI GI	g112741
BLAST score	703
E value	2.0e-74
Match length	133
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147120
Seq. ID	LIB3168-084-P1-K1-D9
Method	BLASTN
NCBI GI	g3869067
BLAST score	401
E value	0.0e+00
Match length	430
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	147121
Seq. ID	LIB3168-084-P1-K1-E1

Method	BLASTN
NCBI GI	g4756963
BLAST score	350
E value	0.0e+00
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	147122
Seq. ID	LIB3168-084-P1-K1-E10
Method	BLASTX
NCBI GI	g3080530
BLAST score	160
E value	8.0e-11
Match length	121
% identity	33
NCBI Description	(AL022600) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	147123
Seq. ID	LIB3168-084-P1-K1-E11
Method	BLASTX
NCBI GI	g2315449
BLAST score	292
E value	3.0e-26
Match length	131
% identity	43
NCBI Description	(AF016448) similar to Saccharomyces cerevisiae nuclear protein SNF7 (SP:P39929)in one region and the chromosome segregation protein SMC2 (SP:P38989) in another [Caenorhabditis elegans]

Seq. No.	147124
Seq. ID	LIB3168-084-P1-K1-E12
Method	BLASTX
NCBI GI	g1107501
BLAST score	369
E value	2.0e-35
Match length	91
% identity	81
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	147125
Seq. ID	LIB3168-084-P1-K1-E3
Method	BLASTX
NCBI GI	g112741
BLAST score	789
E value	1.0e-84
Match length	145
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147126
Seq. ID	LIB3168-084-P1-K1-E4
Method	BLASTX
NCBI GI	g112739
BLAST score	483
E value	1.0e-48
Match length	133
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147127
Seq. ID	LIB3168-084-P1-K1-E5
Method	BLASTN
NCBI GI	g4199934
BLAST score	352
E value	0.0e+00
Match length	392
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	147128
Seq. ID	LIB3168-084-P1-K1-E6
Method	BLASTX
NCBI GI	g3914386
BLAST score	206
E value	3.0e-16
Match length	87
% identity	45
NCBI Description	ALLERGEN MF1 >gi_3445490_dbj_BAA32435_ (AB011804) MF1 [Malassezia furfur]

Seq. No.	147129
Seq. ID	LIB3168-084-P1-K1-E7
Method	BLASTX
NCBI GI	g3157937
BLAST score	653
E value	1.0e-68
Match length	131
% identity	98
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No. 147130

Seq. ID	LIB3168-084-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	620
E value	9.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147131
Seq. ID	LIB3168-084-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	696
E value	1.0e-73
Match length	140
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147132
Seq. ID	LIB3168-084-P1-K1-F10
Method	BLASTX
NCBI GI	g2129657
BLAST score	351
E value	3.0e-33
Match length	102
% identity	75
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147133
Seq. ID	LIB3168-084-P1-K1-F12
Method	BLASTN
NCBI GI	g166609
BLAST score	217
E value	1.0e-119
Match length	217
% identity	100
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	147134
Seq. ID	LIB3168-084-P1-K1-F2
Method	BLASTX
NCBI GI	g4263515
BLAST score	277
E value	1.0e-24
Match length	138
% identity	54

NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147135
Seq. ID	LIB3168-084-P1-K1-F3
Method	BLASTX
NCBI GI	g1070654
BLAST score	318
E value	2.0e-50
Match length	131
% identity	71
NCBI Description	cruciferin 4 precursor - rape

Seq. No.	147136
Seq. ID	LIB3168-084-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	608
E value	2.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147137
Seq. ID	LIB3168-084-P1-K1-F6
Method	BLASTX
NCBI GI	g112737
BLAST score	197
E value	3.0e-15
Match length	65
% identity	65
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147138
Seq. ID	LIB3168-084-P1-K1-F7
Method	BLASTX
NCBI GI	g112739
BLAST score	474
E value	1.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147139

Seq. ID	LIB3168-084-P1-K1-F9
Method	BLASTX
NCBI GI	g112682
BLAST score	56
E value	1.0e-61
Match length	136
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147140
Seq. ID	LIB3168-084-P1-K1-G11
Method	BLASTN
NCBI GI	g4263540
BLAST score	39
E value	5.0e-13
Match length	55
% identity	38
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147141
Seq. ID	LIB3168-084-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	144
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147142
Seq. ID	LIB3168-084-P1-K1-G5
Method	BLASTX
NCBI GI	g3335169
BLAST score	641
E value	3.0e-67
Match length	144
% identity	79
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147143
Seq. ID	LIB3168-084-P1-K1-G6
Method	BLASTN
NCBI GI	g4733952
BLAST score	95
E value	4.0e-46
Match length	219
% identity	80
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic

sequence, complete sequence

Seq. No.	147144
Seq. ID	LIB3168-084-P1-K1-G7
Method	BLASTX
NCBI GI	g112682
BLAST score	588
E value	5.0e-61
Match length	138
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147145
Seq. ID	LIB3168-084-P1-K1-G8
Method	BLASTX
NCBI GI	g4432839
BLAST score	144
E value	6.0e-09
Match length	85
% identity	22
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	147146
Seq. ID	LIB3168-084-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	659
E value	2.0e-69
Match length	138
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147147
Seq. ID	LIB3168-084-P1-K1-H1
Method	BLASTX
NCBI GI	g2129657
BLAST score	271
E value	7.0e-24
Match length	90
% identity	68
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147148
Seq. ID	LIB3168-084-P1-K1-H10
Method	BLASTN
NCBI GI	g4757411

BLAST score	294
E value	1.0e-164
Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	147149
Seq. ID	LIB3168-084-P1-K1-H11
Method	BLASTX
NCBI GI	g2191135
BLAST score	446
E value	2.0e-44
Match length	118
% identity	71
NCBI Description	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]

Seq. No.	147150
Seq. ID	LIB3168-084-P1-K1-H12
Method	BLASTX
NCBI GI	g112682
BLAST score	590
E value	3.0e-61
Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147151
Seq. ID	LIB3168-084-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	719
E value	2.0e-76
Match length	143
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147152
Seq. ID	LIB3168-084-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	4.0e-56
Match length	138
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147153

Seq. ID	LIB3168-084-P1-K1-H4
Method	BLASTX
NCBI GI	g137578
BLAST score	255
E value	5.0e-22
Match length	106
% identity	44
NCBI Description	VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi_81545_pir__S06398 alpha-globulin type A precursor - upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A [Artificial gene] >gi_226119_prf__1410330A vicilin gene A [Saguinus oedipus]

Seq. No.	147154
Seq. ID	LIB3168-084-P1-K1-H5
Method	BLASTX
NCBI GI	g112682
BLAST score	588
E value	5.0e-61
Match length	124
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147155
Seq. ID	LIB3168-084-P1-K1-H6
Method	BLASTX
NCBI GI	g112682
BLAST score	598
E value	3.0e-62
Match length	128
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147156
Seq. ID	LIB3168-084-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147157
Seq. ID	LIB3168-086-P1-K1-A1
Method	BLASTX

NCBI GI	g3738288
BLAST score	407
E value	5.0e-40
Match length	82
% identity	99
NCBI Description	(AC005309) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	147158
Seq. ID	LIB3168-086-P1-K1-A10
Method	BLASTX
NCBI GI	g2795809
BLAST score	362
E value	2.0e-34
Match length	96
% identity	73
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	147159
Seq. ID	LIB3168-086-P1-K1-A11
Method	BLASTX
NCBI GI	g112682
BLAST score	511
E value	6.0e-52
Match length	140
% identity	75
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147160
Seq. ID	LIB3168-086-P1-K1-A12
Method	BLASTX
NCBI GI	g3335169
BLAST score	645
E value	1.0e-67
Match length	130
% identity	94
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147161
Seq. ID	LIB3168-086-P1-K1-A3
Method	BLASTN
NCBI GI	g3894179
BLAST score	412
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147162
Seq. ID	LIB3168-086-P1-K1-A4

Method	BLASTX
NCBI GI	g112737
BLAST score	588
E value	5.0e-61
Match length	140
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147163
Seq. ID	LIB3168-086-P1-K1-A5
Method	BLASTN
NCBI GI	g3242700
BLAST score	369
E value	0.0e+00
Match length	475
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147164
Seq. ID	LIB3168-086-P1-K1-A7
Method	BLASTX
NCBI GI	g3914996
BLAST score	739
E value	1.0e-78
Match length	142
% identity	99
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine aminotransferase [Arabidopsis thaliana]

Seq. No.	147165
Seq. ID	LIB3168-086-P1-K1-A8
Method	BLASTX
NCBI GI	g112739
BLAST score	358
E value	4.0e-34
Match length	110
% identity	67
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147166
Seq. ID	LIB3168-086-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	561
E value	7.0e-58
Match length	134
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147167
Seq. ID	LIB3168-086-P1-K1-B1
Method	BLASTX
NCBI GI	g112682
BLAST score	466
E value	7.0e-47
Match length	109
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147168
Seq. ID	LIB3168-086-P1-K1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	876
E value	1.0e-94
Match length	176
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147169
Seq. ID	LIB3168-086-P1-K1-B11
Method	BLASTX
NCBI GI	g4585924
BLAST score	542
E value	2.0e-55
Match length	174
% identity	64
NCBI Description	(AC007211) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147170
Seq. ID	LIB3168-086-P1-K1-B3
Method	BLASTN
NCBI GI	g2564045
BLAST score	204
E value	1.0e-111
Match length	530
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	147171
Seq. ID	LIB3168-086-P1-K1-B4
Method	BLASTN
NCBI GI	g2564044
BLAST score	131
E value	2.0e-67
Match length	191
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	147172
Seq. ID	LIB3168-086-P1-K1-B5
Method	BLASTX
NCBI GI	g131336
BLAST score	324
E value	6.0e-30
Match length	73
% identity	90
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	147173
Seq. ID	LIB3168-086-P1-K1-B6
Method	BLASTX
NCBI GI	g112737
BLAST score	542
E value	1.0e-55
Match length	118
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147174
Seq. ID	LIB3168-086-P1-K1-B7
Method	BLASTN
NCBI GI	g3482964
BLAST score	167
E value	6.0e-89
Match length	323
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	147175
Seq. ID	LIB3168-086-P1-K1-B8

Method	BLASTX
NCBI GI	g112739
BLAST score	475
E value	1.0e-47
Match length	148
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147176
Seq. ID	LIB3168-086-P1-K1-B9
Method	BLASTX
NCBI GI	g3128189
BLAST score	171
E value	2.0e-19
Match length	93
% identity	61
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	147177
Seq. ID	LIB3168-086-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	541
E value	1.0e-55
Match length	111
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147178
Seq. ID	LIB3168-086-P1-K1-C11
Method	BLASTN
NCBI GI	g3869071
BLAST score	450
E value	0.0e+00
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	147179
Seq. ID	LIB3168-086-P1-K1-C12
Method	BLASTN
NCBI GI	g3869071
BLAST score	453
E value	0.0e+00
Match length	536
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	147180
Seq. ID	LIB3168-086-P1-K1-C2
Method	BLASTX
NCBI GI	g4262222
BLAST score	601
E value	1.0e-62
Match length	119
% identity	100
NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	147181
Seq. ID	LIB3168-086-P1-K1-C3
Method	BLASTX
NCBI GI	g3776561
BLAST score	531
E value	3.0e-54
Match length	119
% identity	95
NCBI Description	(AC005388) Identical to DNA for acyl carrier protein (ACP) gene A2 gb_X57699 from A. thaliana. ESTs gb_W43252, gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955 come from this gene. [Arabidopsis thaliana]

Seq. No.	147182
Seq. ID	LIB3168-086-P1-K1-C4
Method	BLASTX
NCBI GI	g2894599
BLAST score	182
E value	2.0e-13
Match length	125
% identity	28
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	147183
Seq. ID	LIB3168-086-P1-K1-C6
Method	BLASTX
NCBI GI	g3047104
BLAST score	623
E value	5.0e-65
Match length	123
% identity	98
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	147184
Seq. ID	LIB3168-086-P1-K1-C8
Method	BLASTX
NCBI GI	g2961346
BLAST score	271
E value	1.0e-23
Match length	121
% identity	50
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	147185

Seq. ID	LIB3168-086-P1-K1-C9
Method	BLASTX
NCBI GI	g2795809
BLAST score	330
E value	8.0e-31
Match length	79
% identity	82
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	147186
Seq. ID	LIB3168-086-P1-K1-D1
Method	BLASTX
NCBI GI	g112741
BLAST score	847
E value	3.0e-91
Match length	160
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147187
Seq. ID	LIB3168-086-P1-K1-D11
Method	BLASTX
NCBI GI	g2651296
BLAST score	633
E value	4.0e-66
Match length	152
% identity	81
NCBI Description	(AC002336) b-zip DNA-binding protein [Arabidopsis thaliana]

Seq. No.	147188
Seq. ID	LIB3168-086-P1-K1-D12
Method	BLASTX
NCBI GI	g4406780
BLAST score	632
E value	5.0e-66
Match length	154
% identity	82
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	147189
Seq. ID	LIB3168-086-P1-K1-D2
Method	BLASTN
NCBI GI	g3080430
BLAST score	466
E value	0.0e+00
Match length	513
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	147190
Seq. ID	LIB3168-086-P1-K1-D3
Method	BLASTN
NCBI GI	g2842474
BLAST score	278
E value	1.0e-155
Match length	325
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	147191
Seq. ID	LIB3168-086-P1-K1-D5
Method	BLASTX
NCBI GI	g112682
BLAST score	455
E value	2.0e-45
Match length	114
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147192
Seq. ID	LIB3168-086-P1-K1-D9
Method	BLASTX
NCBI GI	g2146741
BLAST score	77
E value	3.0e-33
Match length	98
% identity	77
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	147193
Seq. ID	LIB3168-086-P1-K1-E1
Method	BLASTN
NCBI GI	g4159709
BLAST score	155
E value	7.0e-82
Match length	251
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	147194
Seq. ID	LIB3168-086-P1-K1-E10
Method	BLASTX
NCBI GI	g4204298
BLAST score	607
E value	3.0e-63
Match length	150
% identity	79

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147195
Seq. ID	LIB3168-086-P1-K1-E11
Method	BLASTX
NCBI GI	g4204298
BLAST score	288
E value	7.0e-26
Match length	65
% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147196
Seq. ID	LIB3168-086-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	44
E value	4.0e-58
Match length	144
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147197
Seq. ID	LIB3168-086-P1-K1-E2
Method	BLASTX
NCBI GI	g3273743
BLAST score	536
E value	6.0e-55
Match length	118
% identity	89
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	147198
Seq. ID	LIB3168-086-P1-K1-E3
Method	BLASTX
NCBI GI	g2160133
BLAST score	150
E value	3.0e-10
Match length	49
% identity	67
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	147199
Seq. ID	LIB3168-086-P1-K1-E4
Method	BLASTX
NCBI GI	g112741
BLAST score	753
E value	2.0e-80

Match length	141
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147200
Seq. ID	LIB3168-086-P1-K1-E5
Method	BLASTN
NCBI GI	g2760171
BLAST score	193
E value	1.0e-104
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]

Seq. No.	147201
Seq. ID	LIB3168-086-P1-K1-E6
Method	BLASTN
NCBI GI	g3449320
BLAST score	381
E value	0.0e+00
Match length	473
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	147202
Seq. ID	LIB3168-086-P1-K1-E7
Method	BLASTX
NCBI GI	g112682
BLAST score	594
E value	1.0e-61
Match length	141
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147203
Seq. ID	LIB3168-086-P1-K1-E8
Method	BLASTX
NCBI GI	g2738248
BLAST score	461
E value	1.0e-64
Match length	154
% identity	88
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	147204
Seq. ID	LIB3168-086-P1-K1-E9
Method	BLASTN
NCBI GI	g987013
BLAST score	204
E value	1.0e-111
Match length	300
% identity	92
NCBI Description	A.thaliana mRNA for oleosin (isoform; 841 bp) >gi_987015_emb_Z54165_ATOLEOSN3 A.thaliana mRNA for oleosin (isoform; 841 bp)

Seq. No.	147205
Seq. ID	LIB3168-086-P1-K1-F1
Method	BLASTN
NCBI GI	g4100568
BLAST score	83
E value	3.0e-39
Match length	95
% identity	98
NCBI Description	Arabidopsis thaliana fatty acid desaturase/cytochrome b5 fusion protein mRNA, complete cds

Seq. No.	147206
Seq. ID	LIB3168-086-P1-K1-F10
Method	BLASTN
NCBI GI	g3063690
BLAST score	218
E value	1.0e-119
Match length	437
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	147207
Seq. ID	LIB3168-086-P1-K1-F11
Method	BLASTX
NCBI GI	g4544419
BLAST score	598
E value	4.0e-62
Match length	148
% identity	82
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	147208
Seq. ID	LIB3168-086-P1-K1-F12
Method	BLASTX
NCBI GI	g4204298
BLAST score	582
E value	3.0e-60
Match length	152
% identity	77
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147209
Seq. ID	LIB3168-086-P1-K1-F3

Method	BLASTX
NCBI GI	g112743
BLAST score	704
E value	1.0e-74
Match length	148
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147210
Seq. ID	LIB3168-086-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	549
E value	2.0e-56
Match length	112
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147211
Seq. ID	LIB3168-086-P1-K1-F5
Method	BLASTX
NCBI GI	g2661422
BLAST score	740
E value	1.0e-78
Match length	144
% identity	99
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	147212
Seq. ID	LIB3168-086-P1-K1-F6
Method	BLASTX
NCBI GI	g4006897
BLAST score	42
E value	8.0e-43
Match length	112
% identity	83
NCBI Description	(Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.	147213
Seq. ID	LIB3168-086-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	277
E value	1.0e-27
Match length	96
% identity	66

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147214
Seq. ID	LIB3168-086-P1-K1-F8
Method	BLASTX
NCBI GI	g112741
BLAST score	457
E value	9.0e-51
Match length	101
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147215
Seq. ID	LIB3168-086-P1-K1-F9
Method	BLASTX
NCBI GI	g112682
BLAST score	716
E value	5.0e-76
Match length	145
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147216
Seq. ID	LIB3168-086-P1-K1-G11
Method	BLASTX
NCBI GI	g3660465
BLAST score	471
E value	4.0e-47
Match length	91
% identity	99
NCBI Description	(AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana]

Seq. No.	147217
Seq. ID	LIB3168-086-P1-K1-G12
Method	BLASTX
NCBI GI	g112741
BLAST score	885
E value	1.0e-95
Match length	164
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147218
Seq. ID	LIB3168-086-P1-K1-G2
Method	BLASTX
NCBI GI	g3335171
BLAST score	673
E value	6.0e-71
Match length	134
% identity	96
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	147219
Seq. ID	LIB3168-086-P1-K1-G3
Method	BLASTN
NCBI GI	g3128136
BLAST score	255
E value	1.0e-141
Match length	471
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	147220
Seq. ID	LIB3168-086-P1-K1-G4
Method	BLASTX
NCBI GI	g112741
BLAST score	846
E value	4.0e-91
Match length	157
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147221
Seq. ID	LIB3168-086-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147222
Seq. ID	LIB3168-086-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583

BLAST score	622
E value	7.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147223
Seq. ID	LIB3168-086-P1-K1-G7
Method	BLASTX
NCBI GI	g1628583
BLAST score	524
E value	2.0e-53
Match length	120
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147224
Seq. ID	LIB3168-086-P1-K1-G8
Method	BLASTN
NCBI GI	g3241916
BLAST score	321
E value	0.0e+00
Match length	469
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	147225
Seq. ID	LIB3168-086-P1-K1-G9
Method	BLASTN
NCBI GI	g4006885
BLAST score	324
E value	0.0e+00
Match length	452
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	147226
Seq. ID	LIB3168-086-P1-K1-H1
Method	BLASTX
NCBI GI	g3318611
BLAST score	339
E value	1.0e-31
Match length	66
% identity	94
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	147227
Seq. ID	LIB3168-086-P1-K1-H10
Method	BLASTN
NCBI GI	g4757414

BLAST score	467
E value	0.0e+00
Match length	483
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	147228
Seq. ID	LIB3168-086-P1-K1-H11
Method	BLASTX
NCBI GI	g4006914
BLAST score	609
E value	1.0e-63
Match length	119
% identity	97
NCBI Description	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]

Seq. No.	147229
Seq. ID	LIB3168-086-P1-K1-H12
Method	BLASTX
NCBI GI	g112741
BLAST score	709
E value	4.0e-75
Match length	163
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147230
Seq. ID	LIB3168-086-P1-K1-H2
Method	BLASTX
NCBI GI	g112682
BLAST score	435
E value	3.0e-43
Match length	99
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147231
Seq. ID	LIB3168-086-P1-K1-H3
Method	BLASTN
NCBI GI	g4220632
BLAST score	131
E value	2.0e-67
Match length	387
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	147232
Seq. ID	LIB3168-086-P1-K1-H5
Method	BLASTX
NCBI GI	g2160191
BLAST score	50
E value	1.0e-04
Match length	75
% identity	81
NCBI Description	(AC000132) Identical to A. thaliana AtK-1 (gb_X79279). [Arabidopsis thaliana]

Seq. No.	147233
Seq. ID	LIB3168-086-P1-K1-H6
Method	BLASTX
NCBI GI	g112741
BLAST score	42
E value	1.0e-32
Match length	94
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147234
Seq. ID	LIB3168-086-P1-K1-H7
Method	BLASTX
NCBI GI	g112741
BLAST score	588
E value	6.0e-61
Match length	130
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147235
Seq. ID	LIB3168-086-P1-K1-H8
Method	BLASTX
NCBI GI	g112741
BLAST score	619
E value	3.0e-85
Match length	160
% identity	92
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147236
Seq. ID	LIB3168-087-P1-K1-A10
Method	BLASTX
NCBI GI	g112741
BLAST score	665
E value	5.0e-70
Match length	142
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147237
Seq. ID	LIB3168-087-P1-K1-A11
Method	BLASTX
NCBI GI	g112741
BLAST score	435
E value	3.0e-43
Match length	98
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147238
Seq. ID	LIB3168-087-P1-K1-A12
Method	BLASTX
NCBI GI	g3157947
BLAST score	298
E value	5.0e-49
Match length	131
% identity	54
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	147239
Seq. ID	LIB3168-087-P1-K1-A4
Method	BLASTX
NCBI GI	g112682
BLAST score	412
E value	1.0e-40
Match length	94

% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147240
Seq. ID	LIB3168-087-P1-K1-A5
Method	BLASTX
NCBI GI	g4038491
BLAST score	155
E value	3.0e-10
Match length	110
% identity	33
NCBI Description	(AJ131705) poly(ADP-ribose) polymerase [Arabidopsis thaliana]

Seq. No.	147241
Seq. ID	LIB3168-087-P1-K1-A6
Method	BLASTX
NCBI GI	g112741
BLAST score	301
E value	2.0e-27
Match length	56
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147242
Seq. ID	LIB3168-087-P1-K1-A7
Method	BLASTX
NCBI GI	g112737
BLAST score	460
E value	4.0e-46
Match length	115
% identity	77
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147243
Seq. ID	LIB3168-087-P1-K1-A9
Method	BLASTX
NCBI GI	g2129657
BLAST score	465
E value	2.0e-46
Match length	123

% identity	79
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147244
Seq. ID	LIB3168-087-P1-K1-B1
Method	BLASTX
NCBI GI	g1628583
BLAST score	527
E value	7.0e-54
Match length	120
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147245
Seq. ID	LIB3168-087-P1-K1-B10
Method	BLASTX
NCBI GI	g112737
BLAST score	714
E value	1.0e-75
Match length	164
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147246
Seq. ID	LIB3168-087-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	325
E value	2.0e-30
Match length	89
% identity	72
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147247
Seq. ID	LIB3168-087-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	239
E value	3.0e-56
Match length	128
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147248
Seq. ID	LIB3168-087-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	249
E value	2.0e-21
Match length	49
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147249
Seq. ID	LIB3168-087-P1-K1-B5
Method	BLASTX
NCBI GI	g99742
BLAST score	373
E value	5.0e-36
Match length	94
% identity	79
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	147250
Seq. ID	LIB3168-087-P1-K1-B7
Method	BLASTX
NCBI GI	g112681
BLAST score	854
E value	4.0e-92
Match length	172
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147251
Seq. ID	LIB3168-087-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	416
E value	6.0e-41
Match length	113
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147252
Seq. ID	LIB3168-087-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	474
E value	8.0e-48
Match length	114

% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147253
Seq. ID	LIB3168-087-P1-K1-C10
Method	BLASTX
NCBI GI	g112737
BLAST score	687
E value	1.0e-72
Match length	146
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147254
Seq. ID	LIB3168-087-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	581
E value	5.0e-60
Match length	120
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147255
Seq. ID	LIB3168-087-P1-K1-C4
Method	BLASTN
NCBI GI	g3600045
BLAST score	180
E value	1.0e-96
Match length	372
% identity	94
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	147256
Seq. ID	LIB3168-087-P1-K1-C5
Method	BLASTX
NCBI GI	g3859696
BLAST score	190
E value	2.0e-14
Match length	132
% identity	33
NCBI Description	(AL033497) unknown hypothetical protein [Candida albicans]

Seq. No.	147257
Seq. ID	LIB3168-087-P1-K1-C6
Method	BLASTX
NCBI GI	g112682

BLAST score	465
E value	9.0e-47
Match length	109
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147258
Seq. ID	LIB3168-087-P1-K1-C7
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147259
Seq. ID	LIB3168-087-P1-K1-C8
Method	BLASTX
NCBI GI	g4455338
BLAST score	687
E value	1.0e-72
Match length	133
% identity	100
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	147260
Seq. ID	LIB3168-087-P1-K1-C9
Method	BLASTX
NCBI GI	g112681
BLAST score	744
E value	3.0e-79
Match length	141
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147261
Seq. ID	LIB3168-087-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	358
E value	4.0e-34
Match length	89
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147262
Seq. ID	LIB3168-087-P1-K1-D10
Method	BLASTX
NCBI GI	g3551247
BLAST score	740
E value	9.0e-79
Match length	155
% identity	88
NCBI Description	(AB012703) 181 [Daucus carota]

Seq. No.	147263
Seq. ID	LIB3168-087-P1-K1-D11
Method	BLASTX
NCBI GI	g1628583
BLAST score	644
E value	1.0e-67
Match length	127
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147264
Seq. ID	LIB3168-087-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	698
E value	6.0e-74
Match length	140
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147265
Seq. ID	LIB3168-087-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	678
E value	1.0e-71
Match length	142
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147266
Seq. ID	LIB3168-087-P1-K1-D3
Method	BLASTX
NCBI GI	g1345973
BLAST score	389
E value	9.0e-38
Match length	92
% identity	79
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC

1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	147267
Seq. ID	LIB3168-087-P1-K1-D4
Method	BLASTX
NCBI GI	g4455300
BLAST score	174
E value	2.0e-12
Match length	39
% identity	72
NCBI Description	(AL035528) putative pectate lyase A11 (fragment) [Arabidopsis thaliana]

Seq. No.	147268
Seq. ID	LIB3168-087-P1-K1-D5
Method	BLASTX
NCBI GI	g2832625
BLAST score	523
E value	2.0e-53
Match length	116
% identity	84
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	147269
Seq. ID	LIB3168-087-P1-K1-D6
Method	BLASTN
NCBI GI	g12208
BLAST score	268
E value	1.0e-149
Match length	358
% identity	92
NCBI Description	Sinapis alba plastid trnQ and psbK genes for tRNA-Glu and K proteiH of photosystem II

Seq. No.	147270
Seq. ID	LIB3168-087-P1-K1-D7
Method	BLASTN
NCBI GI	g3176694
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147271
Seq. ID	LIB3168-087-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	491
E value	7.0e-50

Match length	99
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147272
Seq. ID	LIB3168-087-P1-K1-D9
Method	BLASTN
NCBI GI	g4454022
BLAST score	260
E value	1.0e-144
Match length	375
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	147273
Seq. ID	LIB3168-087-P1-K1-E1
Method	BLASTX
NCBI GI	g1107501
BLAST score	389
E value	1.0e-37
Match length	96
% identity	83
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	147274
Seq. ID	LIB3168-087-P1-K1-E10
Method	BLASTX
NCBI GI	g3776005
BLAST score	484
E value	6.0e-49
Match length	110
% identity	86
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	147275
Seq. ID	LIB3168-087-P1-K1-E11
Method	BLASTN
NCBI GI	g1871173
BLAST score	242
E value	1.0e-133
Match length	349
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	147276
Seq. ID	LIB3168-087-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	497
E value	2.0e-50

Match length	98
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147277
Seq. ID	LIB3168-087-P1-K1-E2
Method	BLASTX
NCBI GI	g112682
BLAST score	645
E value	1.0e-84
Match length	158
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147278
Seq. ID	LIB3168-087-P1-K1-E3
Method	BLASTX
NCBI GI	g112682
BLAST score	785
E value	5.0e-84
Match length	176
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147279
Seq. ID	LIB3168-087-P1-K1-E5
Method	BLASTN
NCBI GI	g3510339
BLAST score	262
E value	1.0e-145
Match length	355
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	147280
Seq. ID	LIB3168-087-P1-K1-E7
Method	BLASTX
NCBI GI	g4204299
BLAST score	521
E value	4.0e-53
Match length	103
% identity	98
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147281

Seq. ID LIB3168-087-P1-K1-E8
Method BLASTX
NCBI GI g112739
BLAST score 470
E value 4.0e-47
Match length 133
% identity 72
NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 147282
Seq. ID LIB3168-087-P1-K1-E9
Method BLASTX
NCBI GI g1628583
BLAST score 665
E value 4.0e-70
Match length 127
% identity 99
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147283
Seq. ID LIB3168-087-P1-K1-F1
Method BLASTX
NCBI GI g399091
BLAST score 780
E value 2.0e-83
Match length 175
% identity 89
NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No. 147284
Seq. ID LIB3168-087-P1-K1-F10
Method BLASTX
NCBI GI g112681
BLAST score 691
E value 4.0e-73
Match length 134
% identity 97
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 147285

Seq. ID	LIB3168-087-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	5.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147286
Seq. ID	LIB3168-087-P1-K1-F12
Method	BLASTX
NCBI GI	g2129657
BLAST score	252
E value	9.0e-22
Match length	81
% identity	68
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147287
Seq. ID	LIB3168-087-P1-K1-F2
Method	BLASTN
NCBI GI	g4406776
BLAST score	384
E value	0.0e+00
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147288
Seq. ID	LIB3168-087-P1-K1-F3
Method	BLASTX
NCBI GI	g3193331
BLAST score	177
E value	7.0e-13
Match length	45
% identity	67
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	147289
Seq. ID	LIB3168-087-P1-K1-F4
Method	BLASTX
NCBI GI	g112682
BLAST score	615
E value	3.0e-64
Match length	132
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	147290
Seq. ID	LIB3168-087-P1-K1-F5
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	147291
Seq. ID	LIB3168-087-P1-K1-F6
Method	BLASTN
NCBI GI	g2264302
BLAST score	286
E value	1.0e-160
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	147292
Seq. ID	LIB3168-087-P1-K1-F7
Method	BLASTX
NCBI GI	g1171870
BLAST score	152
E value	9.0e-10
Match length	88
% identity	33
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (COMPLEX I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV) >gi_89670_pir__S16208 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 19K chain - bovine >gi_599681_emb_CAA42218_ (X59697) 19 kDa subunit of NADH:ubiquinone oxidoreductase complex (complex I) [Bos taurus]

Seq. No.	147293
Seq. ID	LIB3168-087-P1-K1-F8
Method	BLASTN
NCBI GI	g1526412
BLAST score	286
E value	1.0e-160
Match length	330
% identity	97
NCBI Description	Arabidopsis thaliana ATPK19 mRNA for ribosomal-protein S6 kinase homolog, complete cds

Seq. No.	147294
Seq. ID	LIB3168-087-P1-K1-F9
Method	BLASTX
NCBI GI	g112741
BLAST score	893
E value	1.0e-96
Match length	164
% identity	100

NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147295
Seq. ID	LIB3168-087-P1-K1-G10
Method	BLASTX
NCBI GI	g115783
BLAST score	561
E value	7.0e-58
Match length	109
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	147296
Seq. ID	LIB3168-087-P1-K1-G12
Method	BLASTN
NCBI GI	g3798730
BLAST score	45
E value	3.0e-16
Match length	73
% identity	90
NCBI Description	Arabidopsis thaliana transgenic line C DNA

Seq. No.	147297
Seq. ID	LIB3168-087-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147298
Seq. ID	LIB3168-087-P1-K1-G4
Method	BLASTN
NCBI GI	g4512656
BLAST score	151
E value	3.0e-79
Match length	357
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	147299
Seq. ID	LIB3168-087-P1-K1-G5
Method	BLASTX

NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147300
Seq. ID	LIB3168-087-P1-K1-G6
Method	BLASTX
NCBI GI	g132074
BLAST score	607
E value	2.0e-63
Match length	123
% identity	93
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	147301
Seq. ID	LIB3168-087-P1-K1-G7
Method	BLASTN
NCBI GI	g3046854
BLAST score	329
E value	0.0e+00
Match length	473
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	147302
Seq. ID	LIB3168-087-P1-K1-G8
Method	BLASTX
NCBI GI	g1354272
BLAST score	671
E value	1.0e-70
Match length	143
% identity	86
NCBI Description	(U51036) aspartic proteinase [Arabidopsis thaliana]

Seq. No.	147303
Seq. ID	LIB3168-087-P1-K1-G9
Method	BLASTX
NCBI GI	g2507477
BLAST score	184
E value	2.0e-13
Match length	120
% identity	37
NCBI Description	TRANSALDOLASE A >gi_1788807 (AE000333) transaldolase A [Escherichia coli] >gi_1799888_dbj_BAA16339_ (D90875) similar to [PIR Accession Number S40535] [Escherichia coli] >gi_2337774_dbj_BAA21821_ (D13159) transaldolase [Escherichia coli]

Seq. No.	147304
Seq. ID	LIB3168-087-P1-K1-H1
Method	BLASTX
NCBI GI	g3894193
BLAST score	431
E value	2.0e-42
Match length	137
% identity	59
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	147305
Seq. ID	LIB3168-087-P1-K1-H12
Method	BLASTN
NCBI GI	g3046853
BLAST score	140
E value	4.0e-73
Match length	148
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	147306
Seq. ID	LIB3168-087-P1-K1-H3
Method	BLASTX
NCBI GI	g112739
BLAST score	470
E value	4.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147307
Seq. ID	LIB3168-087-P1-K1-H4
Method	BLASTX
NCBI GI	g131336
BLAST score	247
E value	5.0e-21
Match length	58
% identity	86
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	147308
Seq. ID	LIB3168-087-P1-K1-H6
Method	BLASTX
NCBI GI	g82051

BLAST score	368
E value	4.0e-35
Match length	151
% identity	50
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	147309
Seq. ID	LIB3168-087-P1-K1-H8
Method	BLASTX
NCBI GI	g633890
BLAST score	450
E value	1.0e-44
Match length	150
% identity	62
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No.	147310
Seq. ID	LIB3168-087-P1-K1-H9
Method	BLASTX
NCBI GI	g112741
BLAST score	653
E value	1.0e-68
Match length	119
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147311
Seq. ID	LIB3168-088-P1-K1-A1
Method	BLASTX
NCBI GI	g1628583
BLAST score	605
E value	5.0e-63
Match length	117
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147312
Seq. ID	LIB3168-088-P1-K1-A10
Method	BLASTX
NCBI GI	g1255951
BLAST score	227
E value	7.0e-32
Match length	103
% identity	70
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	147313
Seq. ID	LIB3168-088-P1-K1-A12
Method	BLASTX
NCBI GI	g1336807
BLAST score	265
E value	3.0e-23
Match length	100
% identity	56
NCBI Description	(S81193) CEN=GTP-binding protein homolog [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum] >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]

Seq. No.	147314
Seq. ID	LIB3168-088-P1-K1-A2
Method	BLASTX
NCBI GI	g3342249
BLAST score	528
E value	4.0e-54
Match length	106
% identity	98
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi_3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	147315
Seq. ID	LIB3168-088-P1-K1-A3
Method	BLASTX
NCBI GI	g82051
BLAST score	331
E value	6.0e-31
Match length	124
% identity	53
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	147316
Seq. ID	LIB3168-088-P1-K1-A4
Method	BLASTX
NCBI GI	g112681
BLAST score	597
E value	4.0e-62
Match length	113
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147317
Seq. ID	LIB3168-088-P1-K1-A5
Method	BLASTX
NCBI GI	g112682
BLAST score	554
E value	5.0e-57

Match length	125
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147318
Seq. ID	LIB3168-088-P1-K1-A6
Method	BLASTX
NCBI GI	g4584346
BLAST score	420
E value	2.0e-41
Match length	91
% identity	90
NCBI Description	(AC007127) unknown protein [Arabidopsis thaliana]

Seq. No.	147319
Seq. ID	LIB3168-088-P1-K1-A7
Method	BLASTX
NCBI GI	g112739
BLAST score	187
E value	2.0e-14
Match length	41
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147320
Seq. ID	LIB3168-088-P1-K1-A8
Method	BLASTX
NCBI GI	g4539301
BLAST score	120
E value	1.0e-12
Match length	66
% identity	56
NCBI Description	(AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	147321
Seq. ID	LIB3168-088-P1-K1-A9
Method	BLASTX
NCBI GI	g112682
BLAST score	628
E value	8.0e-66
Match length	121
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	147322
Seq. ID	LIB3168-088-P1-K1-B1
Method	BLASTX
NCBI GI	g112741
BLAST score	686
E value	2.0e-72
Match length	127
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147323
Seq. ID	LIB3168-088-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	618
E value	1.0e-64
Match length	131
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147324
Seq. ID	LIB3168-088-P1-K1-B11
Method	BLASTX
NCBI GI	g112737
BLAST score	426
E value	4.0e-42
Match length	121
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147325
Seq. ID	LIB3168-088-P1-K1-B12
Method	BLASTX
NCBI GI	g3241945
BLAST score	144
E value	5.0e-09
Match length	65
% identity	43
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	147326
Seq. ID	LIB3168-088-P1-K1-B2
Method	BLASTX
NCBI GI	g3335169
BLAST score	736
E value	2.0e-78
Match length	136
% identity	100
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147327
Seq. ID	LIB3168-088-P1-K1-B3
Method	BLASTX
NCBI GI	g548847
BLAST score	253
E value	9.0e-22
Match length	51
% identity	98
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	147328
Seq. ID	LIB3168-088-P1-K1-B4
Method	BLASTN
NCBI GI	g3241922
BLAST score	137
E value	2.0e-71
Match length	168
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	147329
Seq. ID	LIB3168-088-P1-K1-B5
Method	BLASTX
NCBI GI	g112682
BLAST score	556
E value	3.0e-57
Match length	131
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147330
Seq. ID	LIB3168-088-P1-K1-B6
Method	BLASTX
NCBI GI	g112739
BLAST score	301
E value	1.0e-27

Match length	102
% identity	62
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147331
Seq. ID	LIB3168-088-P1-K1-B7
Method	BLASTX
NCBI GI	g1172676
BLAST score	384
E value	2.0e-37
Match length	80
% identity	93
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi_1262709_dbj_BAA04424.1_ (D17510) PSII 44kDa protein [Pinus thunbergii]

Seq. No.	147332
Seq. ID	LIB3168-088-P1-K1-B9
Method	BLASTX
NCBI GI	g112682
BLAST score	522
E value	2.0e-53
Match length	104
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147333
Seq. ID	LIB3168-088-P1-K1-C1
Method	BLASTX
NCBI GI	g3808062
BLAST score	175
E value	1.0e-12
Match length	73
% identity	44
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	147334
Seq. ID	LIB3168-088-P1-K1-C10
Method	BLASTN
NCBI GI	g2656026
BLAST score	258
E value	1.0e-143
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	147335
Seq. ID	LIB3168-088-P1-K1-C11
Method	BLASTX
NCBI GI	g2129657
BLAST score	335
E value	2.0e-31
Match length	97
% identity	74
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147336
Seq. ID	LIB3168-088-P1-K1-C2
Method	BLASTX
NCBI GI	g2444271
BLAST score	561
E value	7.0e-58
Match length	123
% identity	85
NCBI Description	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No.	147337
Seq. ID	LIB3168-088-P1-K1-C4
Method	BLASTX
NCBI GI	g112737
BLAST score	533
E value	1.0e-54
Match length	130
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147338
Seq. ID	LIB3168-088-P1-K1-C5
Method	BLASTX
NCBI GI	g1628583
BLAST score	718
E value	3.0e-76
Match length	136
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147339
Seq. ID	LIB3168-088-P1-K1-C6
Method	BLASTN
NCBI GI	g4468103
BLAST score	240

E value	1.0e-132
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	147340
Seq. ID	LIB3168-088-P1-K1-C7
Method	BLASTN
NCBI GI	g3128139
BLAST score	392
E value	0.0e+00
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	147341
Seq. ID	LIB3168-088-P1-K1-C8
Method	BLASTX
NCBI GI	g112681
BLAST score	510
E value	6.0e-52
Match length	134
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147342
Seq. ID	LIB3168-088-P1-K1-E10
Method	BLASTX
NCBI GI	g112682
BLAST score	523
E value	1.0e-53
Match length	112
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147343
Seq. ID	LIB3168-088-P1-K1-E11
Method	BLASTX
NCBI GI	g112682
BLAST score	54
E value	2.0e-38
Match length	89
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	147344
Seq. ID	LIB3168-088-P1-K1-E12
Method	BLASTN
NCBI GI	g3108248
BLAST score	54
E value	1.0e-21
Match length	111
% identity	87
NCBI Description	Gossypium barbadense clone pXP027 repetitive DNA sequence

Seq. No.	147345
Seq. ID	LIB3168-088-P1-K1-E5
Method	BLASTX
NCBI GI	g112739
BLAST score	468
E value	5.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147346
Seq. ID	LIB3168-088-P1-K1-E6
Method	BLASTX
NCBI GI	g3929649
BLAST score	237
E value	4.0e-20
Match length	62
% identity	76
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	147347
Seq. ID	LIB3168-088-P1-K1-E7
Method	BLASTN
NCBI GI	g3449314
BLAST score	307
E value	1.0e-172
Match length	370
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]

Seq. No.	147348
Seq. ID	LIB3168-088-P1-K1-E8
Method	BLASTN
NCBI GI	g2864607
BLAST score	331
E value	0.0e+00
Match length	358

% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	147349
Seq. ID	LIB3168-088-P1-K1-E9
Method	BLASTN
NCBI GI	g2138315
BLAST score	289
E value	1.0e-161
Match length	383
% identity	99
NCBI Description	Arabidopsis thaliana root hair defective 3 (RHD3) gene, complete cds

Seq. No.	147350
Seq. ID	LIB3168-088-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	521
E value	3.0e-53
Match length	108
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147351
Seq. ID	LIB3168-088-P1-K1-F10
Method	BLASTN
NCBI GI	g2459406
BLAST score	120
E value	4.0e-61
Match length	212
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147352
Seq. ID	LIB3168-088-P1-K1-F11
Method	BLASTX
NCBI GI	g4204298
BLAST score	277
E value	4.0e-25
Match length	73
% identity	73
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147353
Seq. ID	LIB3168-088-P1-K1-F12
Method	BLASTX
NCBI GI	g112682
BLAST score	592
E value	1.0e-61

Match length	125
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147354
Seq. ID	LIB3168-088-P1-K1-F2
Method	BLASTX
NCBI GI	g112739
BLAST score	432
E value	9.0e-43
Match length	124
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147355
Seq. ID	LIB3168-088-P1-K1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	356
E value	8.0e-34
Match length	69
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147356
Seq. ID	LIB3168-088-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	276
E value	1.0e-24
Match length	72
% identity	75
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147357
Seq. ID	LIB3168-088-P1-K1-F6
Method	BLASTX
NCBI GI	g112682
BLAST score	572
E value	3.0e-59
Match length	119

% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	147358
Seq. ID	LIB3168-088-P1-K1-F7
Method	BLASTN
NCBI GI	g2760172
BLAST score	402
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.	147359
Seq. ID	LIB3168-088-P1-K1-F8
Method	BLASTN
NCBI GI	g4455229
BLAST score	371
E value	0.0e+00
Match length	375
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)
Seq. No.	147360
Seq. ID	LIB3168-088-P1-K1-F9
Method	BLASTX
NCBI GI	g4204299
BLAST score	674
E value	4.0e-71
Match length	129
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	147361
Seq. ID	LIB3168-088-P1-K1-G1
Method	BLASTX
NCBI GI	g2335094
BLAST score	232
E value	3.0e-25
Match length	63
% identity	98
NCBI Description	(AC002339) putative polygalacturonase [Arabidopsis thaliana]
Seq. No.	147362
Seq. ID	LIB3168-088-P1-K1-G10
Method	BLASTX
NCBI GI	g112682
BLAST score	591
E value	2.0e-61

Match length	137
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147363
Seq. ID	LIB3168-088-P1-K1-G11
Method	BLASTX
NCBI GI	g2494896
BLAST score	242
E value	4.0e-21
Match length	54
% identity	81
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	147364
Seq. ID	LIB3168-088-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	668
E value	2.0e-70
Match length	132
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147365
Seq. ID	LIB3168-088-P1-K1-G3
Method	BLASTX
NCBI GI	g112741
BLAST score	695
E value	1.0e-73
Match length	129
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147366
Seq. ID	LIB3168-088-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	646
E value	7.0e-68

Match length	126
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147367
Seq. ID	LIB3168-088-P1-K1-G6
Method	BLASTN
NCBI GI	g2264320
BLAST score	214
E value	1.0e-117
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	147368
Seq. ID	LIB3168-088-P1-K1-G7
Method	BLASTN
NCBI GI	g4557061
BLAST score	328
E value	0.0e+00
Match length	400
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	147369
Seq. ID	LIB3168-088-P1-K1-G9
Method	BLASTN
NCBI GI	g4455229
BLAST score	170
E value	1.0e-90
Match length	256
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	147370
Seq. ID	LIB3168-088-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	610
E value	1.0e-63
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147371
Seq. ID	LIB3168-088-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	73
E value	6.0e-45

Match length	101
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147372
Seq. ID	LIB3168-088-P1-K1-H2
Method	BLASTN
NCBI GI	g2618600
BLAST score	342
E value	0.0e+00
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	147373
Seq. ID	LIB3168-088-P1-K1-H3
Method	BLASTX
NCBI GI	g3044212
BLAST score	580
E value	4.0e-60
Match length	134
% identity	87
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	147374
Seq. ID	LIB3168-088-P1-K1-H5
Method	BLASTN
NCBI GI	g4544435
BLAST score	252
E value	1.0e-140
Match length	252
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	147375
Seq. ID	LIB3168-088-P1-K1-H6
Method	BLASTX
NCBI GI	g112681
BLAST score	575
E value	2.0e-59
Match length	114
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147376
Seq. ID	LIB3168-089-P1-K1-A1
Method	BLASTX
NCBI GI	g112681
BLAST score	199

E value	5.0e-16
Match length	45
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147377
Seq. ID	LIB3168-089-P1-K1-A10
Method	BLASTX
NCBI GI	g112741
BLAST score	597
E value	4.0e-62
Match length	133
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147378
Seq. ID	LIB3168-089-P1-K1-A11
Method	BLASTX
NCBI GI	g112741
BLAST score	648
E value	4.0e-68
Match length	121
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147379
Seq. ID	LIB3168-089-P1-K1-A2
Method	BLASTX
NCBI GI	g4204299
BLAST score	568
E value	1.0e-58
Match length	115
% identity	96
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147380
Seq. ID	LIB3168-089-P1-K1-A3
Method	BLASTX
NCBI GI	g112743
BLAST score	739

E value	1.0e-78
Match length	148
% identity	93
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147381
Seq. ID	LIB3168-089-P1-K1-A4
Method	BLASTN
NCBI GI	g4558586
BLAST score	161
E value	1.0e-85
Match length	193
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	147382
Seq. ID	LIB3168-089-P1-K1-A5
Method	BLASTX
NCBI GI	g2832629
BLAST score	190
E value	2.0e-14
Match length	125
% identity	38
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	147383
Seq. ID	LIB3168-089-P1-K1-A6
Method	BLASTX
NCBI GI	g112681
BLAST score	623
E value	4.0e-65
Match length	143
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147384
Seq. ID	LIB3168-089-P1-K1-A7
Method	BLASTX
NCBI GI	g112741
BLAST score	175
E value	4.0e-13
Match length	67
% identity	57
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147385
Seq. ID	LIB3168-089-P1-K1-A8
Method	BLASTX
NCBI GI	g112741
BLAST score	613
E value	6.0e-64
Match length	122
% identity	93
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147386
Seq. ID	LIB3168-089-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	6.0e-56
Match length	112
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147387
Seq. ID	LIB3168-089-P1-K1-B10
Method	BLASTX
NCBI GI	g112681
BLAST score	523
E value	2.0e-53
Match length	131
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147388
Seq. ID	LIB3168-089-P1-K1-B11
Method	BLASTX
NCBI GI	g1628583
BLAST score	636
E value	1.0e-66
Match length	127
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147389
Seq. ID	LIB3168-089-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	755
E value	1.0e-80
Match length	153
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147390
Seq. ID	LIB3168-089-P1-K1-B3
Method	BLASTX
NCBI GI	g1628583
BLAST score	95
E value	1.0e-57
Match length	148
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147391
Seq. ID	LIB3168-089-P1-K1-B4
Method	BLASTX
NCBI GI	g2129773
BLAST score	554
E value	5.0e-57
Match length	106
% identity	97
NCBI Description	xyloglucan endotransglycosylase-related protein XTR3 - Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	147392
Seq. ID	LIB3168-089-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	555
E value	4.0e-57
Match length	143
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147393
Seq. ID	LIB3168-089-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	672

E value	7.0e-71
Match length	141
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147394
Seq. ID	LIB3168-089-P1-K1-B7
Method	BLASTX
NCBI GI	g112682
BLAST score	607
E value	3.0e-63
Match length	148
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147395
Seq. ID	LIB3168-089-P1-K1-B8
Method	BLASTX
NCBI GI	g112682
BLAST score	615
E value	4.0e-64
Match length	148
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147396
Seq. ID	LIB3168-089-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	604
E value	7.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147397
Seq. ID	LIB3168-089-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	478
E value	4.0e-48
Match length	106
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147398
Seq. ID	LIB3168-089-P1-K1-C10
Method	BLASTX
NCBI GI	g112682
BLAST score	527
E value	7.0e-59
Match length	146
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147399
Seq. ID	LIB3168-089-P1-K1-C11
Method	BLASTX
NCBI GI	g112682
BLAST score	556
E value	3.0e-57
Match length	116
% identity	90
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147400
Seq. ID	LIB3168-089-P1-K1-C2
Method	BLASTX
NCBI GI	g1628583
BLAST score	69
E value	2.0e-52
Match length	108
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147401
Seq. ID	LIB3168-089-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	518
E value	9.0e-53
Match length	139
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147402

Seq. ID	LIB3168-089-P1-K1-C4
Method	BLASTX
NCBI GI	g4689386
BLAST score	342
E value	4.0e-32
Match length	77
% identity	83
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	147403
Seq. ID	LIB3168-089-P1-K1-C5
Method	BLASTX
NCBI GI	g112681
BLAST score	593
E value	1.0e-61
Match length	114
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147404
Seq. ID	LIB3168-089-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	609
E value	2.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147405
Seq. ID	LIB3168-089-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	176
E value	2.0e-26
Match length	124
% identity	60
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147406
Seq. ID	LIB3168-089-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	401
E value	5.0e-39
Match length	89
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147407
Seq. ID	LIB3168-089-P1-K1-D11
Method	BLASTX
NCBI GI	g112682
BLAST score	630
E value	6.0e-66
Match length	139
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147408
Seq. ID	LIB3168-089-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	499
E value	1.0e-50
Match length	120
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147409
Seq. ID	LIB3168-089-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	496
E value	3.0e-50
Match length	131
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147410
Seq. ID	LIB3168-089-P1-K1-D3
Method	BLASTX
NCBI GI	g2129657
BLAST score	445
E value	3.0e-44
Match length	125
% identity	74
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147411
Seq. ID	LIB3168-089-P1-K1-D6
Method	BLASTX

NCBI GI	g112739
BLAST score	414
E value	1.0e-40
Match length	138
% identity	62
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147412
Seq. ID	LIB3168-089-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	562
E value	6.0e-58
Match length	111
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147413
Seq. ID	LIB3168-089-P1-K1-E10
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	6.0e-64
Match length	127
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147414
Seq. ID	LIB3168-089-P1-K1-E12
Method	BLASTX
NCBI GI	g1628583
BLAST score	602
E value	1.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147415
Seq. ID	LIB3168-089-P1-K1-E2
Method	BLASTN
NCBI GI	g1279569
BLAST score	86
E value	2.0e-40
Match length	260
% identity	88

NCBI Description	Nicotiana acuminata chloroplast JLA region, 1-1028bp

Seq. No.	147416
Seq. ID	LIB3168-089-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	387
E value	2.0e-37
Match length	86
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147417
Seq. ID	LIB3168-089-P1-K1-E4
Method	BLASTX
NCBI GI	g1628583
BLAST score	568
E value	1.0e-58
Match length	120
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147418
Seq. ID	LIB3168-089-P1-K1-E5
Method	BLASTN
NCBI GI	g2494106
BLAST score	99
E value	2.0e-48
Match length	166
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147419
Seq. ID	LIB3168-089-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	408
E value	7.0e-40
Match length	109
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147420
Seq. ID	LIB3168-089-P1-K1-E7
Method	BLASTX
NCBI GI	g1526424
BLAST score	350
E value	3.0e-33
Match length	110
% identity	68

NCBI Description	(D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No.	147421
Seq. ID	LIB3168-089-P1-K1-E8
Method	BLASTX
NCBI GI	g2129577
BLAST score	408
E value	4.0e-40
Match length	81
% identity	98
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	147422
Seq. ID	LIB3168-089-P1-K1-E9
Method	BLASTX
NCBI GI	g112743
BLAST score	48
E value	3.0e-23
Match length	117
% identity	54
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147423
Seq. ID	LIB3168-089-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	92
E value	3.0e-51
Match length	131
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147424
Seq. ID	LIB3168-089-P1-K1-F11
Method	BLASTX
NCBI GI	g112681
BLAST score	469
E value	4.0e-47
Match length	121
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147425
Seq. ID	LIB3168-089-P1-K1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	2.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147426
Seq. ID	LIB3168-089-P1-K1-F2
Method	BLASTN
NCBI GI	g2924729
BLAST score	307
E value	1.0e-172
Match length	407
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	147427
Seq. ID	LIB3168-089-P1-K1-F3
Method	BLASTN
NCBI GI	g4006815
BLAST score	286
E value	1.0e-160
Match length	364
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147428
Seq. ID	LIB3168-089-P1-K1-F4
Method	BLASTX
NCBI GI	g112737
BLAST score	623
E value	5.0e-65
Match length	154
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147429
Seq. ID	LIB3168-089-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	573
E value	3.0e-59
Match length	115

% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147430
Seq. ID	LIB3168-089-P1-K1-F6
Method	BLASTX
NCBI GI	g112681
BLAST score	636
E value	1.0e-66
Match length	126
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147431
Seq. ID	LIB3168-089-P1-K1-F7
Method	BLASTX
NCBI GI	g1107501
BLAST score	182
E value	2.0e-13
Match length	94
% identity	47
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	147432
Seq. ID	LIB3168-089-P1-K1-F8
Method	BLASTX
NCBI GI	g21106
BLAST score	265
E value	4.0e-23
Match length	105
% identity	50
NCBI Description	(X59802) cruciferin [Raphanus sativus]

Seq. No.	147433
Seq. ID	LIB3168-089-P1-K1-F9
Method	BLASTX
NCBI GI	g112741
BLAST score	677
E value	2.0e-71
Match length	137
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147434
Seq. ID	LIB3168-089-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583
BLAST score	267
E value	2.0e-23
Match length	75
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147435
Seq. ID	LIB3168-089-P1-K1-G10
Method	BLASTX
NCBI GI	g1361983
BLAST score	621
E value	7.0e-65
Match length	123
% identity	98
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	147436
Seq. ID	LIB3168-089-P1-K1-G11
Method	BLASTN
NCBI GI	g4512656
BLAST score	161
E value	3.0e-85
Match length	426
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	147437
Seq. ID	LIB3168-089-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	80
E value	7.0e-39
Match length	98
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147438
Seq. ID	LIB3168-089-P1-K1-G2
Method	BLASTX
NCBI GI	g21114
BLAST score	131
E value	1.0e-19
Match length	66
% identity	72

NCBI Description	(X59806) cruciferin [Raphanus sativus]

Seq. No.	147439
Seq. ID	LIB3168-089-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	350
E value	4.0e-33
Match length	89
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147440
Seq. ID	LIB3168-089-P1-K1-G6
Method	BLASTN
NCBI GI	g4567259
BLAST score	317
E value	1.0e-178
Match length	389
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	147441
Seq. ID	LIB3168-089-P1-K1-G7
Method	BLASTX
NCBI GI	g112681
BLAST score	720
E value	2.0e-76
Match length	148
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147442
Seq. ID	LIB3168-089-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	55
E value	6.0e-52
Match length	113
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147443
Seq. ID	LIB3168-089-P1-K1-H10
Method	BLASTN
NCBI GI	g3859610
BLAST score	144
E value	2.0e-75

Match length	192
% identity	94
NCBI Description	Arabidopsis thaliana BAC T9E19

Seq. No.	147444
Seq. ID	LIB3168-089-P1-K1-H11
Method	BLASTX
NCBI GI	g112741
BLAST score	584
E value	1.0e-60
Match length	113
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147445
Seq. ID	LIB3168-089-P1-K1-H12
Method	BLASTX
NCBI GI	g3935151
BLAST score	712
E value	2.0e-75
Match length	133
% identity	98
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	147446
Seq. ID	LIB3168-089-P1-K1-H2
Method	BLASTX
NCBI GI	g2129641
BLAST score	600
E value	2.0e-62
Match length	110
% identity	99
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	147447
Seq. ID	LIB3168-089-P1-K1-H3
Method	BLASTX
NCBI GI	g112682
BLAST score	603
E value	1.0e-62
Match length	147
% identity	79
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147448

Seq. ID	LIB3168-089-P1-K1-H4
Method	BLASTN
NCBI GI	g3449314
BLAST score	334
E value	0.0e+00
Match length	414
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]

Seq. No.	147449
Seq. ID	LIB3168-089-P1-K1-H5
Method	BLASTX
NCBI GI	g2134962
BLAST score	376
E value	4.0e-36
Match length	129
% identity	55
NCBI Description	cyclophilin-like protein CyP-60 - human >gi_1199598 (U37219) cyclophilin-like protein CyP-60 [Homo sapiens] >gi_1587642_prf__2207180A cyclophilin:ISOTYPE=CyP-60 [Homo sapiens]

Seq. No.	147450
Seq. ID	LIB3168-089-P1-K1-H6
Method	BLASTX
NCBI GI	g2781394
BLAST score	496
E value	3.0e-50
Match length	107
% identity	95
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	147451
Seq. ID	LIB3168-089-P1-K1-H7
Method	BLASTX
NCBI GI	g112682
BLAST score	542
E value	3.0e-58
Match length	128
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147452
Seq. ID	LIB3168-089-P1-K1-H8
Method	BLASTX
NCBI GI	g112739
BLAST score	300
E value	2.0e-27
Match length	102
% identity	63
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -

Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147453
Seq. ID	LIB3168-089-P1-K1-H9
Method	BLASTX
NCBI GI	g3335169
BLAST score	684
E value	2.0e-73
Match length	147
% identity	89
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147454
Seq. ID	LIB3168-090-P1-K1-A1
Method	BLASTX
NCBI GI	g3929364
BLAST score	701
E value	3.0e-74
Match length	137
% identity	99
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	147455
Seq. ID	LIB3168-090-P1-K1-A11
Method	BLASTN
NCBI GI	g166609
BLAST score	113
E value	6.0e-57
Match length	226
% identity	86
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	147456
Seq. ID	LIB3168-090-P1-K1-A2
Method	BLASTN
NCBI GI	g3869073
BLAST score	258
E value	1.0e-143
Match length	383
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	147457
Seq. ID	LIB3168-090-P1-K1-A3
Method	BLASTN
NCBI GI	g4335711
BLAST score	90
E value	4.0e-43
Match length	256
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147458
Seq. ID	LIB3168-090-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	45
E value	2.0e-57
Match length	120
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147459
Seq. ID	LIB3168-090-P1-K1-A5
Method	BLASTX
NCBI GI	g112737
BLAST score	457
E value	9.0e-46
Match length	98
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147460
Seq. ID	LIB3168-090-P1-K1-A8
Method	BLASTX
NCBI GI	g112681
BLAST score	596
E value	6.0e-62
Match length	124
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147461
Seq. ID	LIB3168-090-P1-K1-A9
Method	BLASTX
NCBI GI	g3757514

BLAST score	641
E value	3.0e-67
Match length	123
% identity	99
NCBI Description	(AC005167) putative plasma membrane intrinsic protein [Arabidopsis thaliana] >gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	147462
Seq. ID	LIB3168-090-P1-K1-B11
Method	BLASTN
NCBI GI	g16131
BLAST score	35
E value	2.0e-10
Match length	146
% identity	84
NCBI Description	Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with 18S rRNA fragment

Seq. No.	147463
Seq. ID	LIB3168-090-P1-K1-B12
Method	BLASTX
NCBI GI	g82214
BLAST score	423
E value	1.0e-41
Match length	129
% identity	78
NCBI Description	hypothetical protein 350 - common tobacco chloroplast >gi_4388761_emb_CAA77394_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	147464
Seq. ID	LIB3168-090-P1-K1-B6
Method	BLASTX
NCBI GI	g114335
BLAST score	665
E value	5.0e-70
Match length	141
% identity	94
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	147465
Seq. ID	LIB3168-090-P1-K1-B7
Method	BLASTN
NCBI GI	g2924257
BLAST score	59
E value	2.0e-24
Match length	83
% identity	93
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	147466
Seq. ID	LIB3168-090-P1-K1-B8

Method	BLASTX
NCBI GI	g1169598
BLAST score	475
E value	7.0e-75
Match length	142
% identity	94
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	147467
Seq. ID	LIB3168-090-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	611
E value	1.0e-63
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147468
Seq. ID	LIB3168-090-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	403
E value	1.0e-39
Match length	89
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147469
Seq. ID	LIB3168-090-P1-K1-C12
Method	BLASTN
NCBI GI	g16231
BLAST score	49
E value	1.0e-18
Match length	133
% identity	83
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	147470
Seq. ID	LIB3168-090-P1-K1-C2
Method	BLASTX
NCBI GI	g3176874
BLAST score	623
E value	4.0e-65
Match length	121
% identity	99
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	147471
Seq. ID	LIB3168-090-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	560
E value	9.0e-58
Match length	131
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147472
Seq. ID	LIB3168-090-P1-K1-C4
Method	BLASTX
NCBI GI	g2129659
BLAST score	45
E value	7.0e-39
Match length	109
% identity	83
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	147473
Seq. ID	LIB3168-090-P1-K1-C5
Method	BLASTX
NCBI GI	g2583125
BLAST score	46
E value	1.0e-26
Match length	126
% identity	56
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	147474
Seq. ID	LIB3168-090-P1-K1-C8
Method	BLASTN
NCBI GI	g2264311
BLAST score	43
E value	3.0e-15
Match length	100
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	147475
Seq. ID	LIB3168-090-P1-K1-C9
Method	BLASTN
NCBI GI	g2842474
BLAST score	71
E value	7.0e-32
Match length	193
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	147476
Seq. ID	LIB3168-090-P1-K1-D1
Method	BLASTX
NCBI GI	g112739
BLAST score	469
E value	5.0e-47
Match length	131
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147477
Seq. ID	LIB3168-090-P1-K1-D11
Method	BLASTX
NCBI GI	g2129657
BLAST score	387
E value	1.0e-37
Match length	113
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147478
Seq. ID	LIB3168-090-P1-K1-D2
Method	BLASTX
NCBI GI	g3924598
BLAST score	213
E value	1.0e-17
Match length	41
% identity	98
NCBI Description	(AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	147479
Seq. ID	LIB3168-090-P1-K1-D4
Method	BLASTX
NCBI GI	g1628583
BLAST score	607
E value	3.0e-63
Match length	127
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147480
Seq. ID	LIB3168-090-P1-K1-D5
Method	BLASTN
NCBI GI	g2828184
BLAST score	187

E value	1.0e-101
Match length	383
% identity	70
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	147481
Seq. ID	LIB3168-090-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	441
E value	6.0e-44
Match length	98
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147482
Seq. ID	LIB3168-090-P1-K1-D7
Method	BLASTX
NCBI GI	g3024434
BLAST score	483
E value	1.0e-48
Match length	117
% identity	85
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	147483
Seq. ID	LIB3168-090-P1-K1-D8
Method	BLASTN
NCBI GI	g2842474
BLAST score	61
E value	1.0e-25
Match length	184
% identity	65
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	147484
Seq. ID	LIB3168-090-P1-K1-D9
Method	BLASTX
NCBI GI	g1345973
BLAST score	728
E value	2.0e-77
Match length	139
% identity	95
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No.	147485
Seq. ID	LIB3168-090-P1-K1-E11
Method	BLASTN
NCBI GI	g4512690
BLAST score	111
E value	2.0e-55
Match length	401
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	147486
Seq. ID	LIB3168-090-P1-K1-E3
Method	BLASTX
NCBI GI	g112741
BLAST score	574
E value	2.0e-59
Match length	107
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147487
Seq. ID	LIB3168-090-P1-K1-E5
Method	BLASTX
NCBI GI	g4204298
BLAST score	470
E value	3.0e-47
Match length	119
% identity	81
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147488
Seq. ID	LIB3168-090-P1-K1-E6
Method	BLASTN
NCBI GI	g2924652
BLAST score	163
E value	2.0e-86
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	147489
Seq. ID	LIB3168-090-P1-K1-E7
Method	BLASTX
NCBI GI	g2506938
BLAST score	527
E value	7.0e-54

Match length	122
% identity	84
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST

Seq. No.	147490
Seq. ID	LIB3168-090-P1-K1-E8
Method	BLASTN
NCBI GI	g2570187
BLAST score	35
E value	1.0e-10
Match length	93
% identity	88
NCBI Description	Arabidopsis thaliana DNA for alcohol dehydrogenase, complete cds >gi_2570191_dbj_D63462_D63462 Arabidopsis thaliana DNA for alcohol dehydrogenase, complete cds

Seq. No.	147491
Seq. ID	LIB3168-090-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	573
E value	3.0e-59
Match length	122
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147492
Seq. ID	LIB3168-090-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	348
E value	7.0e-33
Match length	113
% identity	68
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147493
Seq. ID	LIB3168-090-P1-K1-F11
Method	BLASTN
NCBI GI	g2264367
BLAST score	219
E value	1.0e-120
Match length	370
% identity	95
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	147494
Seq. ID	LIB3168-090-P1-K1-F3
Method	BLASTN
NCBI GI	g2618683
BLAST score	180
E value	1.0e-96
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147495
Seq. ID	LIB3168-090-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	407
E value	5.0e-40
Match length	80
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147496
Seq. ID	LIB3168-090-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	595
E value	7.0e-62
Match length	120
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147497
Seq. ID	LIB3168-090-P1-K1-F8
Method	BLASTX
NCBI GI	g2997591
BLAST score	159
E value	1.0e-10
Match length	82
% identity	51
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No.	147498
Seq. ID	LIB3168-090-P1-K1-F9
Method	BLASTX
NCBI GI	g112681
BLAST score	497
E value	2.0e-50
Match length	99
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147499
Seq. ID	LIB3168-090-P1-K1-G1
Method	BLASTX
NCBI GI	g114335
BLAST score	473
E value	2.0e-47
Match length	126
% identity	74
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	147500
Seq. ID	LIB3168-090-P1-K1-G2
Method	BLASTX
NCBI GI	g1336804
BLAST score	206
E value	3.0e-16
Match length	46
% identity	91
NCBI Description	vacuolar H(+)-ATPase subunit B [Mesembryanthemum crystallinum, leaf, Peptide Partial, 170 aa]

Seq. No.	147501
Seq. ID	LIB3168-090-P1-K1-G3
Method	BLASTX
NCBI GI	g2160146
BLAST score	430
E value	2.0e-42
Match length	127
% identity	69
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F21M12.3,F21M12.1. EST gb_H36326 comes from this gene. [Arabidopsis thaliana]

Seq. No.	147502
Seq. ID	LIB3168-090-P1-K1-G4
Method	BLASTN
NCBI GI	g3449328
BLAST score	173
E value	2.0e-92
Match length	370
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCI2, complete sequence [Arabidopsis thaliana]

Seq. No.	147503
Seq. ID	LIB3168-090-P1-K1-G5
Method	BLASTX
NCBI GI	g2961390
BLAST score	377
E value	1.0e-36
Match length	76

% identity	95
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	147504
Seq. ID	LIB3168-090-P1-K1-G6
Method	BLASTX
NCBI GI	g2252866
BLAST score	192
E value	1.0e-14
Match length	58
% identity	64
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	147505
Seq. ID	LIB3168-090-P1-K1-G7
Method	BLASTX
NCBI GI	g112682
BLAST score	715
E value	7.0e-76
Match length	143
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147506
Seq. ID	LIB3168-090-P1-K1-G8
Method	BLASTX
NCBI GI	g112681
BLAST score	712
E value	1.0e-75
Match length	143
% identity	94
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147507
Seq. ID	LIB3168-090-P1-K1-G9
Method	BLASTX
NCBI GI	g1628583
BLAST score	431
E value	7.0e-43
Match length	95
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147508
Seq. ID	LIB3168-090-P1-K1-H1

Method	BLASTX
NCBI GI	g1628583
BLAST score	515
E value	2.0e-52
Match length	120
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147509
Seq. ID	LIB3168-090-P1-K1-H11
Method	BLASTX
NCBI GI	g112741
BLAST score	330
E value	6.0e-31
Match length	114
% identity	38
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147510
Seq. ID	LIB3168-090-P1-K1-H3
Method	BLASTX
NCBI GI	g112682
BLAST score	619
E value	1.0e-64
Match length	132
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147511
Seq. ID	LIB3168-091-P1-K1-A1
Method	BLASTN
NCBI GI	g2160155
BLAST score	48
E value	7.0e-18
Match length	132
% identity	91
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	147512
Seq. ID	LIB3168-091-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	507
E value	2.0e-51

Match length	147
% identity	69
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147513
Seq. ID	LIB3168-091-P1-K1-A7
Method	BLASTX
NCBI GI	g112737
BLAST score	59
E value	2.0e-61
Match length	142
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147514
Seq. ID	LIB3168-091-P1-K1-B11
Method	BLASTN
NCBI GI	g395203
BLAST score	121
E value	1.0e-61
Match length	278
% identity	63
NCBI Description	A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's

Seq. No.	147515
Seq. ID	LIB3168-091-P1-K1-B12
Method	BLASTN
NCBI GI	g4097693
BLAST score	44
E value	8.0e-16
Match length	103
% identity	83
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	147516
Seq. ID	LIB3168-091-P1-K1-B2
Method	BLASTX
NCBI GI	g112739
BLAST score	328
E value	2.0e-30
Match length	145
% identity	56
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No.	147517
Seq. ID	LIB3168-091-P1-K1-B3
Method	BLASTX
NCBI GI	g3335169
BLAST score	781
E value	1.0e-83
Match length	146
% identity	99
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147518
Seq. ID	LIB3168-091-P1-K1-B4
Method	BLASTX
NCBI GI	g112682
BLAST score	718
E value	3.0e-76
Match length	157
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147519
Seq. ID	LIB3168-091-P1-K1-B6
Method	BLASTX
NCBI GI	g1628583
BLAST score	576
E value	1.0e-59
Match length	135
% identity	84
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147520
Seq. ID	LIB3168-091-P1-K1-B7
Method	BLASTX
NCBI GI	g2129767
BLAST score	434
E value	4.0e-43
Match length	84
% identity	96
NCBI Description	vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No.	147521
Seq. ID	LIB3168-091-P1-K1-B8
Method	BLASTN
NCBI GI	g2252823
BLAST score	69

E value	2.0e-30
Match length	179
% identity	73
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	147522
Seq. ID	LIB3168-091-P1-K1-B9
Method	BLASTN
NCBI GI	g2618677
BLAST score	301
E value	1.0e-169
Match length	339
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	147523
Seq. ID	LIB3168-091-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	49
E value	1.0e-37
Match length	81
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147524
Seq. ID	LIB3168-091-P1-K1-C11
Method	BLASTX
NCBI GI	g1170373
BLAST score	339
E value	1.0e-39
Match length	92
% identity	86
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	147525
Seq. ID	LIB3168-091-P1-K1-C2
Method	BLASTX
NCBI GI	g3264759
BLAST score	541
E value	2.0e-55
Match length	138
% identity	78
NCBI Description	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No.	147526
Seq. ID	LIB3168-091-P1-K1-C3
Method	BLASTX
NCBI GI	g112739
BLAST score	519
E value	7.0e-53

Match length	142
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147527
Seq. ID	LIB3168-091-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	533
E value	1.0e-54
Match length	112
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147528
Seq. ID	LIB3168-091-P1-K1-C5
Method	BLASTX
NCBI GI	g4204299
BLAST score	141
E value	3.0e-09
Match length	49
% identity	65
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147529
Seq. ID	LIB3168-091-P1-K1-C7
Method	BLASTN
NCBI GI	g2656032
BLAST score	82
E value	4.0e-38
Match length	266
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	147530
Seq. ID	LIB3168-091-P1-K1-C8
Method	BLASTX
NCBI GI	g4263704
BLAST score	254
E value	8.0e-22
Match length	84
% identity	56
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	147531
Seq. ID	LIB3168-091-P1-K1-D1

Method	BLASTX
NCBI GI	g112681
BLAST score	617
E value	2.0e-64
Match length	128
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147532
Seq. ID	LIB3168-091-P1-K1-D11
Method	BLASTN
NCBI GI	g1785673
BLAST score	36
E value	6.0e-11
Match length	115
% identity	83
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	147533
Seq. ID	LIB3168-091-P1-K1-D12
Method	BLASTN
NCBI GI	g4079614
BLAST score	40
E value	9.0e-14
Match length	81
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147534
Seq. ID	LIB3168-091-P1-K1-D2
Method	BLASTX
NCBI GI	g112681
BLAST score	630
E value	7.0e-66
Match length	130
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147535
Seq. ID	LIB3168-091-P1-K1-D3
Method	BLASTX
NCBI GI	g1352347
BLAST score	472
E value	2.0e-47
Match length	93
% identity	100
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1

beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	147536
Seq. ID	LIB3168-091-P1-K1-D4
Method	BLASTN
NCBI GI	g3228389
BLAST score	345
E value	0.0e+00
Match length	375
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	147537
Seq. ID	LIB3168-091-P1-K1-D5
Method	BLASTN
NCBI GI	g2244950
BLAST score	205
E value	1.0e-111
Match length	294
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	147538
Seq. ID	LIB3168-091-P1-K1-D6
Method	BLASTN
NCBI GI	g16236
BLAST score	63
E value	7.0e-27
Match length	122
% identity	86
NCBI Description	Arabidopsis CRB gene for 12S seed storage protein >gi_166677_gb_M37248_ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	147539
Seq. ID	LIB3168-091-P1-K1-D7
Method	BLASTX
NCBI GI	g1345592
BLAST score	503
E value	5.0e-51
Match length	106
% identity	94
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	147540
Seq. ID	LIB3168-091-P1-K1-D8
Method	BLASTN
NCBI GI	g4734011
BLAST score	67
E value	3.0e-29
Match length	206
% identity	70

NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	147541
Seq. ID	LIB3168-091-P1-K1-D9
Method	BLASTX
NCBI GI	g112737
BLAST score	547
E value	3.0e-56
Match length	118
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147542
Seq. ID	LIB3168-091-P1-K1-E1
Method	BLASTX
NCBI GI	g112737
BLAST score	668
E value	2.0e-70
Match length	141
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147543
Seq. ID	LIB3168-091-P1-K1-E11
Method	BLASTN
NCBI GI	g4079614
BLAST score	57
E value	3.0e-23
Match length	143
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147544
Seq. ID	LIB3168-091-P1-K1-E12
Method	BLASTX
NCBI GI	g112741
BLAST score	689
E value	8.0e-73
Match length	128
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147545
Seq. ID	LIB3168-091-P1-K1-E2
Method	BLASTX
NCBI GI	g112682
BLAST score	598
E value	3.0e-62
Match length	138
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147546
Seq. ID	LIB3168-091-P1-K1-E3
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	147547
Seq. ID	LIB3168-091-P1-K1-E4
Method	BLASTX
NCBI GI	g112739
BLAST score	510
E value	8.0e-52
Match length	142
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147548
Seq. ID	LIB3168-091-P1-K1-E5
Method	BLASTX
NCBI GI	g112737
BLAST score	684
E value	3.0e-72
Match length	147
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit

1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147549
Seq. ID	LIB3168-091-P1-K1-E6
Method	BLASTN
NCBI GI	g2924505
BLAST score	214
E value	1.0e-117
Match length	427
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	147550
Seq. ID	LIB3168-091-P1-K1-E7
Method	BLASTX
NCBI GI	g4544473
BLAST score	731
E value	9.0e-78
Match length	136
% identity	99
NCBI Description	(AC006580) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	147551
Seq. ID	LIB3168-091-P1-K1-E8
Method	BLASTX
NCBI GI	g112682
BLAST score	62
E value	6.0e-66
Match length	138
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147552
Seq. ID	LIB3168-091-P1-K1-E9
Method	BLASTX
NCBI GI	g1772309
BLAST score	171
E value	4.0e-12
Match length	79
% identity	94
NCBI Description	(D34631) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	147553
Seq. ID	LIB3168-091-P1-K1-F1
Method	BLASTN
NCBI GI	g3985932
BLAST score	269
E value	1.0e-149
Match length	463

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	147554
Seq. ID	LIB3168-091-P1-K1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	227
E value	6.0e-19
Match length	96
% identity	54
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147555
Seq. ID	LIB3168-091-P1-K1-F12
Method	BLASTX
NCBI GI	g461841
BLAST score	185
E value	7.0e-14
Match length	80
% identity	51
NCBI Description	CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN)

Seq. No.	147556
Seq. ID	LIB3168-091-P1-K1-F2
Method	BLASTX
NCBI GI	g112743
BLAST score	731
E value	1.0e-77
Match length	152
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147557
Seq. ID	LIB3168-091-P1-K1-F3
Method	BLASTX
NCBI GI	g112737
BLAST score	684
E value	3.0e-72
Match length	143
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	147558
Seq. ID	LIB3168-091-P1-K1-F4
Method	BLASTX
NCBI GI	g112737
BLAST score	546
E value	4.0e-56
Match length	121
% identity	85
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147559
Seq. ID	LIB3168-091-P1-K1-F5
Method	BLASTX
NCBI GI	g1673426
BLAST score	171
E value	1.0e-12
Match length	71
% identity	58
NCBI Description	(X99979) factor 1-alpha [Forsythia x intermedia]

Seq. No.	147560
Seq. ID	LIB3168-091-P1-K1-F6
Method	BLASTX
NCBI GI	g21913
BLAST score	188
E value	4.0e-14
Match length	84
% identity	43
NCBI Description	(X62626) vicilin [Theobroma cacao]

Seq. No.	147561
Seq. ID	LIB3168-091-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	45
E value	5.0e-15
Match length	76
% identity	62
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147562
Seq. ID	LIB3168-091-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	596
E value	5.0e-62
Match length	124

% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147563
Seq. ID	LIB3168-091-P1-K1-F9
Method	BLASTX
NCBI GI	g1628583
BLAST score	688
E value	1.0e-72
Match length	134
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147564
Seq. ID	LIB3168-091-P1-K1-G1
Method	BLASTX
NCBI GI	g112681
BLAST score	661
E value	1.0e-69
Match length	135
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147565
Seq. ID	LIB3168-091-P1-K1-G10
Method	BLASTN
NCBI GI	g166611
BLAST score	45
E value	3.0e-16
Match length	106
% identity	84
NCBI Description	A.thaliana at2S3 gene encoding albumin 2S subunit 3, complete cds

Seq. No.	147566
Seq. ID	LIB3168-091-P1-K1-G11
Method	BLASTX
NCBI GI	g2129657
BLAST score	299
E value	4.0e-27
Match length	111
% identity	60
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147567
Seq. ID	LIB3168-091-P1-K1-G12

Method	BLASTX
NCBI GI	g133938
BLAST score	515
E value	1.0e-52
Match length	121
% identity	83
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir__R3SP3 ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3 [Spinacia oleracea]

Seq. No.	147568
Seq. ID	LIB3168-091-P1-K1-G2
Method	BLASTX
NCBI GI	g112739
BLAST score	335
E value	2.0e-31
Match length	105
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147569
Seq. ID	LIB3168-091-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	304
E value	6.0e-28
Match length	95
% identity	66
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147570
Seq. ID	LIB3168-091-P1-K1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	594
E value	1.0e-61
Match length	123
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147571
Seq. ID	LIB3168-091-P1-K1-G5
Method	BLASTX
NCBI GI	g2129657
BLAST score	344
E value	3.0e-32

Match length	122
% identity	62
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147572
Seq. ID	LIB3168-091-P1-K1-G6
Method	BLASTX
NCBI GI	g112741
BLAST score	651
E value	2.0e-68
Match length	123
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147573
Seq. ID	LIB3168-091-P1-K1-G7
Method	BLASTX
NCBI GI	g112681
BLAST score	59
E value	1.0e-56
Match length	153
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147574
Seq. ID	LIB3168-091-P1-K1-G8
Method	BLASTX
NCBI GI	g112681
BLAST score	177
E value	4.0e-13
Match length	67
% identity	57
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147575
Seq. ID	LIB3168-091-P1-K1-G9
Method	BLASTX
NCBI GI	g529353
BLAST score	378
E value	2.0e-36

Match length	128
% identity	51
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	147576
Seq. ID	LIB3168-091-P1-K1-H1
Method	BLASTX
NCBI GI	g112682
BLAST score	671
E value	1.0e-70
Match length	151
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147577
Seq. ID	LIB3168-091-P1-K1-H10
Method	BLASTX
NCBI GI	g1628583
BLAST score	261
E value	5.0e-23
Match length	74
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147578
Seq. ID	LIB3168-091-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	443
E value	5.0e-44
Match length	104
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147579
Seq. ID	LIB3168-091-P1-K1-H2
Method	BLASTX
NCBI GI	g112682
BLAST score	625
E value	3.0e-65
Match length	138
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147580

Seq. ID	LIB3168-091-P1-K1-H3
Method	BLASTX
NCBI GI	g112737
BLAST score	694
E value	2.0e-73
Match length	151
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147581
Seq. ID	LIB3168-091-P1-K1-H4
Method	BLASTX
NCBI GI	g112741
BLAST score	711
E value	2.0e-75
Match length	141
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147582
Seq. ID	LIB3168-091-P1-K1-H5
Method	BLASTX
NCBI GI	g112741
BLAST score	659
E value	3.0e-69
Match length	124
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147583
Seq. ID	LIB3168-091-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	406
E value	5.0e-40
Match length	88
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147584
Seq. ID	LIB3168-091-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	544
E value	8.0e-56
Match length	119
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147585
Seq. ID	LIB3168-091-P1-K1-H8
Method	BLASTX
NCBI GI	g112681
BLAST score	667
E value	3.0e-70
Match length	150
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147586
Seq. ID	LIB3168-091-P1-K1-H9
Method	BLASTX
NCBI GI	g112681
BLAST score	566
E value	2.0e-58
Match length	119
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147587
Seq. ID	LIB3168-093-P1-K1-A1
Method	BLASTX
NCBI GI	g4204303
BLAST score	346
E value	5.0e-33
Match length	82
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147588
Seq. ID	LIB3168-093-P1-K1-A10
Method	BLASTN
NCBI GI	g2264311

BLAST score	59
E value	2.0e-24
Match length	87
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	147589
Seq. ID	LIB3168-093-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	649
E value	3.0e-68
Match length	127
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147590
Seq. ID	LIB3168-093-P1-K1-A3
Method	BLASTN
NCBI GI	g4455168
BLAST score	67
E value	4.0e-30
Match length	67
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	147591
Seq. ID	LIB3168-093-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	601
E value	1.0e-62
Match length	125
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147592
Seq. ID	LIB3168-093-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	80
E value	1.0e-58
Match length	126
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147593

Seq. ID	LIB3168-093-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	101
E value	6.0e-04
Match length	77
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147594
Seq. ID	LIB3168-093-P1-K1-A7
Method	BLASTN
NCBI GI	g2828278
BLAST score	166
E value	2.0e-88
Match length	242
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	147595
Seq. ID	LIB3168-093-P1-K1-B1
Method	BLASTX
NCBI GI	g112741
BLAST score	376
E value	1.0e-36
Match length	81
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147596
Seq. ID	LIB3168-093-P1-K1-B10
Method	BLASTX
NCBI GI	g3822223
BLAST score	151
E value	8.0e-10
Match length	104
% identity	39
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	147597
Seq. ID	LIB3168-093-P1-K1-B12
Method	BLASTN
NCBI GI	g4589437
BLAST score	239
E value	1.0e-132
Match length	306
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	147598
Seq. ID	LIB3168-093-P1-K1-B2
Method	BLASTN
NCBI GI	g4584531
BLAST score	32
E value	1.0e-08
Match length	96
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	147599
Seq. ID	LIB3168-093-P1-K1-B3
Method	BLASTX
NCBI GI	g267055
BLAST score	305
E value	2.0e-28
Match length	69
% identity	90
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana >gi_16526_emb_CAA43303_ (X60987) sucrose synthase [Arabidopsis thaliana]

Seq. No.	147600
Seq. ID	LIB3168-093-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	608
E value	2.0e-63
Match length	119
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147601
Seq. ID	LIB3168-093-P1-K1-B5
Method	BLASTX
NCBI GI	g112739
BLAST score	211
E value	2.0e-24
Match length	100
% identity	61
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147602
Seq. ID	LIB3168-093-P1-K1-B6

Method	BLASTX
NCBI GI	g1628583
BLAST score	364
E value	8.0e-35
Match length	78
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147603
Seq. ID	LIB3168-093-P1-K1-B8
Method	BLASTX
NCBI GI	g1109699
BLAST score	497
E value	2.0e-50
Match length	95
% identity	100
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	147604
Seq. ID	LIB3168-093-P1-K1-B9
Method	BLASTX
NCBI GI	g2335106
BLAST score	161
E value	6.0e-11
Match length	133
% identity	8
NCBI Description	(AC002339) salt inducible protein-like [Arabidopsis thaliana]

Seq. No.	147605
Seq. ID	LIB3168-093-P1-K1-C1
Method	BLASTN
NCBI GI	g2252823
BLAST score	75
E value	3.0e-34
Match length	183
% identity	85
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	147606
Seq. ID	LIB3168-093-P1-K1-C10
Method	BLASTN
NCBI GI	g4589969
BLAST score	347
E value	0.0e+00
Match length	421
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	147607
Seq. ID	LIB3168-093-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	202

E value	3.0e-25
Match length	71
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147608
Seq. ID	LIB3168-093-P1-K1-C2
Method	BLASTX
NCBI GI	g136251
BLAST score	452
E value	3.0e-45
Match length	113
% identity	78
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	147609
Seq. ID	LIB3168-093-P1-K1-C4
Method	BLASTX
NCBI GI	g112682
BLAST score	484
E value	5.0e-49
Match length	106
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147610
Seq. ID	LIB3168-093-P1-K1-C6
Method	BLASTX
NCBI GI	g3776023
BLAST score	324
E value	4.0e-30
Match length	73
% identity	86
NCBI Description	(AJ010473) RNA helicase [Arabidopsis thaliana]

Seq. No.	147611
Seq. ID	LIB3168-093-P1-K1-C7
Method	BLASTN
NCBI GI	g3869062
BLAST score	61
E value	9.0e-26
Match length	117
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	147612
Seq. ID	LIB3168-093-P1-K1-C8

Method	BLASTX
NCBI GI	g112737
BLAST score	557
E value	2.0e-57
Match length	137
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147613
Seq. ID	LIB3168-093-P1-K1-C9
Method	BLASTX
NCBI GI	g881615
BLAST score	628
E value	9.0e-66
Match length	123
% identity	98
NCBI Description	(U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No.	147614
Seq. ID	LIB3168-093-P1-K1-D1
Method	BLASTX
NCBI GI	g112737
BLAST score	593
E value	1.0e-61
Match length	130
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147615
Seq. ID	LIB3168-093-P1-K1-D10
Method	BLASTX
NCBI GI	g3335169
BLAST score	563
E value	4.0e-58
Match length	135
% identity	77
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	147616
Seq. ID	LIB3168-093-P1-K1-D11
Method	BLASTX

NCBI GI	g112741
BLAST score	705
E value	9.0e-75
Match length	132
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147617
Seq. ID	LIB3168-093-P1-K1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	612
E value	8.0e-64
Match length	141
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147618
Seq. ID	LIB3168-093-P1-K1-D2
Method	BLASTN
NCBI GI	g2760172
BLAST score	361
E value	0.0e+00
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	147619
Seq. ID	LIB3168-093-P1-K1-D3
Method	BLASTX
NCBI GI	g112737
BLAST score	573
E value	3.0e-59
Match length	122
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147620
Seq. ID	LIB3168-093-P1-K1-D5
Method	BLASTX
NCBI GI	g112741
BLAST score	340

E value	5.0e-32
Match length	110
% identity	65
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147621
Seq. ID	LIB3168-093-P1-K1-D8
Method	BLASTX
NCBI GI	g267083
BLAST score	613
E value	6.0e-64
Match length	136
% identity	83
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	147622
Seq. ID	LIB3168-093-P1-K1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147623
Seq. ID	LIB3168-093-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	580
E value	4.0e-60
Match length	135
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147624
Seq. ID	LIB3168-093-P1-K1-E4
Method	BLASTN
NCBI GI	g2842474
BLAST score	91
E value	2.0e-43
Match length	194
% identity	43

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	147625
Seq. ID	LIB3168-093-P1-K1-E5
Method	BLASTX
NCBI GI	g2129657
BLAST score	354
E value	1.0e-33
Match length	101
% identity	75
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147626
Seq. ID	LIB3168-093-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	455
E value	2.0e-45
Match length	142
% identity	69
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147627
Seq. ID	LIB3168-093-P1-K1-E7
Method	BLASTX
NCBI GI	g1628583
BLAST score	475
E value	8.0e-71
Match length	137
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147628
Seq. ID	LIB3168-093-P1-K1-E8
Method	BLASTX
NCBI GI	g625977
BLAST score	586
E value	8.0e-61
Match length	116
% identity	97
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	147629
Seq. ID	LIB3168-093-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	543

E value	7.0e-56
Match length	117
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147630
Seq. ID	LIB3168-093-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	392
E value	2.0e-38
Match length	82
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147631
Seq. ID	LIB3168-093-P1-K1-F10
Method	BLASTX
NCBI GI	g1628583
BLAST score	52
E value	9.0e-60
Match length	121
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147632
Seq. ID	LIB3168-093-P1-K1-F2
Method	BLASTX
NCBI GI	g4406816
BLAST score	521
E value	3.0e-53
Match length	105
% identity	93
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	147633
Seq. ID	LIB3168-093-P1-K1-F3
Method	BLASTX
NCBI GI	g2253010
BLAST score	122
E value	4.0e-20
Match length	69
% identity	77
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	147634
Seq. ID	LIB3168-093-P1-K1-F5
Method	BLASTX

NCBI GI	g418908
BLAST score	182
E value	2.0e-13
Match length	75
% identity	44
NCBI Description	vicilin precursor - cacao

Seq. No.	147635
Seq. ID	LIB3168-093-P1-K1-F6
Method	BLASTX
NCBI GI	g1864017
BLAST score	513
E value	3.0e-52
Match length	110
% identity	90
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	147636
Seq. ID	LIB3168-093-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	595
E value	7.0e-62
Match length	120
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147637
Seq. ID	LIB3168-093-P1-K1-F9
Method	BLASTX
NCBI GI	g112682
BLAST score	621
E value	6.0e-65
Match length	118
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147638
Seq. ID	LIB3168-093-P1-K1-G1
Method	BLASTX
NCBI GI	g2541876
BLAST score	191
E value	2.0e-14
Match length	121
% identity	34
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	147639
Seq. ID	LIB3168-093-P1-K1-G10
Method	BLASTX

NCBI GI	g112739
BLAST score	439
E value	1.0e-43
Match length	126
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147640
Seq. ID	LIB3168-093-P1-K1-G11
Method	BLASTX
NCBI GI	g2129657
BLAST score	320
E value	1.0e-29
Match length	96
% identity	72
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147641
Seq. ID	LIB3168-093-P1-K1-G12
Method	BLASTX
NCBI GI	g3242709
BLAST score	259
E value	2.0e-22
Match length	70
% identity	70
NCBI Description	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]

Seq. No.	147642
Seq. ID	LIB3168-093-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	530
E value	1.0e-57
Match length	127
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147643
Seq. ID	LIB3168-093-P1-K1-G4
Method	BLASTN
NCBI GI	g4567193
BLAST score	404
E value	0.0e+00
Match length	424
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	147644
Seq. ID	LIB3168-093-P1-K1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	535
E value	8.0e-55
Match length	138
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147645
Seq. ID	LIB3168-093-P1-K1-G6
Method	BLASTN
NCBI GI	g4757413
BLAST score	77
E value	3.0e-35
Match length	289
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	147646
Seq. ID	LIB3168-093-P1-K1-G7
Method	BLASTX
NCBI GI	g4678285
BLAST score	259
E value	2.0e-22
Match length	72
% identity	61
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	147647
Seq. ID	LIB3168-093-P1-K1-G8
Method	BLASTN
NCBI GI	g2623294
BLAST score	202
E value	1.0e-110
Match length	362
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147648
Seq. ID	LIB3168-093-P1-K1-G9
Method	BLASTX
NCBI GI	g3128170
BLAST score	736
E value	2.0e-78
Match length	139
% identity	97

NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.	147649
Seq. ID	LIB3168-093-P1-K1-H10
Method	BLASTN
NCBI GI	g4220510
BLAST score	171
E value	3.0e-91
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	147650
Seq. ID	LIB3168-093-P1-K1-H12
Method	BLASTN
NCBI GI	g4415928
BLAST score	110
E value	5.0e-55
Match length	182
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	147651
Seq. ID	LIB3168-093-P1-K1-H5
Method	BLASTX
NCBI GI	g112682
BLAST score	474
E value	3.0e-55
Match length	131
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	147652
Seq. ID	LIB3168-093-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	563
E value	4.0e-58
Match length	141
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	147653
Seq. ID	LIB3168-093-P1-K1-H7
Method	BLASTX
NCBI GI	g1345973
BLAST score	516
E value	1.0e-52
Match length	106

% identity	88
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	147654
Seq. ID	LIB3168-093-P1-K1-H8
Method	BLASTX
NCBI GI	g3169175
BLAST score	421
E value	2.0e-41
Match length	135
% identity	56
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	147655
Seq. ID	LIB3168-093-P1-K1-H9
Method	BLASTX
NCBI GI	g1628583
BLAST score	500
E value	6.0e-51
Match length	98
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147656
Seq. ID	LIB3168-094-P1-K1-A1
Method	BLASTX
NCBI GI	g112682
BLAST score	240
E value	1.0e-20
Match length	52
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147657
Seq. ID	LIB3168-094-P1-K1-A10
Method	BLASTX
NCBI GI	g1628583
BLAST score	650
E value	2.0e-68
Match length	125
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147658
Seq. ID	LIB3168-094-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	398
E value	7.0e-39
Match length	99
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147659
Seq. ID	LIB3168-094-P1-K1-A12
Method	BLASTX
NCBI GI	g2271477
BLAST score	433
E value	7.0e-43
Match length	101
% identity	83
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	147660
Seq. ID	LIB3168-094-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	528
E value	5.0e-54
Match length	119
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147661
Seq. ID	LIB3168-094-P1-K1-A3
Method	BLASTN
NCBI GI	g1628582
BLAST score	37
E value	2.0e-11
Match length	73
% identity	89
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	147662
Seq. ID	LIB3168-094-P1-K1-A4
Method	BLASTX
NCBI GI	g1628583
BLAST score	704
E value	1.0e-74
Match length	140
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147663
Seq. ID	LIB3168-094-P1-K1-A5
Method	BLASTX
NCBI GI	g112737
BLAST score	356
E value	8.0e-34
Match length	114
% identity	64
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147664
Seq. ID	LIB3168-094-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	261
E value	9.0e-23
Match length	86
% identity	66
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147665
Seq. ID	LIB3168-094-P1-K1-A7
Method	BLASTX
NCBI GI	g4204299
BLAST score	321
E value	2.0e-30
Match length	64
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147666
Seq. ID	LIB3168-094-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	4.0e-04
Match length	113
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147667

Seq. ID	LIB3168-094-P1-K1-B12
Method	BLASTX
NCBI GI	g114649
BLAST score	220
E value	7.0e-18
Match length	46
% identity	100
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67899_pir__LWLVA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - liverwort (Marchantia polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465) atpH [Marchantia polymorpha]

Seq. No.	147668
Seq. ID	LIB3168-094-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	324
E value	3.0e-30
Match length	91
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147669
Seq. ID	LIB3168-094-P1-K1-B3
Method	BLASTX
NCBI GI	g2642158
BLAST score	457
E value	1.0e-45
Match length	117
% identity	71
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147670
Seq. ID	LIB3168-094-P1-K1-B4
Method	BLASTX
NCBI GI	g4584110
BLAST score	328
E value	1.0e-30
Match length	129
% identity	50
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	147671
Seq. ID	LIB3168-094-P1-K1-B5
Method	BLASTX
NCBI GI	g4584110
BLAST score	161
E value	6.0e-11
Match length	87
% identity	40
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	147672
Seq. ID	LIB3168-094-P1-K1-B6

Method	BLASTX
NCBI GI	g1628583
BLAST score	622
E value	5.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147673
Seq. ID	LIB3168-094-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	383
E value	2.0e-37
Match length	78
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147674
Seq. ID	LIB3168-094-P1-K1-B8
Method	BLASTX
NCBI GI	g112737
BLAST score	426
E value	3.0e-42
Match length	93
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147675
Seq. ID	LIB3168-094-P1-K1-C1
Method	BLASTX
NCBI GI	g3941412
BLAST score	178
E value	5.0e-13
Match length	38
% identity	95
NCBI Description	(AF062860) putative transcription factor [Arabidopsis thaliana]

Seq. No.	147676
Seq. ID	LIB3168-094-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	618
E value	1.0e-64
Match length	120
% identity	99

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147677
Seq. ID	LIB3168-094-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147678
Seq. ID	LIB3168-094-P1-K1-C12
Method	BLASTN
NCBI GI	g4159712
BLAST score	361
E value	0.0e+00
Match length	408
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	147679
Seq. ID	LIB3168-094-P1-K1-C3
Method	BLASTX
NCBI GI	g112737
BLAST score	580
E value	5.0e-60
Match length	141
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147680
Seq. ID	LIB3168-094-P1-K1-C4
Method	BLASTX
NCBI GI	g4204299
BLAST score	618
E value	1.0e-64
Match length	139
% identity	87
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147681
Seq. ID	LIB3168-094-P1-K1-C5
Method	BLASTX

NCBI GI	g4204298
BLAST score	640
E value	4.0e-67
Match length	138
% identity	90
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147682
Seq. ID	LIB3168-094-P1-K1-C6
Method	BLASTX
NCBI GI	g2129657
BLAST score	301
E value	2.0e-27
Match length	90
% identity	72
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147683
Seq. ID	LIB3168-094-P1-K1-C7
Method	BLASTX
NCBI GI	g112741
BLAST score	480
E value	2.0e-48
Match length	98
% identity	92
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147684
Seq. ID	LIB3168-094-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	384
E value	2.0e-37
Match length	86
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147685
Seq. ID	LIB3168-094-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	622
E value	5.0e-65
Match length	120
% identity	99

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147686
Seq. ID	LIB3168-094-P1-K1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	613
E value	6.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147687
Seq. ID	LIB3168-094-P1-K1-D11
Method	BLASTX
NCBI GI	g3047082
BLAST score	154
E value	4.0e-10
Match length	41
% identity	68
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	147688
Seq. ID	LIB3168-094-P1-K1-D12
Method	BLASTX
NCBI GI	g99698
BLAST score	481
E value	2.0e-48
Match length	94
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	147689
Seq. ID	LIB3168-094-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	443
E value	5.0e-44
Match length	143
% identity	65
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147690
Seq. ID	LIB3168-094-P1-K1-D3
Method	BLASTN
NCBI GI	g1592685
BLAST score	53
E value	4.0e-21
Match length	227

% identity	82
NCBI Description	A.thaliana mRNA for oleosin type4 protein

Seq. No.	147691
Seq. ID	LIB3168-094-P1-K1-D4
Method	BLASTX
NCBI GI	g112681
BLAST score	567
E value	1.0e-58
Match length	131
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147692
Seq. ID	LIB3168-094-P1-K1-D6
Method	BLASTX
NCBI GI	g2129657
BLAST score	422
E value	1.0e-41
Match length	115
% identity	77
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147693
Seq. ID	LIB3168-094-P1-K1-D7
Method	BLASTX
NCBI GI	g1890281
BLAST score	351
E value	3.0e-33
Match length	114
% identity	22
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No.	147694
Seq. ID	LIB3168-094-P1-K1-E11
Method	BLASTX
NCBI GI	g2160151
BLAST score	540
E value	2.0e-55
Match length	111
% identity	96
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	147695
Seq. ID	LIB3168-094-P1-K1-E12
Method	BLASTX
NCBI GI	g1592677
BLAST score	214

E value	3.0e-17
Match length	113
% identity	43
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No.	147696
Seq. ID	LIB3168-094-P1-K1-E2
Method	BLASTX
NCBI GI	g112743
BLAST score	628
E value	1.0e-65
Match length	132
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147697
Seq. ID	LIB3168-094-P1-K1-E4
Method	BLASTX
NCBI GI	g112681
BLAST score	572
E value	4.0e-59
Match length	140
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147698
Seq. ID	LIB3168-094-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	417
E value	7.0e-41
Match length	79
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147699
Seq. ID	LIB3168-094-P1-K1-E6
Method	BLASTX
NCBI GI	g2088654
BLAST score	552
E value	8.0e-57
Match length	121
% identity	91
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	147700
Seq. ID	LIB3168-094-P1-K1-E7
Method	BLASTX
NCBI GI	g112737
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147701
Seq. ID	LIB3168-094-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	728
E value	2.0e-77
Match length	141
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147702
Seq. ID	LIB3168-094-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	447
E value	2.0e-44
Match length	119
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147703
Seq. ID	LIB3168-094-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	701
E value	3.0e-74
Match length	137
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147704
Seq. ID	LIB3168-094-P1-K1-F12

Method	BLASTN
NCBI GI	g3228389
BLAST score	364
E value	0.0e+00
Match length	403
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	147705
Seq. ID	LIB3168-094-P1-K1-F5
Method	BLASTX
NCBI GI	g4584110
BLAST score	289
E value	6.0e-26
Match length	106
% identity	54
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	147706
Seq. ID	LIB3168-094-P1-K1-F7
Method	BLASTX
NCBI GI	g112737
BLAST score	637
E value	9.0e-67
Match length	136
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147707
Seq. ID	LIB3168-094-P1-K1-F8
Method	BLASTX
NCBI GI	g112681
BLAST score	518
E value	8.0e-53
Match length	139
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147708
Seq. ID	LIB3168-094-P1-K1-F9
Method	BLASTX
NCBI GI	g4204298
BLAST score	550
E value	1.0e-56
Match length	133
% identity	80

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147709
Seq. ID	LIB3168-094-P1-K1-G10
Method	BLASTX
NCBI GI	g4406780
BLAST score	590
E value	3.0e-61
Match length	138
% identity	84
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	147710
Seq. ID	LIB3168-094-P1-K1-G11
Method	BLASTN
NCBI GI	g3036791
BLAST score	413
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No.	147711
Seq. ID	LIB3168-094-P1-K1-G2
Method	BLASTN
NCBI GI	g2618683
BLAST score	379
E value	0.0e+00
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147712
Seq. ID	LIB3168-094-P1-K1-G3
Method	BLASTX
NCBI GI	g3808062
BLAST score	166
E value	1.0e-11
Match length	70
% identity	44
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	147713
Seq. ID	LIB3168-094-P1-K1-G4
Method	BLASTX
NCBI GI	g135535
BLAST score	375
E value	3.0e-36
Match length	76
% identity	99
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_

(D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	147714
Seq. ID	LIB3168-094-P1-K1-G5
Method	BLASTN
NCBI GI	g4589428
BLAST score	158
E value	1.0e-83
Match length	216
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	147715
Seq. ID	LIB3168-094-P1-K1-G6
Method	BLASTX
NCBI GI	g112681
BLAST score	700
E value	4.0e-74
Match length	140
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147716
Seq. ID	LIB3168-094-P1-K1-G7
Method	BLASTX
NCBI GI	g4734005
BLAST score	244
E value	1.0e-20
Match length	77
% identity	58
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147717
Seq. ID	LIB3168-094-P1-K1-G8
Method	BLASTX
NCBI GI	g112681
BLAST score	702
E value	2.0e-74
Match length	133
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147718
Seq. ID	LIB3168-094-P1-K1-G9
Method	BLASTN
NCBI GI	g3176695

BLAST score	150
E value	9.0e-79
Match length	338
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	147719
Seq. ID	LIB3168-094-P1-K1-H1
Method	BLASTX
NCBI GI	g112737
BLAST score	554
E value	5.0e-57
Match length	134
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147720
Seq. ID	LIB3168-094-P1-K1-H10
Method	BLASTX
NCBI GI	g4204298
BLAST score	501
E value	7.0e-51
Match length	125
% identity	78
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147721
Seq. ID	LIB3168-094-P1-K1-H11
Method	BLASTX
NCBI GI	g112741
BLAST score	619
E value	9.0e-65
Match length	117
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147722
Seq. ID	LIB3168-094-P1-K1-H12
Method	BLASTX
NCBI GI	g112739
BLAST score	362
E value	1.0e-34

Match length	110
% identity	68
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	147723
Seq. ID	LIB3168-094-P1-K1-H2
Method	BLASTX
NCBI GI	g112737
BLAST score	573
E value	3.0e-59
Match length	123
% identity	89
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	147724
Seq. ID	LIB3168-094-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	69
E value	8.0e-60
Match length	127
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	147725
Seq. ID	LIB3168-094-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	622
E value	5.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	147726
Seq. ID	LIB3168-094-P1-K1-H6
Method	BLASTX
NCBI GI	g2129657
BLAST score	194
E value	8.0e-15
Match length	93

% identity	51
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147727
Seq. ID	LIB3168-094-P1-K1-H7
Method	BLASTX
NCBI GI	g112681
BLAST score	690
E value	5.0e-73
Match length	139
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147728
Seq. ID	LIB3168-094-P1-K1-H8
Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	8.0e-70
Match length	137
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147729
Seq. ID	LIB3168-094-P1-K1-H9
Method	BLASTX
NCBI GI	g2129657
BLAST score	366
E value	5.0e-35
Match length	104
% identity	76
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	147730
Seq. ID	LIB3168-095-P1-K1-A1
Method	BLASTX
NCBI GI	g1628583
BLAST score	521
E value	3.0e-53
Match length	110
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147731
Seq. ID	LIB3168-095-P1-K1-A10
Method	BLASTX
NCBI GI	g112682
BLAST score	560
E value	9.0e-58
Match length	133
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147732
Seq. ID	LIB3168-095-P1-K1-A11
Method	BLASTX
NCBI GI	g112741
BLAST score	871
E value	4.0e-94
Match length	164
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147733
Seq. ID	LIB3168-095-P1-K1-A12
Method	BLASTX
NCBI GI	g4204299
BLAST score	651
E value	2.0e-68
Match length	126
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147734
Seq. ID	LIB3168-095-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	93
E value	2.0e-58
Match length	120
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147735
Seq. ID	LIB3168-095-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583

BLAST score	433
E value	9.0e-43
Match length	147
% identity	64
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147736
Seq. ID	LIB3168-095-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147737
Seq. ID	LIB3168-095-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	660
E value	2.0e-69
Match length	150
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147738
Seq. ID	LIB3168-095-P1-K1-A7
Method	BLASTX
NCBI GI	g112741
BLAST score	680
E value	7.0e-72
Match length	126
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147739
Seq. ID	LIB3168-095-P1-K1-A8
Method	BLASTN
NCBI GI	g2828181
BLAST score	269
E value	1.0e-149
Match length	498

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE8, complete sequence [Arabidopsis thaliana]

Seq. No.	147740
Seq. ID	LIB3168-095-P1-K1-A9
Method	BLASTX
NCBI GI	g112681
BLAST score	191
E value	4.0e-15
Match length	70
% identity	61
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147741
Seq. ID	LIB3168-095-P1-K1-B1
Method	BLASTX
NCBI GI	g1592670
BLAST score	457
E value	3.0e-46
Match length	132
% identity	72
NCBI Description	(X91920) dehydrin [Arabidopsis thaliana] >gi_4567280_gb_AAD23693.1_AC006841_21 (AC006841) putative dehydrin [Arabidopsis thaliana]

Seq. No.	147742
Seq. ID	LIB3168-095-P1-K1-B10
Method	BLASTX
NCBI GI	g21913
BLAST score	201
E value	1.0e-15
Match length	83
% identity	45
NCBI Description	(X62626) vicilin [Theobroma cacao]

Seq. No.	147743
Seq. ID	LIB3168-095-P1-K1-B11
Method	BLASTX
NCBI GI	g112739
BLAST score	609
E value	2.0e-63
Match length	163
% identity	75
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147744

Seq. ID	LIB3168-095-P1-K1-B12
Method	BLASTX
NCBI GI	g1628583
BLAST score	717
E value	5.0e-76
Match length	172
% identity	83
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147745
Seq. ID	LIB3168-095-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147746
Seq. ID	LIB3168-095-P1-K1-B3
Method	BLASTX
NCBI GI	g112681
BLAST score	664
E value	8.0e-70
Match length	169
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147747
Seq. ID	LIB3168-095-P1-K1-B4
Method	BLASTX
NCBI GI	g1628583
BLAST score	383
E value	4.0e-37
Match length	102
% identity	71
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147748
Seq. ID	LIB3168-095-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	628
E value	1.0e-65
Match length	120
% identity	100

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147749
Seq. ID	LIB3168-095-P1-K1-B6
Method	BLASTX
NCBI GI	g112681
BLAST score	212
E value	4.0e-17
Match length	42
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147750
Seq. ID	LIB3168-095-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	136
E value	1.0e-32
Match length	78
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147751
Seq. ID	LIB3168-095-P1-K1-B8
Method	BLASTX
NCBI GI	g1628583
BLAST score	682
E value	7.0e-72
Match length	167
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147752
Seq. ID	LIB3168-095-P1-K1-B9
Method	BLASTX
NCBI GI	g3738257
BLAST score	504
E value	1.0e-61
Match length	143
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	147753
Seq. ID	LIB3168-095-P1-K1-C10
Method	BLASTN
NCBI GI	g4512656

BLAST score 155
E value 1.0e-81
Match length 499
% identity 83
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No. 147754
Seq. ID LIB3168-095-P1-K1-C11
Method BLASTX
NCBI GI g4249382
BLAST score 505
E value 4.0e-51
Match length 126
% identity 78
NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No. 147755
Seq. ID LIB3168-095-P1-K1-C12
Method BLASTX
NCBI GI g1628583
BLAST score 479
E value 2.0e-48
Match length 101
% identity 91
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147756
Seq. ID LIB3168-095-P1-K1-C2
Method BLASTX
NCBI GI g1628583
BLAST score 665
E value 6.0e-70
Match length 158
% identity 82
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147757
Seq. ID LIB3168-095-P1-K1-C3
Method BLASTX
NCBI GI g1628583
BLAST score 633
E value 4.0e-66
Match length 170
% identity 76
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147758
Seq. ID LIB3168-095-P1-K1-C4

Method	BLASTX
NCBI GI	g1345973
BLAST score	332
E value	3.0e-31
Match length	62
% identity	100
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	147759
Seq. ID	LIB3168-095-P1-K1-C5
Method	BLASTX
NCBI GI	g112682
BLAST score	935
E value	1.0e-101
Match length	178
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147760
Seq. ID	LIB3168-095-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	607
E value	3.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147761
Seq. ID	LIB3168-095-P1-K1-C7
Method	BLASTX
NCBI GI	g4539292
BLAST score	463
E value	3.0e-46
Match length	88
% identity	98
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	147762
Seq. ID	LIB3168-095-P1-K1-C8
Method	BLASTX
NCBI GI	g3273743

BLAST score 620
E value 1.0e-64
Match length 118
% identity 100
NCBI Description (AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 147763
Seq. ID LIB3168-095-P1-K1-C9
Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 9.0e-65
Match length 120
% identity 99
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147764
Seq. ID LIB3168-095-P1-K1-D10
Method BLASTN
NCBI GI g3176695
BLAST score 218
E value 1.0e-119
Match length 270
% identity 95
NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No. 147765
Seq. ID LIB3168-095-P1-K1-D11
Method BLASTN
NCBI GI g4490701
BLAST score 39
E value 6.0e-13
Match length 180
% identity 56
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No. 147766
Seq. ID LIB3168-095-P1-K1-D12
Method BLASTN
NCBI GI g3985954
BLAST score 219
E value 1.0e-120
Match length 342
% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No. 147767
Seq. ID LIB3168-095-P1-K1-D2
Method BLASTX

NCBI GI	g112737
BLAST score	647
E value	7.0e-68
Match length	163
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147768
Seq. ID	LIB3168-095-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147769
Seq. ID	LIB3168-095-P1-K1-D5
Method	BLASTX
NCBI GI	g119143
BLAST score	396
E value	1.0e-47
Match length	103
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	147770
Seq. ID	LIB3168-095-P1-K1-D6
Method	BLASTX
NCBI GI	g112741
BLAST score	846
E value	4.0e-91
Match length	157
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147771
Seq. ID	LIB3168-095-P1-K1-D7
Method	BLASTX
NCBI GI	g1628583
BLAST score	693
E value	3.0e-73
Match length	166
% identity	81
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147772
Seq. ID	LIB3168-095-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147773
Seq. ID	LIB3168-095-P1-K1-E1
Method	BLASTX
NCBI GI	g3287694
BLAST score	151
E value	2.0e-86
Match length	160
% identity	99
NCBI Description	(AC003979) Similar to myb-related transcription factor (THM27) gb_X95296 from Solanum lycopersicum. ESTs gb_T42000, gb_T04118, gb_AA598042, gb_AA394757 and gb_AA598046 come from this gene. [Arabidopsis thaliana]

Seq. No.	147774
Seq. ID	LIB3168-095-P1-K1-E11
Method	BLASTX
NCBI GI	g112737
BLAST score	684
E value	4.0e-72
Match length	145
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147775

Seq. ID	LIB3168-095-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	892
E value	2.0e-96
Match length	171
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147776
Seq. ID	LIB3168-095-P1-K1-E2
Method	BLASTX
NCBI GI	g112681
BLAST score	391
E value	3.0e-46
Match length	139
% identity	77
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147777
Seq. ID	LIB3168-095-P1-K1-E4
Method	BLASTN
NCBI GI	g2864607
BLAST score	202
E value	1.0e-110
Match length	254
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	147778
Seq. ID	LIB3168-095-P1-K1-E5
Method	BLASTX
NCBI GI	g112682
BLAST score	827
E value	7.0e-89
Match length	180
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147779
Seq. ID	LIB3168-095-P1-K1-E6
Method	BLASTX
NCBI GI	g1628583
BLAST score	102

E value	2.0e-60
Match length	120
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147780
Seq. ID	LIB3168-095-P1-K1-E8
Method	BLASTX
NCBI GI	g683553
BLAST score	144
E value	7.0e-09
Match length	117
% identity	30
NCBI Description	(Z48450) oleosin-like protein [Citrus sinensis] >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]

Seq. No.	147781
Seq. ID	LIB3168-095-P1-K1-E9
Method	BLASTX
NCBI GI	g1628583
BLAST score	651
E value	2.0e-68
Match length	139
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147782
Seq. ID	LIB3168-095-P1-K1-F1
Method	BLASTX
NCBI GI	g2702364
BLAST score	212
E value	6.0e-17
Match length	102
% identity	43
NCBI Description	(AF036706) No definition line found [Caenorhabditis elegans]

Seq. No.	147783
Seq. ID	LIB3168-095-P1-K1-F10
Method	BLASTN
NCBI GI	g3869073
BLAST score	230
E value	1.0e-126
Match length	483
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	147784
Seq. ID	LIB3168-095-P1-K1-F11
Method	BLASTX
NCBI GI	g112681
BLAST score	705

E value	1.0e-74
Match length	180
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147785
Seq. ID	LIB3168-095-P1-K1-F12
Method	BLASTN
NCBI GI	g4589445
BLAST score	226
E value	1.0e-124
Match length	409
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	147786
Seq. ID	LIB3168-095-P1-K1-F2
Method	BLASTX
NCBI GI	g112741
BLAST score	631
E value	4.0e-66
Match length	117
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147787
Seq. ID	LIB3168-095-P1-K1-F3
Method	BLASTX
NCBI GI	g119143
BLAST score	735
E value	5.0e-83
Match length	158
% identity	96
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	147788
Seq. ID	LIB3168-095-P1-K1-F4

Method	BLASTN
NCBI GI	g4199934
BLAST score	152
E value	4.0e-80
Match length	196
% identity	68
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	147789
Seq. ID	LIB3168-095-P1-K1-F6
Method	BLASTX
NCBI GI	g112741
BLAST score	849
E value	2.0e-91
Match length	160
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147790
Seq. ID	LIB3168-095-P1-K1-F7
Method	BLASTX
NCBI GI	g4406780
BLAST score	603
E value	9.0e-63
Match length	142
% identity	83
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	147791
Seq. ID	LIB3168-095-P1-K1-F8
Method	BLASTX
NCBI GI	g112681
BLAST score	655
E value	8.0e-69
Match length	150
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147792
Seq. ID	LIB3168-095-P1-K1-F9
Method	BLASTN
NCBI GI	g2864607
BLAST score	389
E value	0.0e+00
Match length	420

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	147793
Seq. ID	LIB3168-095-P1-K1-G11
Method	BLASTN
NCBI GI	g2924257
BLAST score	49
E value	2.0e-18
Match length	89
% identity	89
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	147794
Seq. ID	LIB3168-095-P1-K1-G12
Method	BLASTN
NCBI GI	g4732166
BLAST score	476
E value	0.0e+00
Match length	519
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21I2

Seq. No.	147795
Seq. ID	LIB3168-095-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147796
Seq. ID	LIB3168-095-P1-K1-G3
Method	BLASTX
NCBI GI	g112737
BLAST score	427
E value	4.0e-42
Match length	90
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147797
Seq. ID	LIB3168-095-P1-K1-G5
Method	BLASTX
NCBI GI	g112739
BLAST score	62

E value	8.0e-34
Match length	116
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147798
Seq. ID	LIB3168-095-P1-K1-G6
Method	BLASTX
NCBI GI	g1107501
BLAST score	369
E value	3.0e-35
Match length	91
% identity	81
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	147799
Seq. ID	LIB3168-095-P1-K1-G7
Method	BLASTX
NCBI GI	g4529972
BLAST score	682
E value	5.0e-72
Match length	149
% identity	91
NCBI Description	(AC002330) putative chloroplast outer envelope 86-like protein [Arabidopsis thaliana]

Seq. No.	147800
Seq. ID	LIB3168-095-P1-K1-G8
Method	BLASTX
NCBI GI	g112682
BLAST score	44
E value	2.0e-69
Match length	160
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147801
Seq. ID	LIB3168-095-P1-K1-G9
Method	BLASTX
NCBI GI	g131378
BLAST score	220
E value	6.0e-18
Match length	43
% identity	100

NCBI Description	PHOTOSYSTEM II REACTION CENTRE N PROTEIN >gi_2924272_emb_CAA77424_ (Z00044) PSII N-protein [Nicotiana tabacum]

Seq. No.	147802
Seq. ID	LIB3168-095-P1-K1-H1
Method	BLASTX
NCBI GI	g2920587
BLAST score	349
E value	4.0e-33
Match length	177
% identity	48
NCBI Description	(AF038362) TBP-associated factor 172 [Homo sapiens] >gi_2995136_emb_CAA04475_ (AJ001017) TAFII170 [Homo sapiens]

Seq. No.	147803
Seq. ID	LIB3168-095-P1-K1-H10
Method	BLASTX
NCBI GI	g112737
BLAST score	340
E value	2.0e-32
Match length	81
% identity	83
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147804
Seq. ID	LIB3168-095-P1-K1-H12
Method	BLASTX
NCBI GI	g112681
BLAST score	227
E value	5.0e-19
Match length	89
% identity	55
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147805
Seq. ID	LIB3168-095-P1-K1-H2
Method	BLASTX
NCBI GI	g112681
BLAST score	536
E value	6.0e-55
Match length	144
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147806
Seq. ID	LIB3168-095-P1-K1-H6
Method	BLASTN
NCBI GI	g4539331
BLAST score	33
E value	9.0e-10
Match length	61
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	147807
Seq. ID	LIB3168-095-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147808
Seq. ID	LIB3168-095-P1-K1-H8
Method	BLASTX
NCBI GI	g1628583
BLAST score	548
E value	3.0e-56
Match length	157
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147809
Seq. ID	LIB3168-096-P1-K1-A1
Method	BLASTX
NCBI GI	g2160189
BLAST score	241
E value	2.0e-20
Match length	101
% identity	7
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	147810
Seq. ID	LIB3168-096-P1-K1-A10
Method	BLASTX
NCBI GI	g3169180
BLAST score	568
E value	1.0e-58
Match length	131

% identity	87
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	147811
Seq. ID	LIB3168-096-P1-K1-A11
Method	BLASTX
NCBI GI	g1628583
BLAST score	681
E value	8.0e-72
Match length	136
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147812
Seq. ID	LIB3168-096-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	102
E value	2.0e-62
Match length	123
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147813
Seq. ID	LIB3168-096-P1-K1-A2
Method	BLASTX
NCBI GI	g112741
BLAST score	821
E value	3.0e-88
Match length	152
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147814
Seq. ID	LIB3168-096-P1-K1-A3
Method	BLASTX
NCBI GI	g2288981
BLAST score	396
E value	2.0e-38
Match length	80
% identity	53
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	147815

Seq. ID	LIB3168-096-P1-K1-A4
Method	BLASTX
NCBI GI	g112681
BLAST score	129
E value	4.0e-16
Match length	82
% identity	66
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147816
Seq. ID	LIB3168-096-P1-K1-A5
Method	BLASTX
NCBI GI	g112681
BLAST score	187
E value	2.0e-14
Match length	37
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147817
Seq. ID	LIB3168-096-P1-K1-A6
Method	BLASTX
NCBI GI	g112682
BLAST score	193
E value	1.0e-14
Match length	133
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147818
Seq. ID	LIB3168-096-P1-K1-A7
Method	BLASTN
NCBI GI	g166611
BLAST score	41
E value	7.0e-14
Match length	105
% identity	87
NCBI Description	A.thaliana at2S3 gene encoding albumin 2S subunit 3, complete cds

Seq. No.	147819
Seq. ID	LIB3168-096-P1-K1-A8
Method	BLASTX
NCBI GI	g137465
BLAST score	500

E value	9.0e-51
Match length	102
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	147820
Seq. ID	LIB3168-096-P1-K1-A9
Method	BLASTX
NCBI GI	g4204299
BLAST score	500
E value	1.0e-50
Match length	104
% identity	94
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147821
Seq. ID	LIB3168-096-P1-K1-B1
Method	BLASTX
NCBI GI	g3805849
BLAST score	908
E value	2.0e-98
Match length	177
% identity	99
NCBI Description	(AL031986) cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3) [Arabidopsis thaliana]

Seq. No.	147822
Seq. ID	LIB3168-096-P1-K1-B10
Method	BLASTX
NCBI GI	g1652577
BLAST score	64
E value	2.0e-10
Match length	60
% identity	63
NCBI Description	(D90906) carboxyl-terminal protease [Synechocystis sp.]

Seq. No.	147823
Seq. ID	LIB3168-096-P1-K1-B11
Method	BLASTX
NCBI GI	g112681
BLAST score	67
E value	3.0e-52
Match length	131
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147824
Seq. ID	LIB3168-096-P1-K1-B2

Method	BLASTX
NCBI GI	g1628583
BLAST score	717
E value	5.0e-76
Match length	175
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147825
Seq. ID	LIB3168-096-P1-K1-B4
Method	BLASTX
NCBI GI	g112681
BLAST score	795
E value	4.0e-85
Match length	171
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147826
Seq. ID	LIB3168-096-P1-K1-B5
Method	BLASTX
NCBI GI	g112682
BLAST score	781
E value	2.0e-83
Match length	173
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147827
Seq. ID	LIB3168-096-P1-K1-B6
Method	BLASTX
NCBI GI	g4204298
BLAST score	675
E value	4.0e-71
Match length	171
% identity	80
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147828
Seq. ID	LIB3168-096-P1-K1-B7
Method	BLASTX
NCBI GI	g2462931
BLAST score	287
E value	1.0e-25
Match length	70
% identity	96

NCBI Description	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]

Seq. No.	147829
Seq. ID	LIB3168-096-P1-K1-B8
Method	BLASTN
NCBI GI	g3449334
BLAST score	282
E value	1.0e-157
Match length	471
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	147830
Seq. ID	LIB3168-096-P1-K1-B9
Method	BLASTX
NCBI GI	g112681
BLAST score	135
E value	4.0e-86
Match length	168
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147831
Seq. ID	LIB3168-096-P1-K1-C1
Method	BLASTN
NCBI GI	g4079614
BLAST score	390
E value	0.0e+00
Match length	485
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147832
Seq. ID	LIB3168-096-P1-K1-C10
Method	BLASTX
NCBI GI	g112741
BLAST score	831
E value	2.0e-89
Match length	162
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147833
Seq. ID	LIB3168-096-P1-K1-C11

Method	BLASTX
NCBI GI	g1628583
BLAST score	546
E value	6.0e-56
Match length	120
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147834
Seq. ID	LIB3168-096-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	940
E value	1.0e-102
Match length	187
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147835
Seq. ID	LIB3168-096-P1-K1-C2
Method	BLASTX
NCBI GI	g339878
BLAST score	339
E value	1.0e-31
Match length	154
% identity	48
NCBI Description	(M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No.	147836
Seq. ID	LIB3168-096-P1-K1-C3
Method	BLASTX
NCBI GI	g4204298
BLAST score	845
E value	5.0e-91
Match length	176
% identity	92
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147837
Seq. ID	LIB3168-096-P1-K1-C4
Method	BLASTX
NCBI GI	g3805763
BLAST score	251
E value	2.0e-21
Match length	181
% identity	38
NCBI Description	(AC005693) hypothetical protein [Arabidopsis thaliana]

Seq. No.	147838
Seq. ID	LIB3168-096-P1-K1-C5
Method	BLASTX
NCBI GI	g112682

BLAST score	848
E value	2.0e-91
Match length	174
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147839
Seq. ID	LIB3168-096-P1-K1-C6
Method	BLASTX
NCBI GI	g112741
BLAST score	840
E value	2.0e-90
Match length	157
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147840
Seq. ID	LIB3168-096-P1-K1-C7
Method	BLASTX
NCBI GI	g112681
BLAST score	806
E value	2.0e-86
Match length	176
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147841
Seq. ID	LIB3168-096-P1-K1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	634
E value	3.0e-66
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147842
Seq. ID	LIB3168-096-P1-K1-D1
Method	BLASTX
NCBI GI	g1628583
BLAST score	930

E value	1.0e-101
Match length	178
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147843
Seq. ID	LIB3168-096-P1-K1-D10
Method	BLASTX
NCBI GI	g1419390
BLAST score	847
E value	3.0e-91
Match length	180
% identity	91
NCBI Description	(X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	147844
Seq. ID	LIB3168-096-P1-K1-D11
Method	BLASTX
NCBI GI	g4204299
BLAST score	720
E value	2.0e-76
Match length	141
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147845
Seq. ID	LIB3168-096-P1-K1-D12
Method	BLASTX
NCBI GI	g3915961
BLAST score	805
E value	2.0e-86
Match length	167
% identity	92
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	147846
Seq. ID	LIB3168-096-P1-K1-D2
Method	BLASTX
NCBI GI	g2827524
BLAST score	459
E value	9.0e-46
Match length	81
% identity	100
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	147847
Seq. ID	LIB3168-096-P1-K1-D3
Method	BLASTX
NCBI GI	g112681
BLAST score	733

E value	7.0e-78
Match length	180
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147848
Seq. ID	LIB3168-096-P1-K1-D5
Method	BLASTX
NCBI GI	g112681
BLAST score	831
E value	2.0e-89
Match length	181
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147849
Seq. ID	LIB3168-096-P1-K1-D6
Method	BLASTX
NCBI GI	g112681
BLAST score	87
E value	5.0e-51
Match length	153
% identity	75
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147850
Seq. ID	LIB3168-096-P1-K1-D7
Method	BLASTX
NCBI GI	g112681
BLAST score	810
E value	6.0e-87
Match length	162
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147851
Seq. ID	LIB3168-096-P1-K1-D8
Method	BLASTX
NCBI GI	g1628583
BLAST score	578
E value	1.0e-59

Match length	153
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147852
Seq. ID	LIB3168-096-P1-K1-D9
Method	BLASTX
NCBI GI	g112681
BLAST score	730
E value	2.0e-77
Match length	144
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147853
Seq. ID	LIB3168-096-P1-K1-E10
Method	BLASTN
NCBI GI	g3128138
BLAST score	354
E value	0.0e+00
Match length	450
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]

Seq. No.	147854
Seq. ID	LIB3168-096-P1-K1-E12
Method	BLASTX
NCBI GI	g112741
BLAST score	846
E value	4.0e-91
Match length	157
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147855
Seq. ID	LIB3168-096-P1-K1-E2
Method	BLASTX
NCBI GI	g3522958
BLAST score	622
E value	7.0e-65
Match length	169
% identity	75
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	147856
Seq. ID	LIB3168-096-P1-K1-E3
Method	BLASTX
NCBI GI	g112681
BLAST score	630
E value	8.0e-66
Match length	160
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147857
Seq. ID	LIB3168-096-P1-K1-E4
Method	BLASTX
NCBI GI	g3831440
BLAST score	474
E value	1.0e-47
Match length	127
% identity	73
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	147858
Seq. ID	LIB3168-096-P1-K1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	322
E value	1.0e-29
Match length	100
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147859
Seq. ID	LIB3168-096-P1-K1-E6
Method	BLASTX
NCBI GI	g112737
BLAST score	301
E value	1.0e-27
Match length	83
% identity	73
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147860
Seq. ID	LIB3168-096-P1-K1-E7
Method	BLASTN

NCBI GI	g4199934
BLAST score	269
E value	1.0e-150
Match length	318
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	147861
Seq. ID	LIB3168-096-P1-K1-E8
Method	BLASTX
NCBI GI	g1628583
BLAST score	360
E value	3.0e-34
Match length	147
% identity	55
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147862
Seq. ID	LIB3168-096-P1-K1-E9
Method	BLASTN
NCBI GI	g4235150
BLAST score	267
E value	1.0e-148
Match length	358
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	147863
Seq. ID	LIB3168-096-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	721
E value	2.0e-76
Match length	143
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147864
Seq. ID	LIB3168-096-P1-K1-F10
Method	BLASTX
NCBI GI	g112741
BLAST score	607
E value	4.0e-63
Match length	111
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No.	147865
Seq. ID	LIB3168-096-P1-K1-F11
Method	BLASTX
NCBI GI	g4263791
BLAST score	801
E value	8.0e-86
Match length	181
% identity	87
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	147866
Seq. ID	LIB3168-096-P1-K1-F12
Method	BLASTX
NCBI GI	g112681
BLAST score	978
E value	1.0e-106
Match length	184
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147867
Seq. ID	LIB3168-096-P1-K1-F2
Method	BLASTN
NCBI GI	g4097693
BLAST score	37
E value	2.0e-11
Match length	65
% identity	94
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	147868
Seq. ID	LIB3168-096-P1-K1-F3
Method	BLASTX
NCBI GI	g135406
BLAST score	647
E value	8.0e-68
Match length	122
% identity	99
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	147869
Seq. ID	LIB3168-096-P1-K1-F4
Method	BLASTX
NCBI GI	g112682
BLAST score	728
E value	2.0e-77

Match length	159
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147870
Seq. ID	LIB3168-096-P1-K1-F5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147871
Seq. ID	LIB3168-096-P1-K1-F6
Method	BLASTN
NCBI GI	g3738275
BLAST score	438
E value	0.0e+00
Match length	551
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147872
Seq. ID	LIB3168-096-P1-K1-F7
Method	BLASTX
NCBI GI	g1628583
BLAST score	624
E value	4.0e-65
Match length	119
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147873
Seq. ID	LIB3168-096-P1-K1-F8
Method	BLASTX
NCBI GI	g112681
BLAST score	729
E value	2.0e-77
Match length	177
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147874
Seq. ID	LIB3168-096-P1-K1-F9
Method	BLASTN
NCBI GI	g2618599
BLAST score	106
E value	4.0e-53
Match length	122
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	147875
Seq. ID	LIB3168-096-P1-K1-G1
Method	BLASTX
NCBI GI	g112741
BLAST score	546
E value	4.0e-56
Match length	118
% identity	87
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147876
Seq. ID	LIB3168-096-P1-K1-G10
Method	BLASTX
NCBI GI	g4204299
BLAST score	816
E value	1.0e-87
Match length	174
% identity	90
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147877
Seq. ID	LIB3168-096-P1-K1-G11
Method	BLASTX
NCBI GI	g4455223
BLAST score	505
E value	4.0e-51
Match length	165
% identity	34
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	147878
Seq. ID	LIB3168-096-P1-K1-G12
Method	BLASTX
NCBI GI	g1107501
BLAST score	404
E value	3.0e-39
Match length	99
% identity	82

NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	147879
Seq. ID	LIB3168-096-P1-K1-G2
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147880
Seq. ID	LIB3168-096-P1-K1-G3
Method	BLASTX
NCBI GI	g112739
BLAST score	505
E value	3.0e-51
Match length	139
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147881
Seq. ID	LIB3168-096-P1-K1-G4
Method	BLASTX
NCBI GI	g112682
BLAST score	78
E value	9.0e-44
Match length	118
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147882
Seq. ID	LIB3168-096-P1-K1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	677
E value	2.0e-71
Match length	166
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147883
Seq. ID	LIB3168-096-P1-K1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	562
E value	5.0e-58
Match length	120
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147884
Seq. ID	LIB3168-096-P1-K1-G7
Method	BLASTX
NCBI GI	g112737
BLAST score	727
E value	4.0e-77
Match length	164
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147885
Seq. ID	LIB3168-096-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	420
E value	3.0e-41
Match length	79
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147886
Seq. ID	LIB3168-096-P1-K1-G9
Method	BLASTX
NCBI GI	g112681
BLAST score	657
E value	4.0e-69
Match length	130
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147887
Seq. ID	LIB3168-096-P1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	637
E value	1.0e-66
Match length	122
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147888
Seq. ID	LIB3168-096-P1-K1-H10
Method	BLASTX
NCBI GI	g112681
BLAST score	799
E value	1.0e-85
Match length	176
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147889
Seq. ID	LIB3168-096-P1-K1-H11
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147890
Seq. ID	LIB3168-096-P1-K1-H12
Method	BLASTX
NCBI GI	g2499236
BLAST score	546
E value	5.0e-56
Match length	128
% identity	88
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis thaliana]

Seq. No.	147891
Seq. ID	LIB3168-096-P1-K1-H2
Method	BLASTX
NCBI GI	g1173103
BLAST score	745
E value	3.0e-79

Match length	133
% identity	99
NCBI Description	RIBONUCLEASE 1 PRECURSOR >gi_561998 (U05206) ribonuclease [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease, RNS1 [Arabidopsis thaliana]

Seq. No.	147892
Seq. ID	LIB3168-096-P1-K1-H3
Method	BLASTX
NCBI GI	g112682
BLAST score	643
E value	2.0e-67
Match length	160
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147893
Seq. ID	LIB3168-096-P1-K1-H4
Method	BLASTN
NCBI GI	g4510360
BLAST score	349
E value	0.0e+00
Match length	462
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	147894
Seq. ID	LIB3168-096-P1-K1-H6
Method	BLASTX
NCBI GI	g112739
BLAST score	521
E value	5.0e-53
Match length	146
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147895
Seq. ID	LIB3168-096-P1-K1-H7
Method	BLASTX
NCBI GI	g1628583
BLAST score	660
E value	2.0e-69
Match length	158
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147896
Seq. ID	LIB3168-096-P1-K1-H8
Method	BLASTX
NCBI GI	g112741
BLAST score	78
E value	5.0e-88
Match length	164
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147897
Seq. ID	LIB3168-096-P1-K1-H9
Method	BLASTX
NCBI GI	g112682
BLAST score	788
E value	2.0e-84
Match length	176
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147898
Seq. ID	LIB3168-098-P1-K1-A1
Method	BLASTX
NCBI GI	g4006897
BLAST score	95
E value	1.0e-43
Match length	119
% identity	80
NCBI Description	(Z99708) globulin-like protein [Arabidopsis thaliana]

Seq. No.	147899
Seq. ID	LIB3168-098-P1-K1-A10
Method	BLASTX
NCBI GI	g2642443
BLAST score	578
E value	8.0e-60
Match length	134
% identity	83
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	147900
Seq. ID	LIB3168-098-P1-K1-A2
Method	BLASTX
NCBI GI	g112739
BLAST score	295

E value	1.0e-26
Match length	115
% identity	44
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147901
Seq. ID	LIB3168-098-P1-K1-A3
Method	BLASTX
NCBI GI	g1628583
BLAST score	619
E value	1.0e-64
Match length	129
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147902
Seq. ID	LIB3168-098-P1-K1-A4
Method	BLASTX
NCBI GI	g4741960
BLAST score	467
E value	7.0e-47
Match length	116
% identity	78
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	147903
Seq. ID	LIB3168-098-P1-K1-A5
Method	BLASTN
NCBI GI	g2673901
BLAST score	100
E value	6.0e-49
Match length	386
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147904
Seq. ID	LIB3168-098-P1-K1-A6
Method	BLASTN
NCBI GI	g4678291
BLAST score	233
E value	1.0e-128
Match length	261
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	147905
Seq. ID	LIB3168-098-P1-K1-A7

Method	BLASTX
NCBI GI	g1628583
BLAST score	444
E value	2.0e-44
Match length	100
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147906
Seq. ID	LIB3168-098-P1-K1-A8
Method	BLASTX
NCBI GI	g112739
BLAST score	431
E value	1.0e-42
Match length	130
% identity	69
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147907
Seq. ID	LIB3168-098-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	393
E value	3.0e-38
Match length	81
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147908
Seq. ID	LIB3168-098-P1-K1-B10
Method	BLASTX
NCBI GI	g2661422
BLAST score	399
E value	3.0e-40
Match length	97
% identity	95
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	147909
Seq. ID	LIB3168-098-P1-K1-B11
Method	BLASTX
NCBI GI	g112682
BLAST score	597
E value	4.0e-62

Match length	126
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147910
Seq. ID	LIB3168-098-P1-K1-B12
Method	BLASTX
NCBI GI	g112682
BLAST score	344
E value	8.0e-33
Match length	66
% identity	95
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147911
Seq. ID	LIB3168-098-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	422
E value	5.0e-42
Match length	86
% identity	94
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147912
Seq. ID	LIB3168-098-P1-K1-B3
Method	BLASTN
NCBI GI	g3293260
BLAST score	90
E value	5.0e-43
Match length	178
% identity	88
NCBI Description	Arabidopsis thaliana cystathionine gamma-synthase precursor (CGS1) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	147913
Seq. ID	LIB3168-098-P1-K1-B4
Method	BLASTX
NCBI GI	g112741
BLAST score	516
E value	1.0e-52
Match length	113
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147914
Seq. ID	LIB3168-098-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583
BLAST score	409
E value	4.0e-40
Match length	120
% identity	68
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147915
Seq. ID	LIB3168-098-P1-K1-B6
Method	BLASTN
NCBI GI	g4539378
BLAST score	187
E value	1.0e-101
Match length	208
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	147916
Seq. ID	LIB3168-098-P1-K1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	257
E value	3.0e-22
Match length	69
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147917
Seq. ID	LIB3168-098-P1-K1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	118
E value	6.0e-06
Match length	68
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147918
Seq. ID	LIB3168-098-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	557

E value	2.0e-57
Match length	147
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147919
Seq. ID	LIB3168-098-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	329
E value	4.0e-31
Match length	73
% identity	88
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147920
Seq. ID	LIB3168-098-P1-K1-C12
Method	BLASTN
NCBI GI	g2262155
BLAST score	188
E value	1.0e-101
Match length	393
% identity	97
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	147921
Seq. ID	LIB3168-098-P1-K1-C2
Method	BLASTX
NCBI GI	g3193310
BLAST score	580
E value	4.0e-60
Match length	141
% identity	84
NCBI Description	(AF069300) contains similarity to Nicotiana tabacum hin1 (GB:Y07563) [Arabidopsis thaliana]

Seq. No.	147922
Seq. ID	LIB3168-098-P1-K1-C3
Method	BLASTX
NCBI GI	g99735
BLAST score	461
E value	3.0e-46
Match length	106
% identity	86
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	147923
Seq. ID	LIB3168-098-P1-K1-C4
Method	BLASTX
NCBI GI	g2961390
BLAST score	162

E value	1.0e-11
Match length	31
% identity	97
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	147924
Seq. ID	LIB3168-098-P1-K1-C9
Method	BLASTX
NCBI GI	g112681
BLAST score	221
E value	2.0e-18
Match length	73
% identity	63
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147925
Seq. ID	LIB3168-098-P1-K1-D1
Method	BLASTN
NCBI GI	g166609
BLAST score	227
E value	1.0e-125
Match length	243
% identity	98
NCBI Description	A.thaliana at2S1 gene encoding albumin 2S subunit 1, complete cds

Seq. No.	147926
Seq. ID	LIB3168-098-P1-K1-D10
Method	BLASTX
NCBI GI	g112737
BLAST score	460
E value	5.0e-46
Match length	142
% identity	66
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147927
Seq. ID	LIB3168-098-P1-K1-D11
Method	BLASTN
NCBI GI	g4581084
BLAST score	212
E value	1.0e-116
Match length	351
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	147928
Seq. ID	LIB3168-098-P1-K1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	584
E value	2.0e-60
Match length	147
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147929
Seq. ID	LIB3168-098-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	527
E value	5.0e-54
Match length	104
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147930
Seq. ID	LIB3168-098-P1-K1-D6
Method	BLASTN
NCBI GI	g2815404
BLAST score	38
E value	7.0e-12
Match length	90
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	147931
Seq. ID	LIB3168-098-P1-K1-D8
Method	BLASTN
NCBI GI	g1769896
BLAST score	330
E value	0.0e+00
Match length	386
% identity	46
NCBI Description	A.thaliana lectin receptor kinase gene

Seq. No.	147932
Seq. ID	LIB3168-098-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	319
E value	1.0e-29
Match length	66
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147933
Seq. ID	LIB3168-098-P1-K1-E1
Method	BLASTX
NCBI GI	g112682
BLAST score	512
E value	3.0e-52
Match length	117
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147934
Seq. ID	LIB3168-098-P1-K1-E11
Method	BLASTX
NCBI GI	g1345973
BLAST score	179
E value	2.0e-13
Match length	49
% identity	73
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	147935
Seq. ID	LIB3168-098-P1-K1-E12
Method	BLASTX
NCBI GI	g112681
BLAST score	203
E value	3.0e-16
Match length	50
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147936
Seq. ID	LIB3168-098-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	225
E value	4.0e-19
Match length	64
% identity	73

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147937
Seq. ID	LIB3168-098-P1-K1-E6
Method	BLASTX
NCBI GI	g112681
BLAST score	373
E value	3.0e-37
Match length	113
% identity	80
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147938
Seq. ID	LIB3168-098-P1-K1-E9
Method	BLASTX
NCBI GI	g112682
BLAST score	231
E value	1.0e-23
Match length	72
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147939
Seq. ID	LIB3168-098-P1-K1-F1
Method	BLASTX
NCBI GI	g1628583
BLAST score	59
E value	2.0e-26
Match length	95
% identity	65
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147940
Seq. ID	LIB3168-098-P1-K1-F10
Method	BLASTX
NCBI GI	g112681
BLAST score	480
E value	2.0e-60
Match length	145
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147941
Seq. ID	LIB3168-098-P1-K1-F11
Method	BLASTX
NCBI GI	g112739
BLAST score	386
E value	2.0e-37
Match length	116
% identity	69
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	147942
Seq. ID	LIB3168-098-P1-K1-F12
Method	BLASTN
NCBI GI	g4314354
BLAST score	309
E value	1.0e-173
Match length	450
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147943
Seq. ID	LIB3168-098-P1-K1-F2
Method	BLASTX
NCBI GI	g112681
BLAST score	47
E value	3.0e-30
Match length	106
% identity	70
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147944
Seq. ID	LIB3168-098-P1-K1-F3
Method	BLASTN
NCBI GI	g4159705
BLAST score	278
E value	1.0e-155
Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	147945
Seq. ID	LIB3168-098-P1-K1-F4
Method	BLASTX
NCBI GI	g112682

BLAST score	540
E value	2.0e-55
Match length	134
% identity	78
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147946
Seq. ID	LIB3168-098-P1-K1-F5
Method	BLASTX
NCBI GI	g112743
BLAST score	420
E value	2.0e-41
Match length	82
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	147947
Seq. ID	LIB3168-098-P1-K1-F7
Method	BLASTX
NCBI GI	g4204298
BLAST score	437
E value	2.0e-43
Match length	86
% identity	97
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147948
Seq. ID	LIB3168-098-P1-K1-F8
Method	BLASTN
NCBI GI	g2584827
BLAST score	58
E value	2.0e-24
Match length	78
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147949
Seq. ID	LIB3168-098-P1-K1-F9
Method	BLASTX
NCBI GI	g1174805
BLAST score	224
E value	2.0e-18
Match length	140
% identity	41
NCBI Description	TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55

SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi_1074717_pir__B64170 hypothetical protein HI1289 - Haemophilus influenzae (strain Rd KW20) >gi_1574748 (U32809) tRNA pseudouridine 55 synthase (truB) [Haemophilus influenzae Rd]

Seq. No.	147950
Seq. ID	LIB3168-098-P1-K1-G1
Method	BLASTX
NCBI GI	g3947690
BLAST score	249
E value	3.0e-21
Match length	146
% identity	40
NCBI Description	(AJ131245) Sec24B protein [Homo sapiens]

Seq. No.	147951
Seq. ID	LIB3168-098-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	408
E value	4.0e-40
Match length	100
% identity	82
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147952
Seq. ID	LIB3168-098-P1-K1-G11
Method	BLASTX
NCBI GI	g4204299
BLAST score	606
E value	3.0e-63
Match length	125
% identity	96
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	147953
Seq. ID	LIB3168-098-P1-K1-G2
Method	BLASTX
NCBI GI	g82051
BLAST score	320
E value	1.0e-29
Match length	125
% identity	50
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]

Seq. No.	147954
Seq. ID	LIB3168-098-P1-K1-G4
Method	BLASTN
NCBI GI	g4159712
BLAST score	67

E value	1.0e-29
Match length	138
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	147955
Seq. ID	LIB3168-098-P1-K1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	187
E value	2.0e-14
Match length	36
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147956
Seq. ID	LIB3168-098-P1-K1-G8
Method	BLASTX
NCBI GI	g112681
BLAST score	459
E value	4.0e-46
Match length	101
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147957
Seq. ID	LIB3168-098-P1-K1-G9
Method	BLASTX
NCBI GI	g112682
BLAST score	322
E value	3.0e-34
Match length	110
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147958
Seq. ID	LIB3168-098-P1-K1-H1
Method	BLASTN
NCBI GI	g3128142
BLAST score	211
E value	1.0e-115
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	147959
Seq. ID	LIB3168-098-P1-K1-H11
Method	BLASTX
NCBI GI	g112681
BLAST score	247
E value	2.0e-26
Match length	89
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147960
Seq. ID	LIB3168-098-P1-K1-H12
Method	BLASTN
NCBI GI	g4159704
BLAST score	357
E value	0.0e+00
Match length	400
% identity	54
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	147961
Seq. ID	LIB3168-098-P1-K1-H2
Method	BLASTX
NCBI GI	g1346831
BLAST score	154
E value	9.0e-11
Match length	32
% identity	94
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) >gi_984310 (U26948) photosystem I component [Glycine max]

Seq. No.	147962
Seq. ID	LIB3168-098-P1-K1-H3
Method	BLASTX
NCBI GI	g3004557
BLAST score	496
E value	2.0e-50
Match length	98
% identity	99
NCBI Description	(AC003673) plasma membrane proton pump H+ ATPase, PMA1 [Arabidopsis thaliana]

Seq. No.	147963
Seq. ID	LIB3168-098-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	540
E value	2.0e-55
Match length	138
% identity	78

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147964
Seq. ID	LIB3168-098-P1-K1-H5
Method	BLASTN
NCBI GI	g4455339
BLAST score	38
E value	2.0e-12
Match length	114
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	147965
Seq. ID	LIB3168-098-P1-K1-H7
Method	BLASTN
NCBI GI	g725259
BLAST score	105
E value	2.0e-52
Match length	132
% identity	95
NCBI Description	Arabidopsis thaliana oleosin mRNA, complete cds

Seq. No.	147966
Seq. ID	LIB3168-099-P1-K1-A1
Method	BLASTX
NCBI GI	g1628583
BLAST score	335
E value	1.0e-42
Match length	124
% identity	75
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147967
Seq. ID	LIB3168-099-P1-K1-A10
Method	BLASTX
NCBI GI	g112741
BLAST score	744
E value	3.0e-79
Match length	143
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	147968
Seq. ID	LIB3168-099-P1-K1-A11
Method	BLASTX
NCBI GI	g112737

BLAST score	624
E value	3.0e-65
Match length	148
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147969
Seq. ID	LIB3168-099-P1-K1-A12
Method	BLASTN
NCBI GI	g4263038
BLAST score	359
E value	0.0e+00
Match length	383
% identity	82
NCBI Description	Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	147970
Seq. ID	LIB3168-099-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	525
E value	1.0e-53
Match length	111
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147971
Seq. ID	LIB3168-099-P1-K1-A3
Method	BLASTN
NCBI GI	g4589419
BLAST score	181
E value	2.0e-97
Match length	261
% identity	69
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	147972
Seq. ID	LIB3168-099-P1-K1-A4
Method	BLASTX
NCBI GI	g226120
BLAST score	248
E value	4.0e-21
Match length	123
% identity	40
NCBI Description	vicilin gene B [Saguinus oedipus]

Seq. No. 147973

Seq. ID	LIB3168-099-P1-K1-A5
Method	BLASTX
NCBI GI	g1628583
BLAST score	769
E value	3.0e-82
Match length	153
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147974
Seq. ID	LIB3168-099-P1-K1-A7
Method	BLASTX
NCBI GI	g1628583
BLAST score	165
E value	1.0e-11
Match length	36
% identity	89
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147975
Seq. ID	LIB3168-099-P1-K1-A8
Method	BLASTX
NCBI GI	g1628583
BLAST score	536
E value	5.0e-55
Match length	107
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147976
Seq. ID	LIB3168-099-P1-K1-B1
Method	BLASTN
NCBI GI	g2739359
BLAST score	88
E value	1.0e-41
Match length	215
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147977
Seq. ID	LIB3168-099-P1-K1-B10
Method	BLASTX
NCBI GI	g112682
BLAST score	693
E value	3.0e-73
Match length	148
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147978
Seq. ID	LIB3168-099-P1-K1-B11
Method	BLASTX
NCBI GI	g3157944
BLAST score	751
E value	4.0e-80
Match length	145
% identity	99
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	147979
Seq. ID	LIB3168-099-P1-K1-B2
Method	BLASTX
NCBI GI	g881615
BLAST score	655
E value	6.0e-69
Match length	128
% identity	99
NCBI Description	(U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No.	147980
Seq. ID	LIB3168-099-P1-K1-B3
Method	BLASTX
NCBI GI	g112681
BLAST score	533
E value	1.0e-54
Match length	126
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147981
Seq. ID	LIB3168-099-P1-K1-B4
Method	BLASTX
NCBI GI	g4454042
BLAST score	297
E value	6.0e-27
Match length	97
% identity	53
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	147982
Seq. ID	LIB3168-099-P1-K1-B5
Method	BLASTX
NCBI GI	g1628583

BLAST score	54
E value	8.0e-79
Match length	153
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147983
Seq. ID	LIB3168-099-P1-K1-B6
Method	BLASTN
NCBI GI	g4567259
BLAST score	335
E value	0.0e+00
Match length	413
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	147984
Seq. ID	LIB3168-099-P1-K1-B7
Method	BLASTX
NCBI GI	g4678226
BLAST score	546
E value	4.0e-56
Match length	131
% identity	86
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	147985
Seq. ID	LIB3168-099-P1-K1-B8
Method	BLASTX
NCBI GI	g2828296
BLAST score	593
E value	1.0e-61
Match length	117
% identity	96
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	147986
Seq. ID	LIB3168-099-P1-K1-B9
Method	BLASTX
NCBI GI	g112682
BLAST score	589
E value	4.0e-61
Match length	138
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147987
Seq. ID	LIB3168-099-P1-K1-C1
Method	BLASTX

NCBI GI	g1628583
BLAST score	435
E value	4.0e-43
Match length	114
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147988
Seq. ID	LIB3168-099-P1-K1-C10
Method	BLASTX
NCBI GI	g112681
BLAST score	643
E value	2.0e-67
Match length	150
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147989
Seq. ID	LIB3168-099-P1-K1-C11
Method	BLASTN
NCBI GI	g3738088
BLAST score	41
E value	1.0e-13
Match length	507
% identity	38
NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147990
Seq. ID	LIB3168-099-P1-K1-C12
Method	BLASTX
NCBI GI	g1628583
BLAST score	587
E value	5.0e-61
Match length	121
% identity	93
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147991
Seq. ID	LIB3168-099-P1-K1-C2
Method	BLASTN
NCBI GI	g2656029
BLAST score	296
E value	1.0e-166
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	147992
Seq. ID	LIB3168-099-P1-K1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	655
E value	9.0e-69
Match length	128
% identity	97
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	147993
Seq. ID	LIB3168-099-P1-K1-C4
Method	BLASTX
NCBI GI	g1628583
BLAST score	607
E value	3.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147994
Seq. ID	LIB3168-099-P1-K1-C5
Method	BLASTX
NCBI GI	g112737
BLAST score	617
E value	2.0e-64
Match length	152
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	147995
Seq. ID	LIB3168-099-P1-K1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	558
E value	2.0e-57
Match length	119
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147996
Seq. ID	LIB3168-099-P1-K1-C7
Method	BLASTN

NCBI GI	g2656030
BLAST score	223
E value	1.0e-122
Match length	414
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	147997
Seq. ID	LIB3168-099-P1-K1-C8
Method	BLASTN
NCBI GI	g4263540
BLAST score	37
E value	3.0e-11
Match length	49
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	147998
Seq. ID	LIB3168-099-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	671
E value	1.0e-70
Match length	132
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	147999
Seq. ID	LIB3168-099-P1-K1-D1
Method	BLASTX
NCBI GI	g3935148
BLAST score	568
E value	1.0e-58
Match length	131
% identity	85
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	148000
Seq. ID	LIB3168-099-P1-K1-D10
Method	BLASTX
NCBI GI	g4512684
BLAST score	677
E value	2.0e-71
Match length	136
% identity	100
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	148001
Seq. ID	LIB3168-099-P1-K1-D12
Method	BLASTX
NCBI GI	g112682

BLAST score	646
E value	9.0e-68
Match length	147
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148002
Seq. ID	LIB3168-099-P1-K1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	423
E value	6.0e-42
Match length	95
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148003
Seq. ID	LIB3168-099-P1-K1-D5
Method	BLASTX
NCBI GI	g112682
BLAST score	653
E value	1.0e-68
Match length	134
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148004
Seq. ID	LIB3168-099-P1-K1-D6
Method	BLASTX
NCBI GI	g1628583
BLAST score	603
E value	1.0e-62
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148005
Seq. ID	LIB3168-099-P1-K1-D8
Method	BLASTN
NCBI GI	g4580400
BLAST score	50
E value	9.0e-20
Match length	95
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T16I21 genomic

sequence, complete sequence

Seq. No.	148006
Seq. ID	LIB3168-099-P1-K1-E1
Method	BLASTX
NCBI GI	g1592670
BLAST score	370
E value	1.0e-35
Match length	99
% identity	71
NCBI Description	(X91920) dehydrin [Arabidopsis thaliana] >gi_4567280_gb_AAD23693.1_AC006841_21 (AC006841) putative dehydrin [Arabidopsis thaliana]

Seq. No.	148007
Seq. ID	LIB3168-099-P1-K1-E10
Method	BLASTN
NCBI GI	g3241920
BLAST score	183
E value	2.0e-98
Match length	400
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	148008
Seq. ID	LIB3168-099-P1-K1-E11
Method	BLASTX
NCBI GI	g4455338
BLAST score	831
E value	2.0e-89
Match length	148
% identity	100
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	148009
Seq. ID	LIB3168-099-P1-K1-E2
Method	BLASTN
NCBI GI	g3746057
BLAST score	449
E value	0.0e+00
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148010
Seq. ID	LIB3168-099-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	634
E value	2.0e-66
Match length	123
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148011
Seq. ID	LIB3168-099-P1-K1-E4
Method	BLASTX
NCBI GI	g112741
BLAST score	731
E value	1.0e-77
Match length	139
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148012
Seq. ID	LIB3168-099-P1-K1-E5
Method	BLASTX
NCBI GI	g1723958
BLAST score	235
E value	1.0e-19
Match length	96
% identity	49
NCBI Description	PUTATIVE KINESIN-LIKE PROTEIN YGL216W >gi_2131622_pir__S64238 hypothetical protein YGL216w - yeast (Saccharomyces cerevisiae) >gi_1322862_emb_CAA96933_ (Z72739) ORF YGL216w [Saccharomyces cerevisiae]

Seq. No.	148013
Seq. ID	LIB3168-099-P1-K1-E6
Method	BLASTX
NCBI GI	g112682
BLAST score	608
E value	2.0e-63
Match length	144
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148014
Seq. ID	LIB3168-099-P1-K1-E7
Method	BLASTN
NCBI GI	g4589437
BLAST score	253
E value	1.0e-140
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	148015
Seq. ID	LIB3168-099-P1-K1-E8

Method	BLASTX
NCBI GI	g1628583
BLAST score	541
E value	1.0e-55
Match length	117
% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148016
Seq. ID	LIB3168-099-P1-K1-E9
Method	BLASTN
NCBI GI	g16472
BLAST score	42
E value	2.0e-14
Match length	138
% identity	83
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	148017
Seq. ID	LIB3168-099-P1-K1-F10
Method	BLASTX
NCBI GI	g4455192
BLAST score	374
E value	7.0e-36
Match length	134
% identity	58
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	148018
Seq. ID	LIB3168-099-P1-K1-F12
Method	BLASTX
NCBI GI	g2129657
BLAST score	309
E value	9.0e-37
Match length	119
% identity	72
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	148019
Seq. ID	LIB3168-099-P1-K1-F2
Method	BLASTN
NCBI GI	g2264312
BLAST score	309
E value	1.0e-173
Match length	443
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	148020
Seq. ID	LIB3168-099-P1-K1-F3
Method	BLASTX

NCBI GI	g112741
BLAST score	430
E value	8.0e-43
Match length	86
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148021
Seq. ID	LIB3168-099-P1-K1-F5
Method	BLASTX
NCBI GI	g2244906
BLAST score	460
E value	5.0e-46
Match length	88
% identity	99
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	148022
Seq. ID	LIB3168-099-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	450
E value	6.0e-45
Match length	117
% identity	78
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148023
Seq. ID	LIB3168-099-P1-K1-F7
Method	BLASTN
NCBI GI	g4079614
BLAST score	372
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148024
Seq. ID	LIB3168-099-P1-K1-F9
Method	BLASTN
NCBI GI	g3402747
BLAST score	415
E value	0.0e+00
Match length	444
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)

Seq. No.	148025
Seq. ID	LIB3168-099-P1-K1-G1
Method	BLASTX
NCBI GI	g112737
BLAST score	182
E value	4.0e-47
Match length	137
% identity	74
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148026
Seq. ID	LIB3168-099-P1-K1-G11
Method	BLASTX
NCBI GI	g112743
BLAST score	778
E value	3.0e-83
Match length	151
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	148027
Seq. ID	LIB3168-099-P1-K1-G12
Method	BLASTX
NCBI GI	g135535
BLAST score	501
E value	9.0e-51
Match length	106
% identity	96
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	148028
Seq. ID	LIB3168-099-P1-K1-G3
Method	BLASTX
NCBI GI	g112741
BLAST score	608
E value	2.0e-63
Match length	114
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148029
Seq. ID	LIB3168-099-P1-K1-G4
Method	BLASTX
NCBI GI	g4204308
BLAST score	425
E value	7.0e-42
Match length	85
% identity	84
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	148030
Seq. ID	LIB3168-099-P1-K1-G5
Method	BLASTN
NCBI GI	g304110
BLAST score	309
E value	1.0e-173
Match length	346
% identity	99
NCBI Description	Arabidopsis thaliana signal recognition particle 54 kDa subunit (Srp54-1) gene, complete cds

Seq. No.	148031
Seq. ID	LIB3168-099-P1-K1-G6
Method	BLASTX
NCBI GI	g3264805
BLAST score	705
E value	9.0e-75
Match length	136
% identity	97
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	148032
Seq. ID	LIB3168-099-P1-K1-G8
Method	BLASTX
NCBI GI	g1628583
BLAST score	499
E value	2.0e-50
Match length	101
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148033
Seq. ID	LIB3168-099-P1-K1-G9
Method	BLASTX
NCBI GI	g4204299

BLAST score	87
E value	1.0e-68
Match length	139
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	148034
Seq. ID	LIB3168-099-P1-K1-H1
Method	BLASTX
NCBI GI	g112682
BLAST score	590
E value	3.0e-61
Match length	117
% identity	96
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148035
Seq. ID	LIB3168-099-P1-K1-H10
Method	BLASTN
NCBI GI	g2583106
BLAST score	168
E value	1.0e-89
Match length	241
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148036
Seq. ID	LIB3168-099-P1-K1-H12
Method	BLASTX
NCBI GI	g112681
BLAST score	663
E value	9.0e-70
Match length	150
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148037
Seq. ID	LIB3168-099-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	642
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148038
Seq. ID	LIB3168-099-P1-K1-H3
Method	BLASTX
NCBI GI	g112682
BLAST score	696
E value	1.0e-73
Match length	157
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148039
Seq. ID	LIB3168-099-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	314
E value	4.0e-29
Match length	69
% identity	87
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148040
Seq. ID	LIB3168-099-P1-K1-H5
Method	BLASTN
NCBI GI	g4097693
BLAST score	79
E value	5.0e-37
Match length	95
% identity	96
NCBI Description	Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds

Seq. No.	148041
Seq. ID	LIB3168-099-P1-K1-H7
Method	BLASTN
NCBI GI	g4580454
BLAST score	383
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	148042
Seq. ID	LIB3168-099-P1-K1-H8
Method	BLASTX
NCBI GI	g1628583
BLAST score	811
E value	4.0e-87
Match length	156
% identity	99

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148043
Seq. ID	LIB3168-100-P1-K1-A1
Method	BLASTX
NCBI GI	g112739
BLAST score	337
E value	2.0e-51
Match length	131
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	148044
Seq. ID	LIB3168-100-P1-K1-A10
Method	BLASTN
NCBI GI	g4510338
BLAST score	433
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	148045
Seq. ID	LIB3168-100-P1-K1-A11
Method	BLASTX
NCBI GI	g112682
BLAST score	639
E value	6.0e-67
Match length	146
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148046
Seq. ID	LIB3168-100-P1-K1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	599
E value	2.0e-62
Match length	126
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148047
Seq. ID	LIB3168-100-P1-K1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	626
E value	2.0e-65
Match length	123
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148048
Seq. ID	LIB3168-100-P1-K1-A3
Method	BLASTN
NCBI GI	g4586098
BLAST score	244
E value	1.0e-135
Match length	437
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	148049
Seq. ID	LIB3168-100-P1-K1-A4
Method	BLASTX
NCBI GI	g1170505
BLAST score	531
E value	3.0e-54
Match length	105
% identity	97
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	148050
Seq. ID	LIB3168-100-P1-K1-A6
Method	BLASTX
NCBI GI	g2505876
BLAST score	332
E value	5.0e-31
Match length	72
% identity	86
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	148051
Seq. ID	LIB3168-100-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	433
E value	8.0e-43
Match length	144
% identity	61

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	148052
Seq. ID	LIB3168-100-P1-K1-A8
Method	BLASTN
NCBI GI	g2564049
BLAST score	305
E value	1.0e-171
Match length	372
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.	148053
Seq. ID	LIB3168-100-P1-K1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	529
E value	5.0e-54
Match length	120
% identity	85
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	148054
Seq. ID	LIB3168-100-P1-K1-B1
Method	BLASTX
NCBI GI	g112737
BLAST score	600
E value	2.0e-62
Match length	143
% identity	81
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	148055
Seq. ID	LIB3168-100-P1-K1-B11
Method	BLASTX
NCBI GI	g67842
BLAST score	225
E value	1.0e-18
Match length	80
% identity	60
NCBI Description	H+-transporting ATP synthase (EC 3.6.1.34) beta chain - spinach chloroplast >gi_343355 (J01441) ATPase beta subunit [Spinacia oleracea] >gi_223530_prf__0811259A ATPase beta [Spinacia oleracea]

Seq. No.	148056
Seq. ID	LIB3168-100-P1-K1-B12
Method	BLASTX
NCBI GI	g112681
BLAST score	737
E value	2.0e-78
Match length	140
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148057
Seq. ID	LIB3168-100-P1-K1-B2
Method	BLASTX
NCBI GI	g1628583
BLAST score	404
E value	2.0e-39
Match length	112
% identity	73
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148058
Seq. ID	LIB3168-100-P1-K1-B3
Method	BLASTX
NCBI GI	g542157
BLAST score	585
E value	1.0e-60
Match length	136
% identity	81
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	148059
Seq. ID	LIB3168-100-P1-K1-B6
Method	BLASTX
NCBI GI	g3269286
BLAST score	453
E value	9.0e-57
Match length	141
% identity	90
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	148060
Seq. ID	LIB3168-100-P1-K1-B7
Method	BLASTN
NCBI GI	g3046852
BLAST score	268
E value	1.0e-149
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	148061
Seq. ID	LIB3168-100-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148062
Seq. ID	LIB3168-100-P1-K1-C1
Method	BLASTN
NCBI GI	g2564049
BLAST score	171
E value	1.0e-91
Match length	171
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	148063
Seq. ID	LIB3168-100-P1-K1-C10
Method	BLASTX
NCBI GI	g1628583
BLAST score	752
E value	3.0e-80
Match length	145
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148064
Seq. ID	LIB3168-100-P1-K1-C11
Method	BLASTX
NCBI GI	g112741
BLAST score	771
E value	2.0e-82
Match length	143
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148065
Seq. ID	LIB3168-100-P1-K1-C12
Method	BLASTN
NCBI GI	g4753195
BLAST score	227

E value	1.0e-124
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	148066
Seq. ID	LIB3168-100-P1-K1-C2
Method	BLASTX
NCBI GI	g112737
BLAST score	598
E value	4.0e-62
Match length	124
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148067
Seq. ID	LIB3168-100-P1-K1-C3
Method	BLASTX
NCBI GI	g1169598
BLAST score	629
E value	9.0e-66
Match length	126
% identity	90
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	148068
Seq. ID	LIB3168-100-P1-K1-C6
Method	BLASTX
NCBI GI	g112681
BLAST score	646
E value	9.0e-68
Match length	148
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148069
Seq. ID	LIB3168-100-P1-K1-C7
Method	BLASTN
NCBI GI	g16231
BLAST score	112
E value	4.0e-56
Match length	176
% identity	95
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein

>gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	148070
Seq. ID	LIB3168-100-P1-K1-C8
Method	BLASTX
NCBI GI	g112741
BLAST score	764
E value	1.0e-81
Match length	145
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148071
Seq. ID	LIB3168-100-P1-K1-C9
Method	BLASTX
NCBI GI	g1628583
BLAST score	441
E value	9.0e-44
Match length	149
% identity	62
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148072
Seq. ID	LIB3168-100-P1-K1-D1
Method	BLASTX
NCBI GI	g112682
BLAST score	555
E value	3.0e-57
Match length	126
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148073
Seq. ID	LIB3168-100-P1-K1-D10
Method	BLASTN
NCBI GI	g4733991
BLAST score	38
E value	7.0e-12
Match length	82
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T4D8 genomic sequence, complete sequence

Seq. No. 148074

Seq. ID	LIB3168-100-P1-K1-D11
Method	BLASTX
NCBI GI	g112681
BLAST score	631
E value	5.0e-66
Match length	144
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148075
Seq. ID	LIB3168-100-P1-K1-D12
Method	BLASTX
NCBI GI	g112682
BLAST score	650
E value	3.0e-68
Match length	136
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148076
Seq. ID	LIB3168-100-P1-K1-D2
Method	BLASTX
NCBI GI	g112737
BLAST score	624
E value	3.0e-65
Match length	146
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148077
Seq. ID	LIB3168-100-P1-K1-D3
Method	BLASTX
NCBI GI	g1628583
BLAST score	153
E value	5.0e-10
Match length	81
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148078
Seq. ID	LIB3168-100-P1-K1-D4

Method	BLASTX
NCBI GI	g112737
BLAST score	605
E value	5.0e-63
Match length	143
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148079
Seq. ID	LIB3168-100-P1-K1-D5
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	3.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148080
Seq. ID	LIB3168-100-P1-K1-D6
Method	BLASTX
NCBI GI	g2288981
BLAST score	312
E value	1.0e-28
Match length	64
% identity	52
NCBI Description	(AC002335) calcium binding protein isolog [Arabidopsis thaliana] >gi_3763938 (AC004450) putative calcium binding protein [Arabidopsis thaliana]

Seq. No.	148081
Seq. ID	LIB3168-100-P1-K1-D7
Method	BLASTN
NCBI GI	g4490701
BLAST score	147
E value	4.0e-77
Match length	147
% identity	53
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	148082
Seq. ID	LIB3168-100-P1-K1-D8
Method	BLASTX
NCBI GI	g2827621
BLAST score	312
E value	1.0e-28
Match length	136
% identity	45

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 148083
Seq. ID LIB3168-100-P1-K1-D9
Method BLASTN
NCBI GI g4455262
BLAST score 316
E value 1.0e-178
Match length 436
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No. 148084
Seq. ID LIB3168-100-P1-K1-E1
Method BLASTX
NCBI GI g1628583
BLAST score 467
E value 6.0e-47
Match length 100
% identity 88
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148085
Seq. ID LIB3168-100-P1-K1-E10
Method BLASTX
NCBI GI g1628583
BLAST score 669
E value 2.0e-70
Match length 148
% identity 88
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148086
Seq. ID LIB3168-100-P1-K1-E11
Method BLASTN
NCBI GI g4584351
BLAST score 75
E value 5.0e-34
Match length 299
% identity 89
NCBI Description Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No. 148087
Seq. ID LIB3168-100-P1-K1-E12
Method BLASTX
NCBI GI g112741
BLAST score 750
E value 6.0e-80
Match length 141
% identity 99
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148088
Seq. ID	LIB3168-100-P1-K1-E2
Method	BLASTX
NCBI GI	g112681
BLAST score	648
E value	5.0e-68
Match length	147
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148089
Seq. ID	LIB3168-100-P1-K1-E3
Method	BLASTX
NCBI GI	g1628583
BLAST score	557
E value	2.0e-57
Match length	119
% identity	90
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148090
Seq. ID	LIB3168-100-P1-K1-E4
Method	BLASTX
NCBI GI	g112737
BLAST score	517
E value	4.0e-59
Match length	147
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148091
Seq. ID	LIB3168-100-P1-K1-E5
Method	BLASTX
NCBI GI	g2462749
BLAST score	231
E value	4.0e-19
Match length	117
% identity	38

NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	148092
Seq. ID	LIB3168-100-P1-K1-E6
Method	BLASTN
NCBI GI	g3327922
BLAST score	146
E value	3.0e-76
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148093
Seq. ID	LIB3168-100-P1-K1-E8
Method	BLASTX
NCBI GI	g112737
BLAST score	619
E value	1.0e-64
Match length	146
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148094
Seq. ID	LIB3168-100-P1-K1-F1
Method	BLASTX
NCBI GI	g3935148
BLAST score	736
E value	2.0e-78
Match length	147
% identity	97
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	148095
Seq. ID	LIB3168-100-P1-K1-F11
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	7.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	148096
Seq. ID	LIB3168-100-P1-K1-F12
Method	BLASTX
NCBI GI	g112741
BLAST score	50
E value	4.0e-69

Match length	135
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148097
Seq. ID	LIB3168-100-P1-K1-F4
Method	BLASTX
NCBI GI	g112739
BLAST score	398
E value	9.0e-39
Match length	119
% identity	69
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	148098
Seq. ID	LIB3168-100-P1-K1-F5
Method	BLASTX
NCBI GI	g112741
BLAST score	572
E value	2.0e-73
Match length	136
% identity	95
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148099
Seq. ID	LIB3168-100-P1-K1-F6
Method	BLASTX
NCBI GI	g1628583
BLAST score	430
E value	9.0e-43
Match length	96
% identity	86
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148100
Seq. ID	LIB3168-100-P1-K1-F7
Method	BLASTX

NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148101
Seq. ID	LIB3168-100-P1-K1-F8
Method	BLASTX
NCBI GI	g1628583
BLAST score	699
E value	5.0e-74
Match length	136
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148102
Seq. ID	LIB3168-100-P1-K1-F9
Method	BLASTX
NCBI GI	g1724100
BLAST score	319
E value	2.0e-29
Match length	149
% identity	41
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	148103
Seq. ID	LIB3168-100-P1-K1-G1
Method	BLASTX
NCBI GI	g1628583
BLAST score	595
E value	8.0e-62
Match length	146
% identity	80
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148104
Seq. ID	LIB3168-100-P1-K1-G10
Method	BLASTX
NCBI GI	g1628583
BLAST score	622
E value	6.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148105
Seq. ID	LIB3168-100-P1-K1-G11

Method	BLASTX
NCBI GI	g1628583
BLAST score	621
E value	7.0e-65
Match length	120
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148106
Seq. ID	LIB3168-100-P1-K1-G12
Method	BLASTX
NCBI GI	g1628583
BLAST score	763
E value	2.0e-81
Match length	151
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148107
Seq. ID	LIB3168-100-P1-K1-G3
Method	BLASTX
NCBI GI	g1628583
BLAST score	605
E value	6.0e-63
Match length	120
% identity	97
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148108
Seq. ID	LIB3168-100-P1-K1-G4
Method	BLASTN
NCBI GI	g511598
BLAST score	129
E value	2.0e-66
Match length	241
% identity	84
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	148109
Seq. ID	LIB3168-100-P1-K1-G5
Method	BLASTX
NCBI GI	g1628583
BLAST score	485
E value	5.0e-49
Match length	128
% identity	76
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148110
Seq. ID	LIB3168-100-P1-K1-G6
Method	BLASTX
NCBI GI	g3935137
BLAST score	243
E value	1.0e-20
Match length	48
% identity	98
NCBI Description	(AC005106) T25N20.1 [Arabidopsis thaliana]

Seq. No.	148111
Seq. ID	LIB3168-100-P1-K1-G7
Method	BLASTX
NCBI GI	g4678327
BLAST score	437
E value	2.0e-43
Match length	90
% identity	92
NCBI Description	(AL049658) putative cyclic nucleotide-gated channel [Arabidopsis thaliana]

Seq. No.	148112
Seq. ID	LIB3168-100-P1-K1-G8
Method	BLASTX
NCBI GI	g112682
BLAST score	680
E value	8.0e-72
Match length	141
% identity	91
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148113
Seq. ID	LIB3168-100-P1-K1-G9
Method	BLASTX
NCBI GI	g2352921
BLAST score	269
E value	1.0e-23
Match length	94
% identity	79
NCBI Description	(AF012862) cytosolic glucose-6-phosphate dehydrogenase 1 [Petroselinum crispum]

Seq. No.	148114
Seq. ID	LIB3168-100-P1-K1-H1
Method	BLASTX
NCBI GI	g112681
BLAST score	643
E value	2.0e-67
Match length	148
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148115
Seq. ID	LIB3168-100-P1-K1-H10
Method	BLASTX
NCBI GI	g112737
BLAST score	605
E value	5.0e-63
Match length	143
% identity	82
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	148116
Seq. ID	LIB3168-100-P1-K1-H12
Method	BLASTX
NCBI GI	g1628583
BLAST score	227
E value	6.0e-19
Match length	48
% identity	92
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148117
Seq. ID	LIB3168-100-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	788
E value	2.0e-84
Match length	151
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148118
Seq. ID	LIB3168-100-P1-K1-H4
Method	BLASTX
NCBI GI	g112737
BLAST score	617
E value	2.0e-64
Match length	128
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No.	148119
Seq. ID	LIB3168-100-P1-K1-H6
Method	BLASTX
NCBI GI	g1628583
BLAST score	121
E value	2.0e-55
Match length	118
% identity	95
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148120
Seq. ID	LIB3168-100-P1-K1-H7
Method	BLASTN
NCBI GI	g4159710
BLAST score	453
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	148121
Seq. ID	LIB3168-100-P1-K1-H8
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148122
Seq. ID	LIB3168-100-P1-K1-H9
Method	BLASTX
NCBI GI	g2924509
BLAST score	208
E value	2.0e-16
Match length	84
% identity	48
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	148123
Seq. ID	LIB3175-001-Q1-K1-A1
Method	BLASTN
NCBI GI	g4263694
BLAST score	227
E value	1.0e-124
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148124
Seq. ID	LIB3175-001-Q1-K1-A10
Method	BLASTX
NCBI GI	g2497753
BLAST score	263
E value	6.0e-23
Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	148125
Seq. ID	LIB3175-001-Q1-K1-A12
Method	BLASTX
NCBI GI	g2462746
BLAST score	212
E value	4.0e-17
Match length	52
% identity	87
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	148126
Seq. ID	LIB3175-001-Q1-K1-A2
Method	BLASTX
NCBI GI	g166765
BLAST score	621
E value	6.0e-65
Match length	118
% identity	100
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	148127
Seq. ID	LIB3175-001-Q1-K1-A3
Method	BLASTX
NCBI GI	g132074
BLAST score	550
E value	1.0e-56
Match length	104
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	148128
Seq. ID	LIB3175-001-Q1-K1-A4
Method	BLASTX
NCBI GI	g3885943
BLAST score	605
E value	5.0e-63
Match length	119
% identity	100
NCBI Description	(AF095455) PII protein [Arabidopsis thaliana]

>gi_4558559_gb_AAD22652.1_AC007138_16 (AC007138) P II nitrogen sensing protein GLB I [Arabidopsis thaliana]

Seq. No.	148129
Seq. ID	LIB3175-001-Q1-K1-A6
Method	BLASTN
NCBI GI	g3702730
BLAST score	42
E value	2.0e-14
Match length	205
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No.	148130
Seq. ID	LIB3175-001-Q1-K1-A7
Method	BLASTX
NCBI GI	g16245
BLAST score	649
E value	3.0e-68
Match length	130
% identity	97
NCBI Description	(X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana]

Seq. No.	148131
Seq. ID	LIB3175-001-Q1-K1-A9
Method	BLASTX
NCBI GI	g3860277
BLAST score	71
E value	2.0e-34
Match length	80
% identity	98
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	148132
Seq. ID	LIB3175-001-Q1-K1-B1
Method	BLASTX
NCBI GI	g2129538
BLAST score	320
E value	1.0e-29
Match length	62
% identity	100
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	148133
Seq. ID	LIB3175-001-Q1-K1-B10
Method	BLASTN
NCBI GI	g3650026
BLAST score	202
E value	1.0e-110
Match length	222
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148134
Seq. ID	LIB3175-001-Q1-K1-B11
Method	BLASTX
NCBI GI	g2342734
BLAST score	614
E value	7.0e-67
Match length	121
% identity	95
NCBI Description	(AC002341) DNA-binding protein isolog [Arabidopsis thaliana]

Seq. No.	148135
Seq. ID	LIB3175-001-Q1-K1-B12
Method	BLASTX
NCBI GI	g4544412
BLAST score	237
E value	7.0e-20
Match length	84
% identity	45
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148136
Seq. ID	LIB3175-001-Q1-K1-B3
Method	BLASTN
NCBI GI	g2961335
BLAST score	396
E value	0.0e+00
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	148137
Seq. ID	LIB3175-001-Q1-K1-B4
Method	BLASTN
NCBI GI	g4263694
BLAST score	207
E value	1.0e-113
Match length	375
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148138
Seq. ID	LIB3175-001-Q1-K1-B5
Method	BLASTX
NCBI GI	g2827636
BLAST score	514
E value	2.0e-52
Match length	106
% identity	98
NCBI Description	(AL021636) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No. 148139

Seq. ID	LIB3175-001-Q1-K1-B6
Method	BLASTN
NCBI GI	g3080352
BLAST score	19
E value	1.3e+00
Match length	389
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	148140
Seq. ID	LIB3175-001-Q1-K1-B7
Method	BLASTN
NCBI GI	g3869064
BLAST score	51
E value	1.0e-19
Match length	148
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1013, complete sequence [Arabidopsis thaliana]

Seq. No.	148141
Seq. ID	LIB3175-001-Q1-K1-B8
Method	BLASTX
NCBI GI	g2262167
BLAST score	670
E value	1.0e-70
Match length	128
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	148142
Seq. ID	LIB3175-001-Q1-K1-B9
Method	BLASTX
NCBI GI	g2660677
BLAST score	702
E value	2.0e-74
Match length	132
% identity	100
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	148143
Seq. ID	LIB3175-001-Q1-K1-C1
Method	BLASTX
NCBI GI	g2497542
BLAST score	598
E value	3.0e-62
Match length	132
% identity	87
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	148144
Seq. ID	LIB3175-001-Q1-K1-C10

Method	BLASTX
NCBI GI	g3879145
BLAST score	195
E value	6.0e-15
Match length	73
% identity	51
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	148145
Seq. ID	LIB3175-001-Q1-K1-C11
Method	BLASTN
NCBI GI	g556473
BLAST score	298
E value	1.0e-167
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for ERD14 protein, complete cds

Seq. No.	148146
Seq. ID	LIB3175-001-Q1-K1-C12
Method	BLASTX
NCBI GI	g3860277
BLAST score	410
E value	3.0e-40
Match length	81
% identity	100
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	148147
Seq. ID	LIB3175-001-Q1-K1-C4
Method	BLASTX
NCBI GI	g4107099
BLAST score	302
E value	9.0e-34
Match length	90
% identity	80
NCBI Description	(AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No.	148148
Seq. ID	LIB3175-001-Q1-K1-C5
Method	BLASTN
NCBI GI	g3046852
BLAST score	302
E value	1.0e-169
Match length	404
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	148149
Seq. ID	LIB3175-001-Q1-K1-C6

Method	BLASTN
NCBI GI	g4757395
BLAST score	359
E value	0.0e+00
Match length	390
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	148150
Seq. ID	LIB3175-001-Q1-K1-C8
Method	BLASTX
NCBI GI	g4559339
BLAST score	153
E value	5.0e-10
Match length	58
% identity	59
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	148151
Seq. ID	LIB3175-001-Q1-K1-C9
Method	BLASTX
NCBI GI	g2146734
BLAST score	212
E value	6.0e-17
Match length	37
% identity	92
NCBI Description	GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana

Seq. No.	148152
Seq. ID	LIB3175-001-Q1-K1-D1
Method	BLASTX
NCBI GI	g3738261
BLAST score	288
E value	7.0e-26
Match length	98
% identity	68
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	148153
Seq. ID	LIB3175-001-Q1-K1-D10
Method	BLASTX
NCBI GI	g4115377
BLAST score	368
E value	3.0e-35
Match length	109
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	148154
Seq. ID	LIB3175-001-Q1-K1-D11
Method	BLASTN
NCBI GI	g4309747
BLAST score	292
E value	1.0e-163

Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148155
Seq. ID	LIB3175-001-Q1-K1-D12
Method	BLASTX
NCBI GI	g2130051
BLAST score	379
E value	1.0e-36
Match length	100
% identity	70
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	148156
Seq. ID	LIB3175-001-Q1-K1-D2
Method	BLASTX
NCBI GI	g1169476
BLAST score	570
E value	6.0e-59
Match length	120
% identity	93
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	148157
Seq. ID	LIB3175-001-Q1-K1-D3
Method	BLASTN
NCBI GI	g4049332
BLAST score	284
E value	1.0e-158
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	148158
Seq. ID	LIB3175-001-Q1-K1-D5
Method	BLASTX
NCBI GI	g4678935
BLAST score	525
E value	1.0e-53
Match length	104
% identity	98
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	148159
Seq. ID	LIB3175-001-Q1-K1-D6
Method	BLASTN
NCBI GI	g3176695
BLAST score	208
E value	1.0e-113

Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	148160
Seq. ID	LIB3175-001-Q1-K1-D8
Method	BLASTX
NCBI GI	g99752
BLAST score	438
E value	2.0e-43
Match length	113
% identity	84
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	148161
Seq. ID	LIB3175-001-Q1-K1-D9
Method	BLASTX
NCBI GI	g2738248
BLAST score	535
E value	7.0e-55
Match length	102
% identity	100
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	148162
Seq. ID	LIB3175-001-Q1-K1-E1
Method	BLASTX
NCBI GI	g1550740
BLAST score	577
E value	9.0e-60
Match length	111
% identity	100
NCBI Description	(Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No.	148163
Seq. ID	LIB3175-001-Q1-K1-E10
Method	BLASTX
NCBI GI	g4006834
BLAST score	614
E value	4.0e-64
Match length	120
% identity	100
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	148164
Seq. ID	LIB3175-001-Q1-K1-E11
Method	BLASTX
NCBI GI	g116527
BLAST score	556
E value	3.0e-57
Match length	120
% identity	87

NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196) >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]
Seq. No.	148165
Seq. ID	LIB3175-001-Q1-K1-E3
Method	BLASTX
NCBI GI	g4589398
BLAST score	373
E value	7.0e-36
Match length	81
% identity	81
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
Seq. No.	148166
Seq. ID	LIB3175-001-Q1-K1-E4
Method	BLASTX
NCBI GI	g2499542
BLAST score	515
E value	2.0e-52
Match length	123
% identity	78
NCBI Description	IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP) >gi_1218042 (U48448) secreted purple acid phosphatase precursor [Arabidopsis thaliana]
Seq. No.	148167
Seq. ID	LIB3175-001-Q1-K1-E5
Method	BLASTX
NCBI GI	g231587
BLAST score	64
E value	2.0e-40
Match length	115
% identity	76
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]
Seq. No.	148168
Seq. ID	LIB3175-001-Q1-K1-E6
Method	BLASTX
NCBI GI	g3201632
BLAST score	285
E value	1.0e-25
Match length	104
% identity	54
NCBI Description	(AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.	148169
Seq. ID	LIB3175-001-Q1-K1-E7
Method	BLASTX
NCBI GI	g3123271
BLAST score	499
E value	1.0e-50

Match length	114
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	148170
Seq. ID	LIB3175-001-Q1-K1-E8
Method	BLASTX
NCBI GI	g399013
BLAST score	478
E value	4.0e-48
Match length	93
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	148171
Seq. ID	LIB3175-001-Q1-K1-E9
Method	BLASTX
NCBI GI	g2245030
BLAST score	410
E value	3.0e-40
Match length	113
% identity	74
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	148172
Seq. ID	LIB3175-001-Q1-K1-F1
Method	BLASTX
NCBI GI	g3763919
BLAST score	517
E value	9.0e-53
Match length	125
% identity	82
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana] >gi_4531436_gb_AAD22121.1_AC006224_3 (AC006224) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	148173
Seq. ID	LIB3175-001-Q1-K1-F10
Method	BLASTX
NCBI GI	g1237102
BLAST score	207
E value	2.0e-16
Match length	87
% identity	53
NCBI Description	(L40358) calmodulin-binding protein [Arabidopsis thaliana] >gi_1589171_prf__2210340A calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	148174
Seq. ID	LIB3175-001-Q1-K1-F11
Method	BLASTX
NCBI GI	g2252840
BLAST score	470
E value	3.0e-47
Match length	125
% identity	67
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	148175
Seq. ID	LIB3175-001-Q1-K1-F12
Method	BLASTX
NCBI GI	g1550740
BLAST score	568
E value	1.0e-58
Match length	110
% identity	99
NCBI Description	(Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No.	148176
Seq. ID	LIB3175-001-Q1-K1-F2
Method	BLASTN
NCBI GI	g3869073
BLAST score	120
E value	6.0e-61
Match length	337
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	148177
Seq. ID	LIB3175-001-Q1-K1-F3
Method	BLASTX
NCBI GI	g2117612
BLAST score	717
E value	3.0e-76
Match length	131
% identity	100
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	148178
Seq. ID	LIB3175-001-Q1-K1-F4
Method	BLASTX
NCBI GI	g1669387
BLAST score	439
E value	1.0e-43
Match length	82
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	148179
Seq. ID	LIB3175-001-Q1-K1-F5
Method	BLASTX
NCBI GI	g115778
BLAST score	85

E value	9.0e-16
Match length	79
% identity	65
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_282896_pir__S22511 chlorophyll a/b-binding protein (cab-1) - white mustard >gi_21138_emb_CAA34459_ (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi_21140_emb_CAA33903_ (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]

Seq. No.	148180
Seq. ID	LIB3175-001-Q1-K1-F6
Method	BLASTX
NCBI GI	g1246019
BLAST score	576
E value	1.0e-59
Match length	115
% identity	96
NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No.	148181
Seq. ID	LIB3175-001-Q1-K1-F7
Method	BLASTN
NCBI GI	g4220510
BLAST score	220
E value	1.0e-120
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	148182
Seq. ID	LIB3175-001-Q1-K1-F8
Method	BLASTX
NCBI GI	g4538943
BLAST score	493
E value	6.0e-50
Match length	126
% identity	79
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	148183
Seq. ID	LIB3175-001-Q1-K1-F9
Method	BLASTX
NCBI GI	g1718097
BLAST score	322
E value	7.0e-30
Match length	95
% identity	60
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	148184
Seq. ID	LIB3175-001-Q1-K1-G1
Method	BLASTX
NCBI GI	g4262180
BLAST score	699
E value	4.0e-74
Match length	131
% identity	99
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	148185
Seq. ID	LIB3175-001-Q1-K1-G11
Method	BLASTX
NCBI GI	g1698582
BLAST score	253
E value	9.0e-22
Match length	75
% identity	72
NCBI Description	(U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No.	148186
Seq. ID	LIB3175-001-Q1-K1-G12
Method	BLASTN
NCBI GI	g2924653
BLAST score	228
E value	1.0e-125
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	148187
Seq. ID	LIB3175-001-Q1-K1-G3
Method	BLASTX
NCBI GI	g1350680
BLAST score	662
E value	1.0e-69
Match length	126
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	148188
Seq. ID	LIB3175-001-Q1-K1-G4
Method	BLASTX
NCBI GI	g1695719
BLAST score	569
E value	8.0e-59
Match length	135
% identity	86
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No.	148189
Seq. ID	LIB3175-001-Q1-K1-G5
Method	BLASTX
NCBI GI	g417381
BLAST score	629
E value	7.0e-66

Match length	125
% identity	98
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	148190
Seq. ID	LIB3175-001-Q1-K1-G6
Method	BLASTX
NCBI GI	g4586265
BLAST score	531
E value	2.0e-54
Match length	120
% identity	81
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148191
Seq. ID	LIB3175-001-Q1-K1-G7
Method	BLASTX
NCBI GI	g2129759
BLAST score	453
E value	3.0e-45
Match length	90
% identity	100
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	148192
Seq. ID	LIB3175-001-Q1-K1-G8
Method	BLASTN
NCBI GI	g3367567
BLAST score	311
E value	1.0e-175
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	148193
Seq. ID	LIB3175-001-Q1-K1-G9
Method	BLASTX
NCBI GI	g112741
BLAST score	661
E value	1.0e-69
Match length	123
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	148194
Seq. ID	LIB3175-001-Q1-K1-H10

Method	BLASTX
NCBI GI	g4567249
BLAST score	518
E value	7.0e-53
Match length	113
% identity	87
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148195
Seq. ID	LIB3175-001-Q1-K1-H11
Method	BLASTX
NCBI GI	g120667
BLAST score	518
E value	6.0e-53
Match length	116
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	148196
Seq. ID	LIB3175-001-Q1-K1-H12
Method	BLASTN
NCBI GI	g2252823
BLAST score	247
E value	1.0e-136
Match length	296
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	148197
Seq. ID	LIB3175-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g3850568
BLAST score	475
E value	8.0e-48
Match length	106
% identity	90
NCBI Description	(AC005278) Similar to hypothetical protein SPAC2F7.14c gi_1052797 from Schizosaccharomyces pombe cosmid gb_Z50142. [Arabidopsis thaliana]

Seq. No.	148198
Seq. ID	LIB3175-001-Q1-K1-H3
Method	BLASTX
NCBI GI	g4262186
BLAST score	521
E value	2.0e-53
Match length	105
% identity	95
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	148199
Seq. ID	LIB3175-001-Q1-K1-H4
Method	BLASTX
NCBI GI	g4538963
BLAST score	460
E value	5.0e-46
Match length	117
% identity	77
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	148200
Seq. ID	LIB3175-001-Q1-K1-H5
Method	BLASTN
NCBI GI	g4581084
BLAST score	283
E value	1.0e-158
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	148201
Seq. ID	LIB3175-001-Q1-K1-H6
Method	BLASTX
NCBI GI	g2347192
BLAST score	289
E value	1.0e-54
Match length	113
% identity	95
NCBI Description	(AC002338) spliceosomal protein U2B isolog [Arabidopsis thaliana]

Seq. No.	148202
Seq. ID	LIB3175-001-Q1-K1-H7
Method	BLASTX
NCBI GI	g4218123
BLAST score	336
E value	2.0e-31
Match length	125
% identity	58
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	148203
Seq. ID	LIB3175-002-Q1-K1-A10
Method	BLASTX
NCBI GI	g1669389
BLAST score	252
E value	7.0e-22
Match length	47
% identity	100
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	148204
Seq. ID	LIB3175-002-Q1-K1-A11

Method	BLASTN
NCBI GI	g1069997
BLAST score	132
E value	4.0e-68
Match length	264
% identity	95
NCBI Description	B.napus chloroplast accD gene

Seq. No.	148205
Seq. ID	LIB3175-002-Q1-K1-A2
Method	BLASTX
NCBI GI	g2911055
BLAST score	317
E value	1.0e-29
Match length	87
% identity	72
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	148206
Seq. ID	LIB3175-002-Q1-K1-A4
Method	BLASTN
NCBI GI	g2288979
BLAST score	293
E value	1.0e-164
Match length	297
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148207
Seq. ID	LIB3175-002-Q1-K1-A6
Method	BLASTN
NCBI GI	g4519191
BLAST score	180
E value	8.0e-97
Match length	234
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	148208
Seq. ID	LIB3175-002-Q1-K1-A8
Method	BLASTX
NCBI GI	g2129578
BLAST score	274
E value	2.0e-24
Match length	55
% identity	95
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	148209
Seq. ID	LIB3175-002-Q1-K1-A9
Method	BLASTX

NCBI GI	g2781394
BLAST score	362
E value	8.0e-35
Match length	75
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	148210
Seq. ID	LIB3175-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g3582341
BLAST score	294
E value	8.0e-27
Match length	96
% identity	64
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	148211
Seq. ID	LIB3175-002-Q1-K1-B11
Method	BLASTN
NCBI GI	g4589411
BLAST score	272
E value	1.0e-151
Match length	296
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	148212
Seq. ID	LIB3175-002-Q1-K1-B12
Method	BLASTX
NCBI GI	g3176874
BLAST score	398
E value	5.0e-39
Match length	79
% identity	97
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	148213
Seq. ID	LIB3175-002-Q1-K1-B2
Method	BLASTX
NCBI GI	g3914740
BLAST score	387
E value	9.0e-38
Match length	84
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	148214
Seq. ID	LIB3175-002-Q1-K1-B4
Method	BLASTN
NCBI GI	g4757403
BLAST score	128
E value	9.0e-66

Match length	266
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	148215
Seq. ID	LIB3175-002-Q1-K1-B5
Method	BLASTX
NCBI GI	g2088652
BLAST score	423
E value	6.0e-42
Match length	94
% identity	86
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	148216
Seq. ID	LIB3175-002-Q1-K1-B6
Method	BLASTX
NCBI GI	g4432860
BLAST score	483
E value	6.0e-49
Match length	99
% identity	20
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	148217
Seq. ID	LIB3175-002-Q1-K1-B7
Method	BLASTX
NCBI GI	g115783
BLAST score	324
E value	2.0e-30
Match length	62
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	148218
Seq. ID	LIB3175-002-Q1-K1-B9
Method	BLASTX
NCBI GI	g4544399
BLAST score	169
E value	4.0e-12
Match length	74
% identity	41
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	148219
Seq. ID	LIB3175-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g4263704

BLAST score	204
E value	3.0e-16
Match length	72
% identity	53
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	148220
Seq. ID	LIB3175-002-Q1-K1-C10
Method	BLASTX
NCBI GI	g2623962
BLAST score	273
E value	2.0e-24
Match length	55
% identity	95
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	148221
Seq. ID	LIB3175-002-Q1-K1-C11
Method	BLASTX
NCBI GI	g1172977
BLAST score	439
E value	8.0e-44
Match length	90
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	148222
Seq. ID	LIB3175-002-Q1-K1-C2
Method	BLASTN
NCBI GI	g3080430
BLAST score	294
E value	1.0e-165
Match length	298
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	148223
Seq. ID	LIB3175-002-Q1-K1-C3
Method	BLASTX
NCBI GI	g3421123
BLAST score	472
E value	1.0e-47
Match length	95
% identity	98
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	148224
Seq. ID	LIB3175-002-Q1-K1-C4
Method	BLASTN
NCBI GI	g4757403
BLAST score	140
E value	6.0e-73

Match length 300
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No. 148225
Seq. ID LIB3175-002-Q1-K1-C6
Method BLASTX
NCBI GI g113026
BLAST score 271
E value 4.0e-24
Match length 99
% identity 59
NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No. 148226
Seq. ID LIB3175-002-Q1-K1-C7
Method BLASTN
NCBI GI g4519187
BLAST score 137
E value 2.0e-71
Match length 137
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No. 148227
Seq. ID LIB3175-002-Q1-K1-C8
Method BLASTX
NCBI GI g4191778
BLAST score 392
E value 3.0e-38
Match length 98
% identity 76
NCBI Description (AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No. 148228
Seq. ID LIB3175-002-Q1-K1-C9
Method BLASTX
NCBI GI g3806098
BLAST score 461
E value 2.0e-46
Match length 84
% identity 100
NCBI Description (AF079100) arginine-tRNA-protein transferase 1; Ate1p [Arabidopsis thaliana]

Seq. No. 148229
Seq. ID LIB3175-002-Q1-K1-D1
Method BLASTN

NCBI GI	g2264317
BLAST score	111
E value	1.0e-55
Match length	118
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	148230
Seq. ID	LIB3175-002-Q1-K1-D10
Method	BLASTX
NCBI GI	g1362007
BLAST score	457
E value	6.0e-46
Match length	87
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	148231
Seq. ID	LIB3175-002-Q1-K1-D12
Method	BLASTN
NCBI GI	g4490734
BLAST score	204
E value	1.0e-111
Match length	298
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	148232
Seq. ID	LIB3175-002-Q1-K1-D3
Method	BLASTX
NCBI GI	g3122387
BLAST score	381
E value	5.0e-37
Match length	82
% identity	88
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394229 (AF016846) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	148233
Seq. ID	LIB3175-002-Q1-K1-D4
Method	BLASTN
NCBI GI	g3046852
BLAST score	213
E value	1.0e-116
Match length	300
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	148234
Seq. ID	LIB3175-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g2129583

BLAST score 388
E value 8.0e-38
Match length 92
% identity 86
NCBI Description ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_ (X94248) ferritin [Arabidopsis thaliana]

Seq. No. 148235
Seq. ID LIB3175-002-Q1-K1-D6
Method BLASTX
NCBI GI g4585882
BLAST score 284
E value 1.0e-25
Match length 56
% identity 100
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 148236
Seq. ID LIB3175-002-Q1-K1-D8
Method BLASTN
NCBI GI g450879
BLAST score 78
E value 2.0e-36
Match length 90
% identity 97
NCBI Description A.thaliana hsc70-1 gene

Seq. No. 148237
Seq. ID LIB3175-002-Q1-K1-D9
Method BLASTN
NCBI GI g3702728
BLAST score 38
E value 4.0e-12
Match length 94
% identity 85
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No. 148238
Seq. ID LIB3175-002-Q1-K1-E10
Method BLASTX
NCBI GI g2702268
BLAST score 414
E value 7.0e-41
Match length 79
% identity 100
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 148239
Seq. ID LIB3175-002-Q1-K1-E12
Method BLASTN
NCBI GI g3702731
BLAST score 296
E value 1.0e-166
Match length 296
% identity 100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	148240
Seq. ID	LIB3175-002-Q1-K1-E2
Method	BLASTX
NCBI GI	g4263525
BLAST score	403
E value	1.0e-39
Match length	99
% identity	80
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	148241
Seq. ID	LIB3175-002-Q1-K1-E3
Method	BLASTX
NCBI GI	g2088654
BLAST score	340
E value	3.0e-32
Match length	78
% identity	86
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	148242
Seq. ID	LIB3175-002-Q1-K1-E4
Method	BLASTX
NCBI GI	g462181
BLAST score	150
E value	6.0e-10
Match length	83
% identity	36
NCBI Description	GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_294445 (L12410) unnamed protein product [Pyrococcus furiosus]

Seq. No.	148243
Seq. ID	LIB3175-002-Q1-K1-E5
Method	BLASTN
NCBI GI	g4585952
BLAST score	294
E value	1.0e-165
Match length	298
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	148244
Seq. ID	LIB3175-002-Q1-K1-E6
Method	BLASTX
NCBI GI	g3875246
BLAST score	241
E value	1.0e-20
Match length	86
% identity	52
NCBI Description	(Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No.	148245
Seq. ID	LIB3175-002-Q1-K1-E7
Method	BLASTN
NCBI GI	g4220640
BLAST score	210
E value	1.0e-114
Match length	294
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	148246
Seq. ID	LIB3175-002-Q1-K1-E8
Method	BLASTX
NCBI GI	g4741940
BLAST score	540
E value	1.0e-55
Match length	97
% identity	65
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	148247
Seq. ID	LIB3175-002-Q1-K1-E9
Method	BLASTX
NCBI GI	g3892050
BLAST score	220
E value	4.0e-18
Match length	62
% identity	69
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148248
Seq. ID	LIB3175-002-Q1-K1-F1
Method	BLASTN
NCBI GI	g3241916
BLAST score	70
E value	2.0e-31
Match length	123
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	148249
Seq. ID	LIB3175-002-Q1-K1-F10
Method	BLASTN
NCBI GI	g3063690
BLAST score	278
E value	1.0e-155
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	148250
Seq. ID	LIB3175-002-Q1-K1-F11
Method	BLASTX
NCBI GI	g3176685
BLAST score	519
E value	3.0e-53
Match length	98
% identity	100
NCBI Description	(AC003671) Strong similarity to spermidine synthase 1, gb_Y08252 and possibly closer similarity to spermidine synthase 2 gb_Y08253 from Datura stramonium. ESTs gb_N38155, gb_T41738, gb_AA597626, gb_AA712967 and gb_AA712346 come from this ge

Seq. No.	148251
Seq. ID	LIB3175-002-Q1-K1-F12
Method	BLASTN
NCBI GI	g1765898
BLAST score	227
E value	1.0e-125
Match length	227
% identity	100
NCBI Description	A.thaliana mRNA for Spot 3 protein

Seq. No.	148252
Seq. ID	LIB3175-002-Q1-K1-F2
Method	BLASTX
NCBI GI	g2586127
BLAST score	243
E value	8.0e-21
Match length	94
% identity	52
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	148253
Seq. ID	LIB3175-002-Q1-K1-F6
Method	BLASTX
NCBI GI	g1703220
BLAST score	453
E value	2.0e-45
Match length	97
% identity	90
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	148254
Seq. ID	LIB3175-002-Q1-K1-F7
Method	BLASTX
NCBI GI	g2130051
BLAST score	214
E value	2.0e-17
Match length	70
% identity	59
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	148255
Seq. ID	LIB3175-002-Q1-K1-F8
Method	BLASTX
NCBI GI	g2129579
BLAST score	474
E value	6.0e-48
Match length	90
% identity	100
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	148256
Seq. ID	LIB3175-002-Q1-K1-F9
Method	BLASTX
NCBI GI	g1109699
BLAST score	506
E value	1.0e-51
Match length	96
% identity	100
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	148257
Seq. ID	LIB3175-002-Q1-K1-G1
Method	BLASTN
NCBI GI	g3241917
BLAST score	69
E value	1.0e-30
Match length	157
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	148258
Seq. ID	LIB3175-002-Q1-K1-G11
Method	BLASTX
NCBI GI	g115783
BLAST score	396
E value	9.0e-39
Match length	74
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	148259
Seq. ID	LIB3175-002-Q1-K1-G12
Method	BLASTX
NCBI GI	g629669
BLAST score	169
E value	2.0e-12
Match length	61
% identity	51
NCBI Description	hypothetical protein - tomato

Seq. No.	148260

Seq. ID	LIB3175-002-Q1-K1-G2
Method	BLASTX
NCBI GI	g4538963
BLAST score	278
E value	5.0e-25
Match length	84
% identity	68
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	148261
Seq. ID	LIB3175-002-Q1-K1-G5
Method	BLASTX
NCBI GI	g267073
BLAST score	382
E value	4.0e-37
Match length	70
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	148262
Seq. ID	LIB3175-002-Q1-K1-G6
Method	BLASTX
NCBI GI	g2245000
BLAST score	430
E value	1.0e-42
Match length	85
% identity	100
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148263
Seq. ID	LIB3175-002-Q1-K1-G7
Method	BLASTX
NCBI GI	g2459421
BLAST score	438
E value	1.0e-43
Match length	97
% identity	88
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	148264
Seq. ID	LIB3175-002-Q1-K1-G8
Method	BLASTN
NCBI GI	g4262276
BLAST score	79
E value	3.0e-37
Match length	79
% identity	100
NCBI Description	Arabidopsis thaliana gamma-glutamylcysteine synthetase gene, complete cds

Seq. No.	148265

Seq. ID	LIB3175-002-Q1-K1-H1
Method	BLASTN
NCBI GI	g4589950
BLAST score	185
E value	1.0e-100
Match length	300
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	148266
Seq. ID	LIB3175-002-Q1-K1-H10
Method	BLASTX
NCBI GI	g4544456
BLAST score	434
E value	3.0e-43
Match length	97
% identity	89
NCBI Description	(AC006592) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148267
Seq. ID	LIB3175-002-Q1-K1-H11
Method	BLASTX
NCBI GI	g1619602
BLAST score	217
E value	9.0e-18
Match length	54
% identity	78
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	148268
Seq. ID	LIB3175-002-Q1-K1-H12
Method	BLASTN
NCBI GI	g4455321
BLAST score	75
E value	1.0e-34
Match length	114
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	148269
Seq. ID	LIB3175-002-Q1-K1-H2
Method	BLASTN
NCBI GI	g4220632
BLAST score	136
E value	2.0e-70
Match length	232
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	148270
Seq. ID	LIB3175-002-Q1-K1-H5
Method	BLASTX
NCBI GI	g3024702
BLAST score	166

E value	8.0e-12
Match length	47
% identity	70
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) >gi_1871210 (U91327) T-complex protein 1, Beta subunit (TCP-1-BETA) [Homo sapiens]

Seq. No.	148271
Seq. ID	LIB3175-002-Q1-K1-H7
Method	BLASTN
NCBI GI	g2351062
BLAST score	272
E value	1.0e-151
Match length	276
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	148272
Seq. ID	LIB3175-002-Q1-K1-H9
Method	BLASTX
NCBI GI	g417381
BLAST score	341
E value	2.0e-32
Match length	94
% identity	76
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	148273
Seq. ID	LIB3175-003-P1-K1-A11
Method	BLASTX
NCBI GI	g2244919
BLAST score	506
E value	2.0e-51
Match length	131
% identity	85
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148274
Seq. ID	LIB3175-003-P1-K1-A12
Method	BLASTX
NCBI GI	g629541
BLAST score	661
E value	2.0e-69
Match length	140
% identity	93
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	148275
Seq. ID	LIB3175-003-P1-K1-A2
Method	BLASTX
NCBI GI	g4587615
BLAST score	406

E value	1.0e-39
Match length	123
% identity	67
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	148276
Seq. ID	LIB3175-003-P1-K1-A3
Method	BLASTX
NCBI GI	g421826
BLAST score	667
E value	3.0e-70
Match length	144
% identity	88
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	148277
Seq. ID	LIB3175-003-P1-K1-A4
Method	BLASTN
NCBI GI	g4733953
BLAST score	229
E value	1.0e-126
Match length	288
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	148278
Seq. ID	LIB3175-003-P1-K1-A5
Method	BLASTX
NCBI GI	g3790548
BLAST score	781
E value	1.0e-83
Match length	150
% identity	99
NCBI Description	(AF064064) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	148279
Seq. ID	LIB3175-003-P1-K1-A6
Method	BLASTX
NCBI GI	g3123188
BLAST score	729
E value	2.0e-77
Match length	142
% identity	99
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	148280
Seq. ID	LIB3175-003-P1-K1-A9
Method	BLASTX
NCBI GI	g4063749
BLAST score	170

E value	5.0e-12
Match length	68
% identity	26
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148281
Seq. ID	LIB3175-003-P1-K1-B1
Method	BLASTN
NCBI GI	g4539331
BLAST score	67
E value	2.0e-29
Match length	203
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	148282
Seq. ID	LIB3175-003-P1-K1-B10
Method	BLASTN
NCBI GI	g2351066
BLAST score	151
E value	3.0e-79
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	148283
Seq. ID	LIB3175-003-P1-K1-B11
Method	BLASTX
NCBI GI	g1773330
BLAST score	634
E value	2.0e-66
Match length	141
% identity	87
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	148284
Seq. ID	LIB3175-003-P1-K1-B12
Method	BLASTX
NCBI GI	g3540199
BLAST score	475
E value	1.0e-47
Match length	139
% identity	73
NCBI Description	(AC004260) Putative monosaccharide transport protein [Arabidopsis thaliana]

Seq. No.	148285
Seq. ID	LIB3175-003-P1-K1-B2
Method	BLASTN
NCBI GI	g2281081
BLAST score	41
E value	1.0e-13
Match length	199
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148286
Seq. ID	LIB3175-003-P1-K1-B3
Method	BLASTX
NCBI GI	g2633727
BLAST score	191
E value	2.0e-14
Match length	106
% identity	42
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	148287
Seq. ID	LIB3175-003-P1-K1-B4
Method	BLASTN
NCBI GI	g4263753
BLAST score	269
E value	1.0e-149
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	148288
Seq. ID	LIB3175-003-P1-K1-B5
Method	BLASTX
NCBI GI	g3687252
BLAST score	673
E value	6.0e-71
Match length	137
% identity	37
NCBI Description	(AC005169) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No.	148289
Seq. ID	LIB3175-003-P1-K1-B6
Method	BLASTN
NCBI GI	g3688169
BLAST score	210
E value	1.0e-115
Match length	228
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	148290
Seq. ID	LIB3175-003-P1-K1-B7
Method	BLASTX
NCBI GI	g2459443
BLAST score	673
E value	5.0e-71
Match length	133
% identity	97
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No. 148291

Seq. ID	LIB3175-003-P1-K1-B8
Method	BLASTN
NCBI GI	g2947056
BLAST score	277
E value	1.0e-154
Match length	466
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148292
Seq. ID	LIB3175-003-P1-K1-B9
Method	BLASTN
NCBI GI	g2827538
BLAST score	396
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	148293
Seq. ID	LIB3175-003-P1-K1-C1
Method	BLASTX
NCBI GI	g2244896
BLAST score	575
E value	1.0e-59
Match length	127
% identity	88
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	148294
Seq. ID	LIB3175-003-P1-K1-C10
Method	BLASTX
NCBI GI	g3157937
BLAST score	657
E value	1.0e-68
Match length	150
% identity	86
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	148295
Seq. ID	LIB3175-003-P1-K1-C11
Method	BLASTX
NCBI GI	g3402751
BLAST score	43
E value	8.0e-72
Match length	146
% identity	51
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 148296

Seq. ID	LIB3175-003-P1-K1-C2
Method	BLASTX
NCBI GI	g2633727
BLAST score	192
E value	1.0e-14
Match length	103
% identity	42
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	148297
Seq. ID	LIB3175-003-P1-K1-C3
Method	BLASTN
NCBI GI	g4063735
BLAST score	125
E value	8.0e-64
Match length	377
% identity	99
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	148298
Seq. ID	LIB3175-003-P1-K1-C4
Method	BLASTX
NCBI GI	g2244904
BLAST score	570
E value	7.0e-59
Match length	136
% identity	91
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	148299
Seq. ID	LIB3175-003-P1-K1-C5
Method	BLASTX
NCBI GI	g2058282
BLAST score	518
E value	9.0e-53
Match length	125
% identity	82
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	148300
Seq. ID	LIB3175-003-P1-K1-C6
Method	BLASTX
NCBI GI	g1076708
BLAST score	698
E value	7.0e-74
Match length	140
% identity	25
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus

annuus]

Seq. No.	148301
Seq. ID	LIB3175-003-P1-K1-C7
Method	BLASTX
NCBI GI	g3168840
BLAST score	383
E value	6.0e-37
Match length	121
% identity	67
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	148302
Seq. ID	LIB3175-003-P1-K1-C8
Method	BLASTX
NCBI GI	g2618721
BLAST score	392
E value	5.0e-38
Match length	94
% identity	82
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	148303
Seq. ID	LIB3175-003-P1-K1-C9
Method	BLASTX
NCBI GI	g1175013
BLAST score	521
E value	3.0e-53
Match length	109
% identity	94
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	148304
Seq. ID	LIB3175-003-P1-K1-D1
Method	BLASTX
NCBI GI	g2244896
BLAST score	302
E value	5.0e-59
Match length	127
% identity	83
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	148305
Seq. ID	LIB3175-003-P1-K1-D10
Method	BLASTX
NCBI GI	g1173345
BLAST score	513
E value	3.0e-52
Match length	139
% identity	76
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_1076403_pir__S51838 sedoheptulose-1,7-biphosphatase -

Arabidopsis thaliana >gi_786466_bbs_159034 (S74719) sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37} [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa] [Arabidopsis thaliana]

Seq. No.	148306
Seq. ID	LIB3175-003-P1-K1-D11
Method	BLASTX
NCBI GI	g542157
BLAST score	596
E value	6.0e-62
Match length	138
% identity	81
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	148307
Seq. ID	LIB3175-003-P1-K1-D12
Method	BLASTX
NCBI GI	g115767
BLAST score	770
E value	2.0e-82
Match length	146
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	148308
Seq. ID	LIB3175-003-P1-K1-D2
Method	BLASTX
NCBI GI	g4586265
BLAST score	532
E value	2.0e-54
Match length	130
% identity	78
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148309
Seq. ID	LIB3175-003-P1-K1-D3
Method	BLASTX
NCBI GI	g4371297
BLAST score	303
E value	1.0e-27
Match length	59
% identity	100
NCBI Description	(AC006260) phenylalanine ammonia-lyase 1, 3' partial [Arabidopsis thaliana]

Seq. No.	148310
Seq. ID	LIB3175-003-P1-K1-D4
Method	BLASTX
NCBI GI	g3157944
BLAST score	725

E value	5.0e-77
Match length	140
% identity	99
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	148311
Seq. ID	LIB3175-003-P1-K1-D5
Method	BLASTX
NCBI GI	g2645971
BLAST score	531
E value	8.0e-74
Match length	141
% identity	96
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	148312
Seq. ID	LIB3175-003-P1-K1-D7
Method	BLASTX
NCBI GI	g132074
BLAST score	782
E value	1.0e-83
Match length	148
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	148313
Seq. ID	LIB3175-003-P1-K1-D8
Method	BLASTX
NCBI GI	g3915032
BLAST score	481
E value	2.0e-48
Match length	122
% identity	75
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_508603 (L34346) stearoyl-acyl carrier protein desaturase [Glycine max]

Seq. No.	148314
Seq. ID	LIB3175-003-P1-K1-D9
Method	BLASTN
NCBI GI	g4006815
BLAST score	206
E value	1.0e-112
Match length	443
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 148315

Seq. ID	LIB3175-003-P1-K1-E1
Method	BLASTX
NCBI GI	g2911050
BLAST score	449
E value	1.0e-44
Match length	135
% identity	49
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	148316
Seq. ID	LIB3175-003-P1-K1-E11
Method	BLASTX
NCBI GI	g166867
BLAST score	667
E value	3.0e-70
Match length	147
% identity	88
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	148317
Seq. ID	LIB3175-003-P1-K1-E2
Method	BLASTX
NCBI GI	g2914703
BLAST score	374
E value	7.0e-36
Match length	127
% identity	55
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	148318
Seq. ID	LIB3175-003-P1-K1-E3
Method	BLASTX
NCBI GI	g4006890
BLAST score	642
E value	3.0e-67
Match length	136
% identity	92
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	148319
Seq. ID	LIB3175-003-P1-K1-E4
Method	BLASTX
NCBI GI	g115783
BLAST score	675
E value	4.0e-71
Match length	133
% identity	95
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	148320
Seq. ID	LIB3175-003-P1-K1-E5
Method	BLASTX

NCBI GI	g3157937
BLAST score	47
E value	4.0e-61
Match length	134
% identity	91
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	148321
Seq. ID	LIB3175-003-P1-K1-E6
Method	BLASTN
NCBI GI	g3395421
BLAST score	440
E value	0.0e+00
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148322
Seq. ID	LIB3175-003-P1-K1-E7
Method	BLASTX
NCBI GI	g602076
BLAST score	376
E value	3.0e-36
Match length	84
% identity	20
NCBI Description	(X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No.	148323
Seq. ID	LIB3175-003-P1-K1-E8
Method	BLASTX
NCBI GI	g135444
BLAST score	582
E value	2.0e-60
Match length	120
% identity	94
NCBI Description	TUBULIN BETA-1 CHAIN >gi_16122_emb_CAA38630_ (X54852) beta-tubulin [Avena sativa]

Seq. No.	148324
Seq. ID	LIB3175-003-P1-K1-E9
Method	BLASTX
NCBI GI	g1084415
BLAST score	335
E value	2.0e-31
Match length	111
% identity	60
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_ (D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]

Seq. No.	148325
Seq. ID	LIB3175-003-P1-K1-F1

Method	BLASTX
NCBI GI	g2781354
BLAST score	169
E value	2.0e-31
Match length	125
% identity	63
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	148326
Seq. ID	LIB3175-003-P1-K1-F10
Method	BLASTX
NCBI GI	g119143
BLAST score	639
E value	6.0e-67
Match length	123
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	148327
Seq. ID	LIB3175-003-P1-K1-F12
Method	BLASTN
NCBI GI	g1305454
BLAST score	72
E value	5.0e-32
Match length	147
% identity	93
NCBI Description	Arabidopsis thaliana cytosolic cyclophilin (ROC3) mRNA, complete cds

Seq. No.	148328
Seq. ID	LIB3175-003-P1-K1-F2
Method	BLASTX
NCBI GI	g4006827
BLAST score	360
E value	3.0e-34
Match length	150
% identity	46
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	148329
Seq. ID	LIB3175-003-P1-K1-F3
Method	BLASTX
NCBI GI	g2462834
BLAST score	199
E value	2.0e-15
Match length	107
% identity	41
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148330
Seq. ID	LIB3175-003-P1-K1-F4
Method	BLASTX
NCBI GI	g132102
BLAST score	246
E value	5.0e-21
Match length	79
% identity	68
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	148331
Seq. ID	LIB3175-003-P1-K1-F6
Method	BLASTX
NCBI GI	g2642158
BLAST score	429
E value	3.0e-42
Match length	117
% identity	68
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148332
Seq. ID	LIB3175-003-P1-K1-F7
Method	BLASTX
NCBI GI	g543565
BLAST score	218
E value	1.0e-17
Match length	87
% identity	44
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	148333
Seq. ID	LIB3175-003-P1-K1-F9
Method	BLASTX
NCBI GI	g2244759
BLAST score	606
E value	4.0e-63
Match length	144
% identity	75
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	148334
Seq. ID	LIB3175-003-P1-K1-G1
Method	BLASTX
NCBI GI	g3402713
BLAST score	731
E value	1.0e-77
Match length	147
% identity	97

NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.	148335
Seq. ID	LIB3175-003-P1-K1-G12
Method	BLASTX
NCBI GI	g3915826
BLAST score	589
E value	4.0e-61
Match length	137
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L5
Seq. No.	148336
Seq. ID	LIB3175-003-P1-K1-G2
Method	BLASTN
NCBI GI	g4467094
BLAST score	411
E value	0.0e+00
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)
Seq. No.	148337
Seq. ID	LIB3175-003-P1-K1-G5
Method	BLASTX
NCBI GI	g3157927
BLAST score	288
E value	8.0e-26
Match length	90
% identity	63
NCBI Description	(AC002131) Contains similarity to GDP-dissociation inhibitor gb_L07918 from Mus musculus. [Arabidopsis thaliana]
Seq. No.	148338
Seq. ID	LIB3175-003-P1-K1-G6
Method	BLASTX
NCBI GI	g2129978
BLAST score	571
E value	6.0e-59
Match length	122
% identity	60
NCBI Description	calmodulin (clone PCM5) - potato >gi_677903 (U20295) calmodulin [Solanum tuberosum] >gi_687704 (U20294) calmodulin [Solanum tuberosum] >gi_687706 (U20296) calmodulin [Solanum tuberosum] >gi_687708 (U20297) calmodulin [Solanum tuberosum]
Seq. No.	148339
Seq. ID	LIB3175-003-P1-K1-G7
Method	BLASTN
NCBI GI	g2737903
BLAST score	387
E value	0.0e+00
Match length	419
% identity	98

NCBI Description	Arabidopsis thaliana retrotransposon TSCL genomic sequence

Seq. No.	148340
Seq. ID	LIB3175-003-P1-K1-G8
Method	BLASTX
NCBI GI	g267070
BLAST score	622
E value	5.0e-65
Match length	118
% identity	97
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]

Seq. No.	148341
Seq. ID	LIB3175-003-P1-K1-G9
Method	BLASTX
NCBI GI	g4337175
BLAST score	613
E value	6.0e-64
Match length	140
% identity	87
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	148342
Seq. ID	LIB3175-003-P1-K1-H1
Method	BLASTX
NCBI GI	g2245141
BLAST score	509
E value	1.0e-51
Match length	98
% identity	99
NCBI Description	(Z97344) acetylornithine deacetylase [Arabidopsis thaliana]

Seq. No.	148343
Seq. ID	LIB3175-003-P1-K1-H10
Method	BLASTX
NCBI GI	g3024666
BLAST score	585
E value	1.0e-60
Match length	137
% identity	84
NCBI Description	STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713) strictosidine synthase [Arabidopsis thaliana] >gi_1754985 (U43945) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	148344
Seq. ID	LIB3175-003-P1-K1-H11
Method	BLASTX
NCBI GI	g2497753
BLAST score	263
E value	7.0e-23

Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	148345
Seq. ID	LIB3175-003-P1-K1-H12
Method	BLASTN
NCBI GI	g4519187
BLAST score	368
E value	0.0e+00
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No.	148346
Seq. ID	LIB3175-003-P1-K1-H2
Method	BLASTX
NCBI GI	g1351239
BLAST score	355
E value	1.0e-33
Match length	99
% identity	65
NCBI Description	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_481594_pir__S38909 thioredoxin m precursor - garden pea >gi_431957_emb_CAA53900_ (X76269) thioredoxin m [Pisum sativum]

Seq. No.	148347
Seq. ID	LIB3175-003-P1-K1-H3
Method	BLASTX
NCBI GI	g2981475
BLAST score	563
E value	5.0e-58
Match length	140
% identity	74
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	148348
Seq. ID	LIB3175-003-P1-K1-H6
Method	BLASTX
NCBI GI	g2911797
BLAST score	217
E value	1.0e-17
Match length	85
% identity	47
NCBI Description	(AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	148349
Seq. ID	LIB3175-003-P1-K1-H8
Method	BLASTN
NCBI GI	g3335356
BLAST score	299

E value	1.0e-167
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148350
Seq. ID	LIB3175-003-P1-K1-H9
Method	BLASTX
NCBI GI	g132110
BLAST score	49
E value	2.0e-67
Match length	136
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	148351
Seq. ID	LIB3175-004-P1-K1-A1
Method	BLASTN
NCBI GI	g2351072
BLAST score	47
E value	1.0e-17
Match length	125
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No.	148352
Seq. ID	LIB3175-004-P1-K1-A10
Method	BLASTX
NCBI GI	g3859606
BLAST score	596
E value	5.0e-62
Match length	132
% identity	79
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	148353
Seq. ID	LIB3175-004-P1-K1-A11
Method	BLASTN
NCBI GI	g3176701
BLAST score	117
E value	3.0e-59
Match length	247
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148354
Seq. ID	LIB3175-004-P1-K1-A12
Method	BLASTN

NCBI GI	g4220631
BLAST score	121
E value	2.0e-61
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	148355
Seq. ID	LIB3175-004-P1-K1-A3
Method	BLASTX
NCBI GI	g2911057
BLAST score	199
E value	5.0e-16
Match length	51
% identity	82
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	148356
Seq. ID	LIB3175-004-P1-K1-A5
Method	BLASTX
NCBI GI	g3668175
BLAST score	582
E value	3.0e-60
Match length	119
% identity	94
NCBI Description	(AB006778) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	148357
Seq. ID	LIB3175-004-P1-K1-A6
Method	BLASTX
NCBI GI	g4567232
BLAST score	64
E value	1.0e-34
Match length	87
% identity	93
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]

Seq. No.	148358
Seq. ID	LIB3175-004-P1-K1-A8
Method	BLASTX
NCBI GI	g2760833
BLAST score	357
E value	5.0e-34
Match length	74
% identity	99
NCBI Description	(AC003105) unknown protein [Arabidopsis thaliana]

Seq. No.	148359
Seq. ID	LIB3175-004-P1-K1-B10
Method	BLASTX
NCBI GI	g2146728
BLAST score	144
E value	6.0e-09

Match length	98
% identity	46
NCBI Description	cyclin cyc1b - Arabidopsis thaliana >gi_1360646 (L27223) cyclin [Arabidopsis thaliana]

Seq. No.	148360
Seq. ID	LIB3175-004-P1-K1-B12
Method	BLASTN
NCBI GI	g4159709
BLAST score	364
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	148361
Seq. ID	LIB3175-004-P1-K1-B3
Method	BLASTX
NCBI GI	g4567235
BLAST score	550
E value	2.0e-56
Match length	119
% identity	91
NCBI Description	(AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	148362
Seq. ID	LIB3175-004-P1-K1-B4
Method	BLASTX
NCBI GI	g3785978
BLAST score	682
E value	5.0e-72
Match length	140
% identity	93
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	148363
Seq. ID	LIB3175-004-P1-K1-B6
Method	BLASTX
NCBI GI	g4033467
BLAST score	416
E value	5.0e-41
Match length	86
% identity	51
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	148364
Seq. ID	LIB3175-004-P1-K1-B7
Method	BLASTX
NCBI GI	g4678943
BLAST score	266
E value	2.0e-23
Match length	102
% identity	30

NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]
Seq. No.	148365
Seq. ID	LIB3175-004-P1-K1-B9
Method	BLASTX
NCBI GI	g1246019
BLAST score	670
E value	1.0e-70
Match length	131
% identity	97
NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
Seq. No.	148366
Seq. ID	LIB3175-004-P1-K1-C1
Method	BLASTN
NCBI GI	g2244788
BLAST score	323
E value	0.0e+00
Match length	408
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	148367
Seq. ID	LIB3175-004-P1-K1-C10
Method	BLASTX
NCBI GI	g67842
BLAST score	360
E value	3.0e-34
Match length	84
% identity	89
NCBI Description	H+-transporting ATP synthase (EC 3.6.1.34) beta chain - spinach chloroplast >gi_343355 (J01441) ATPase beta subunit [Spinacia oleracea] >gi_223530_prf__0811259A ATPase beta [Spinacia oleracea]
Seq. No.	148368
Seq. ID	LIB3175-004-P1-K1-C11
Method	BLASTX
NCBI GI	g3661595
BLAST score	370
E value	2.0e-35
Match length	68
% identity	100
NCBI Description	(AF091844) aminoalcoholphosphotransferase [Arabidopsis thaliana]
Seq. No.	148369
Seq. ID	LIB3175-004-P1-K1-C12
Method	BLASTX
NCBI GI	g2944446
BLAST score	320
E value	1.0e-29
Match length	77
% identity	78
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus

communis]

Seq. No.	148370
Seq. ID	LIB3175-004-P1-K1-C2
Method	BLASTN
NCBI GI	g1707006
BLAST score	245
E value	1.0e-135
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148371
Seq. ID	LIB3175-004-P1-K1-C3
Method	BLASTN
NCBI GI	g3702731
BLAST score	302
E value	1.0e-169
Match length	357
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	148372
Seq. ID	LIB3175-004-P1-K1-C4
Method	BLASTN
NCBI GI	g2351062
BLAST score	48
E value	9.0e-18
Match length	147
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	148373
Seq. ID	LIB3175-004-P1-K1-C5
Method	BLASTX
NCBI GI	g3122673
BLAST score	609
E value	2.0e-63
Match length	140
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	148374
Seq. ID	LIB3175-004-P1-K1-C6
Method	BLASTX
NCBI GI	g3914370
BLAST score	631
E value	5.0e-66
Match length	149
% identity	84
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_419754_pir__S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis

thaliana >gi_217845_dbj_BAA00575_ (D00672) glycerol-3-phosphate acyltransferase [Arabidopsis thaliana] >gi_217847_dbj_BAA00576_ (D00673) glycerol-3-phosphate acyltransferase precursor [Arabidopsis thaliana]

Seq. No.	148375
Seq. ID	LIB3175-004-P1-K1-C7
Method	BLASTN
NCBI GI	g3128135
BLAST score	318
E value	1.0e-179
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	148376
Seq. ID	LIB3175-004-P1-K1-C8
Method	BLASTX
NCBI GI	g4587525
BLAST score	142
E value	8.0e-09
Match length	95
% identity	34
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	148377
Seq. ID	LIB3175-004-P1-K1-D1
Method	BLASTX
NCBI GI	g481031
BLAST score	478
E value	4.0e-48
Match length	127
% identity	44
NCBI Description	transcription factor SF3 - common sunflower

Seq. No.	148378
Seq. ID	LIB3175-004-P1-K1-D10
Method	BLASTX
NCBI GI	g3337356
BLAST score	178
E value	2.0e-13
Match length	36
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	148379
Seq. ID	LIB3175-004-P1-K1-D11
Method	BLASTN
NCBI GI	g4469002
BLAST score	254
E value	1.0e-141
Match length	399

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	148380
Seq. ID	LIB3175-004-P1-K1-D2
Method	BLASTX
NCBI GI	g3184100
BLAST score	181
E value	2.0e-13
Match length	51
% identity	61
NCBI Description	(AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	148381
Seq. ID	LIB3175-004-P1-K1-D3
Method	BLASTX
NCBI GI	g4314363
BLAST score	564
E value	3.0e-58
Match length	121
% identity	49
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148382
Seq. ID	LIB3175-004-P1-K1-D5
Method	BLASTN
NCBI GI	g16452
BLAST score	52
E value	6.0e-21
Match length	81
% identity	91
NCBI Description	Arabidopsis thaliana ats1A gene for ribulose 1.5-biphoshate carboxylase small subunit (EC 4.1.1.39)

Seq. No.	148383
Seq. ID	LIB3175-004-P1-K1-D8
Method	BLASTX
NCBI GI	g3687239
BLAST score	612
E value	8.0e-64
Match length	123
% identity	95
NCBI Description	(AC005169) putative clathrin coat assembly protein [Arabidopsis thaliana]

Seq. No.	148384
Seq. ID	LIB3175-004-P1-K1-D9
Method	BLASTX
NCBI GI	g4589366
BLAST score	275
E value	2.0e-24
Match length	117
% identity	47
NCBI Description	(AF140505) DEAD box RNA helicase [Candida albicans]

Seq. No.	148385

Seq. ID LIB3175-004-P1-K1-E1
Method BLASTX
NCBI GI g2497486
BLAST score 628
E value 1.0e-65
Match length 123
% identity 99
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No. 148386
Seq. ID LIB3175-004-P1-K1-E11
Method BLASTX
NCBI GI g166834
BLAST score 84
E value 3.0e-68
Match length 137
% identity 97
NCBI Description (M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No. 148387
Seq. ID LIB3175-004-P1-K1-E12
Method BLASTN
NCBI GI g2182287
BLAST score 327
E value 0.0e+00
Match length 355
% identity 98
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No. 148388
Seq. ID LIB3175-004-P1-K1-E2
Method BLASTX
NCBI GI g4490331
BLAST score 583
E value 2.0e-60
Match length 131
% identity 87
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 148389
Seq. ID LIB3175-004-P1-K1-E3
Method BLASTX
NCBI GI g3024697
BLAST score 379
E value 1.0e-36
Match length 79
% identity 96
NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No. 148390

Seq. ID	LIB3175-004-P1-K1-E5
Method	BLASTX
NCBI GI	g4102839
BLAST score	251
E value	2.0e-21
Match length	136
% identity	40
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	148391
Seq. ID	LIB3175-004-P1-K1-E6
Method	BLASTN
NCBI GI	g3702735
BLAST score	41
E value	7.0e-14
Match length	61
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	148392
Seq. ID	LIB3175-004-P1-K1-E7
Method	BLASTX
NCBI GI	g4455215
BLAST score	146
E value	2.0e-09
Match length	87
% identity	41
NCBI Description	(AL035440) putative homeodomain protein [Arabidopsis thaliana]

Seq. No.	148393
Seq. ID	LIB3175-004-P1-K1-E8
Method	BLASTX
NCBI GI	g2829899
BLAST score	224
E value	1.0e-18
Match length	71
% identity	61
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	148394
Seq. ID	LIB3175-004-P1-K1-F1
Method	BLASTX
NCBI GI	g2493646
BLAST score	267
E value	1.0e-23
Match length	70
% identity	74
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 (L21008) chaperonin 60 [Zea mays] >gi_309561 (L21006) mitochondrial chaperonin 60 [Zea mays]

Seq. No.	148395
Seq. ID	LIB3175-004-P1-K1-F11

Method	BLASTX
NCBI GI	g4006848
BLAST score	309
E value	3.0e-28
Match length	107
% identity	53
NCBI Description	(AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No.	148396
Seq. ID	LIB3175-004-P1-K1-F12
Method	BLASTX
NCBI GI	g2129639
BLAST score	184
E value	9.0e-14
Match length	72
% identity	57
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	148397
Seq. ID	LIB3175-004-P1-K1-F3
Method	BLASTX
NCBI GI	g2760843
BLAST score	345
E value	2.0e-32
Match length	142
% identity	56
NCBI Description	(AC003105) unknown protein [Arabidopsis thaliana]

Seq. No.	148398
Seq. ID	LIB3175-004-P1-K1-F4
Method	BLASTX
NCBI GI	g4741960
BLAST score	597
E value	5.0e-62
Match length	132
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	148399
Seq. ID	LIB3175-004-P1-K1-G1
Method	BLASTX
NCBI GI	g1174162
BLAST score	461
E value	4.0e-46
Match length	82
% identity	99
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	148400
Seq. ID	LIB3175-004-P1-K1-G10
Method	BLASTN
NCBI GI	g4096078

BLAST score	48
E value	7.0e-18
Match length	175
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148401
Seq. ID	LIB3175-004-P1-K1-G11
Method	BLASTX
NCBI GI	g4417271
BLAST score	755
E value	1.0e-80
Match length	143
% identity	98
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	148402
Seq. ID	LIB3175-004-P1-K1-G12
Method	BLASTX
NCBI GI	g1175012
BLAST score	626
E value	2.0e-65
Match length	136
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	148403
Seq. ID	LIB3175-004-P1-K1-G2
Method	BLASTX
NCBI GI	g1408473
BLAST score	343
E value	2.0e-32
Match length	79
% identity	85
NCBI Description	(U48939) actin depolymerizing factor 2 [Arabidopsis thaliana]

Seq. No.	148404
Seq. ID	LIB3175-004-P1-K1-G3
Method	BLASTX
NCBI GI	g4138137
BLAST score	363
E value	1.0e-34
Match length	128
% identity	55
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	148405
Seq. ID	LIB3175-004-P1-K1-G4
Method	BLASTX
NCBI GI	g3157937
BLAST score	640
E value	4.0e-67

Match length	132
% identity	97
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	148406
Seq. ID	LIB3175-004-P1-K1-G5
Method	BLASTN
NCBI GI	g3650026
BLAST score	397
E value	0.0e+00
Match length	445
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148407
Seq. ID	LIB3175-004-P1-K1-G6
Method	BLASTX
NCBI GI	g3747111
BLAST score	573
E value	3.0e-59
Match length	127
% identity	87
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	148408
Seq. ID	LIB3175-004-P1-K1-G7
Method	BLASTN
NCBI GI	g3367500
BLAST score	288
E value	1.0e-161
Match length	428
% identity	98
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	148409
Seq. ID	LIB3175-004-P1-K1-G8
Method	BLASTX
NCBI GI	g3668080
BLAST score	383
E value	4.0e-37
Match length	96
% identity	82
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	148410
Seq. ID	LIB3175-004-P1-K1-G9
Method	BLASTX
NCBI GI	g3107903
BLAST score	254
E value	5.0e-22
Match length	66

% identity	68
NCBI Description	(D83719) polycomb-like protein [Daucus carota]

Seq. No.	148411
Seq. ID	LIB3175-004-P1-K1-H1
Method	BLASTN
NCBI GI	g4263774
BLAST score	426
E value	0.0e+00
Match length	442
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148412
Seq. ID	LIB3175-004-P1-K1-H10
Method	BLASTN
NCBI GI	g2342717
BLAST score	97
E value	4.0e-47
Match length	282
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148413
Seq. ID	LIB3175-004-P1-K1-H11
Method	BLASTN
NCBI GI	g3355463
BLAST score	37
E value	2.0e-11
Match length	357
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148414
Seq. ID	LIB3175-004-P1-K1-H2
Method	BLASTX
NCBI GI	g535780
BLAST score	706
E value	8.0e-75
Match length	134
% identity	100
NCBI Description	(D26609) transmembrane protein [Arabidopsis thaliana]

Seq. No.	148415
Seq. ID	LIB3175-004-P1-K1-H3
Method	BLASTX
NCBI GI	g81952
BLAST score	662
E value	1.0e-69
Match length	147
% identity	87
NCBI Description	tubulin beta-2 chain - garden pea (fragment)

Seq. No.	148416

Seq. ID	LIB3175-004-P1-K1-H4
Method	BLASTX
NCBI GI	g2493045
BLAST score	566
E value	2.0e-58
Match length	131
% identity	84
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	148417
Seq. ID	LIB3175-004-P1-K1-H6
Method	BLASTX
NCBI GI	g4586265
BLAST score	375
E value	4.0e-42
Match length	129
% identity	71
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148418
Seq. ID	LIB3175-004-P1-K1-H7
Method	BLASTX
NCBI GI	g1172872
BLAST score	468
E value	5.0e-47
Match length	119
% identity	79
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	148419
Seq. ID	LIB3175-004-P1-K1-H8
Method	BLASTX
NCBI GI	g4741962
BLAST score	409
E value	5.0e-40
Match length	118
% identity	55
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	148420
Seq. ID	LIB3175-004-P1-K1-H9
Method	BLASTN
NCBI GI	g3046847
BLAST score	143
E value	1.0e-74
Match length	355
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	148421
Seq. ID	LIB3175-005-P1-K1-A1
Method	BLASTN
NCBI GI	g2160716
BLAST score	349
E value	0.0e+00
Match length	386
% identity	97
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	148422
Seq. ID	LIB3175-005-P1-K1-A2
Method	BLASTX
NCBI GI	g4741940
BLAST score	609
E value	2.0e-63
Match length	135
% identity	62
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	148423
Seq. ID	LIB3175-005-P1-K1-A3
Method	BLASTX
NCBI GI	g3860258
BLAST score	84
E value	5.0e-14
Match length	79
% identity	56
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	148424
Seq. ID	LIB3175-005-P1-K1-A4
Method	BLASTX
NCBI GI	g4539303
BLAST score	604
E value	7.0e-63
Match length	139
% identity	78
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	148425
Seq. ID	LIB3175-005-P1-K1-A5
Method	BLASTX
NCBI GI	g119143
BLAST score	50
E value	6.0e-65
Match length	129
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]

>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	148426
Seq. ID	LIB3175-005-P1-K1-A6
Method	BLASTX
NCBI GI	g4091810
BLAST score	254
E value	7.0e-22
Match length	79
% identity	70
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	148427
Seq. ID	LIB3175-005-P1-K1-A7
Method	BLASTX
NCBI GI	g4185505
BLAST score	370
E value	2.0e-35
Match length	101
% identity	73
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	148428
Seq. ID	LIB3175-005-P1-K1-A8
Method	BLASTN
NCBI GI	g3176695
BLAST score	32
E value	1.0e-08
Match length	68
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	148429
Seq. ID	LIB3175-005-P1-K1-A9
Method	BLASTX
NCBI GI	g4140326
BLAST score	252
E value	1.0e-21
Match length	98
% identity	42
NCBI Description	(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to many (archae)bacterial, worm and yeast hypothetical proteins) [Homo sapiens]

Seq. No.	148430
Seq. ID	LIB3175-005-P1-K1-B10
Method	BLASTX
NCBI GI	g3360289
BLAST score	464
E value	6.0e-47
Match length	131
% identity	68
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No.	148431
Seq. ID	LIB3175-005-P1-K1-B11
Method	BLASTN
NCBI GI	g3241917
BLAST score	331
E value	0.0e+00
Match length	343
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	148432
Seq. ID	LIB3175-005-P1-K1-B2
Method	BLASTX
NCBI GI	g1332579
BLAST score	535
E value	8.0e-55
Match length	109
% identity	10
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	148433
Seq. ID	LIB3175-005-P1-K1-B3
Method	BLASTN
NCBI GI	g2191126
BLAST score	325
E value	0.0e+00
Match length	381
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	148434
Seq. ID	LIB3175-005-P1-K1-B4
Method	BLASTX
NCBI GI	g4678276
BLAST score	589
E value	3.0e-61
Match length	117
% identity	97
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	148435
Seq. ID	LIB3175-005-P1-K1-B5
Method	BLASTX
NCBI GI	g115767
BLAST score	643
E value	2.0e-67
Match length	126
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	148436
Seq. ID	LIB3175-005-P1-K1-B6
Method	BLASTX
NCBI GI	g4741940
BLAST score	536
E value	4.0e-55
Match length	105
% identity	96
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	148437
Seq. ID	LIB3175-005-P1-K1-B7
Method	BLASTX
NCBI GI	g2829899
BLAST score	370
E value	2.0e-35
Match length	102
% identity	67
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	148438
Seq. ID	LIB3175-005-P1-K1-B8
Method	BLASTN
NCBI GI	g4589427
BLAST score	166
E value	3.0e-88
Match length	301
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	148439
Seq. ID	LIB3175-005-P1-K1-B9
Method	BLASTN
NCBI GI	g3080430
BLAST score	219
E value	1.0e-120
Match length	283
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	148440
Seq. ID	LIB3175-005-P1-K1-C1
Method	BLASTN
NCBI GI	g2435510
BLAST score	196
E value	1.0e-106
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	148441

Seq. ID	LIB3175-005-P1-K1-C2
Method	BLASTX
NCBI GI	g1350680
BLAST score	628
E value	1.0e-65
Match length	123
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	148442
Seq. ID	LIB3175-005-P1-K1-C3
Method	BLASTX
NCBI GI	g2213622
BLAST score	380
E value	1.0e-36
Match length	79
% identity	99
NCBI Description	(AC000103) F21J9.25 [Arabidopsis thaliana]

Seq. No.	148443
Seq. ID	LIB3175-005-P1-K1-C5
Method	BLASTX
NCBI GI	g1531762
BLAST score	191
E value	2.0e-14
Match length	36
% identity	100
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	148444
Seq. ID	LIB3175-005-P1-K1-C6
Method	BLASTN
NCBI GI	g2264319
BLAST score	102
E value	4.0e-50
Match length	298
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	148445
Seq. ID	LIB3175-005-P1-K1-D1
Method	BLASTX
NCBI GI	g115783
BLAST score	623
E value	4.0e-65
Match length	126
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	148446
Seq. ID	LIB3175-005-P1-K1-D10
Method	BLASTX

NCBI GI	g4263703
BLAST score	202
E value	1.0e-15
Match length	89
% identity	54
NCBI Description	(AC006223) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148447
Seq. ID	LIB3175-005-P1-K1-D3
Method	BLASTN
NCBI GI	g2696018
BLAST score	44
E value	7.0e-16
Match length	76
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	148448
Seq. ID	LIB3175-005-P1-K1-D4
Method	BLASTX
NCBI GI	g120675
BLAST score	472
E value	2.0e-47
Match length	116
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	148449
Seq. ID	LIB3175-005-P1-K1-D6
Method	BLASTX
NCBI GI	g2244977
BLAST score	462
E value	3.0e-46
Match length	106
% identity	85
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	148450
Seq. ID	LIB3175-005-P1-K1-D7
Method	BLASTN
NCBI GI	g2760172
BLAST score	126
E value	9.0e-65
Match length	170
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	148451
Seq. ID	LIB3175-005-P1-K1-D8
Method	BLASTX
NCBI GI	g417103

BLAST score	335
E value	1.0e-31
Match length	68
% identity	99
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	148452
Seq. ID	LIB3175-005-P1-K1-D9
Method	BLASTN
NCBI GI	g710625
BLAST score	36
E value	7.0e-11
Match length	140
% identity	81
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	148453
Seq. ID	LIB3175-005-P1-K1-E1
Method	BLASTX
NCBI GI	g4455253
BLAST score	476
E value	5.0e-48
Match length	98
% identity	92
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	148454
Seq. ID	LIB3175-005-P1-K1-E10
Method	BLASTX
NCBI GI	g3738092
BLAST score	90
E value	2.0e-51
Match length	118
% identity	88
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	148455

Seq. ID	LIB3175-005-P1-K1-E11
Method	BLASTX
NCBI GI	g1076366
BLAST score	696
E value	1.0e-73
Match length	131
% identity	98
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	148456
Seq. ID	LIB3175-005-P1-K1-E2
Method	BLASTN
NCBI GI	g3510343
BLAST score	303
E value	1.0e-170
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	148457
Seq. ID	LIB3175-005-P1-K1-E3
Method	BLASTX
NCBI GI	g1352663
BLAST score	481
E value	2.0e-48
Match length	91
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana >gi_466441 (M96841) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4559341_gb_AAD23003.1_AC007087_22 (AC007087) serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] >gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956) serine/threonine protein phosphatase [Arabidopsis thaliana]

Seq. No.	148458
Seq. ID	LIB3175-005-P1-K1-E4
Method	BLASTX
NCBI GI	g3193293
BLAST score	670
E value	1.0e-70
Match length	143
% identity	96
NCBI Description	(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana]

Seq. No. 148459

Seq. ID	LIB3175-005-P1-K1-E5
Method	BLASTX
NCBI GI	g3152596
BLAST score	262
E value	1.0e-26
Match length	92
% identity	74
NCBI Description	(AC002986) YUP8H12R.36 [Arabidopsis thaliana]

Seq. No.	148460
Seq. ID	LIB3175-005-P1-K1-E6
Method	BLASTX
NCBI GI	g3785983
BLAST score	546
E value	4.0e-56
Match length	105
% identity	99
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148461
Seq. ID	LIB3175-005-P1-K1-E7
Method	BLASTX
NCBI GI	g543565
BLAST score	145
E value	2.0e-09
Match length	43
% identity	51
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	148462
Seq. ID	LIB3175-005-P1-K1-E9
Method	BLASTX
NCBI GI	g3056594
BLAST score	528
E value	5.0e-54
Match length	110
% identity	95
NCBI Description	(AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No.	148463
Seq. ID	LIB3175-005-P1-K1-F1
Method	BLASTX
NCBI GI	g2781354
BLAST score	609
E value	5.0e-64
Match length	123
% identity	100
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	148464
Seq. ID	LIB3175-005-P1-K1-F10
Method	BLASTX
NCBI GI	g4582468
BLAST score	529

E value	4.0e-54
Match length	108
% identity	99
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	148465
Seq. ID	LIB3175-005-P1-K1-F11
Method	BLASTN
NCBI GI	g3702732
BLAST score	37
E value	1.0e-11
Match length	156
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	148466
Seq. ID	LIB3175-005-P1-K1-F3
Method	BLASTX
NCBI GI	g2317725
BLAST score	304
E value	8.0e-28
Match length	109
% identity	52
NCBI Description	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]

Seq. No.	148467
Seq. ID	LIB3175-005-P1-K1-F4
Method	BLASTX
NCBI GI	g2245093
BLAST score	461
E value	4.0e-46
Match length	132
% identity	76
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	148468
Seq. ID	LIB3175-005-P1-K1-F6
Method	BLASTX
NCBI GI	g4105772
BLAST score	408
E value	5.0e-40
Match length	86
% identity	43
NCBI Description	(AF049917) PGP9B [Petunia x hybrida]

Seq. No.	148469
Seq. ID	LIB3175-005-P1-K1-F7
Method	BLASTN
NCBI GI	g3341716
BLAST score	43
E value	4.0e-15
Match length	190
% identity	80
NCBI Description	Arabidopsis thaliana ACC oxidase (ACO2) mRNA, complete cds

Seq. No.	148470
Seq. ID	LIB3175-005-P1-K1-G10
Method	BLASTN
NCBI GI	g3402745
BLAST score	59
E value	1.0e-24
Match length	197
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	148471
Seq. ID	LIB3175-005-P1-K1-G2
Method	BLASTX
NCBI GI	g3850573
BLAST score	632
E value	8.0e-69
Match length	137
% identity	98
NCBI Description	(AC005278) Similar to gi_1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb_D90908. ESTs gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from this gene. [Arabidopsis thaliana]

Seq. No.	148472
Seq. ID	LIB3175-005-P1-K1-G3
Method	BLASTX
NCBI GI	g3157947
BLAST score	629
E value	8.0e-66
Match length	120
% identity	52
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	148473
Seq. ID	LIB3175-005-P1-K1-G6
Method	BLASTX
NCBI GI	g4587525
BLAST score	221
E value	5.0e-18
Match length	104
% identity	38
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	148474
Seq. ID	LIB3175-005-P1-K1-G7
Method	BLASTX
NCBI GI	g2766448
BLAST score	307

E value	3.0e-28
Match length	103
% identity	54
NCBI Description	(AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No.	148475
Seq. ID	LIB3175-005-P1-K1-G8
Method	BLASTX
NCBI GI	g120667
BLAST score	480
E value	2.0e-48
Match length	120
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	148476
Seq. ID	LIB3175-005-P1-K1-G9
Method	BLASTX
NCBI GI	g2827139
BLAST score	355
E value	7.0e-34
Match length	66
% identity	100
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	148477
Seq. ID	LIB3175-005-P1-K1-H1
Method	BLASTX
NCBI GI	g3157944
BLAST score	638
E value	7.0e-67
Match length	122
% identity	100
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	148478
Seq. ID	LIB3175-005-P1-K1-H2
Method	BLASTX
NCBI GI	g3953466
BLAST score	585
E value	8.0e-61
Match length	118
% identity	97
NCBI Description	(AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No.	148479
Seq. ID	LIB3175-005-P1-K1-H3
Method	BLASTX
NCBI GI	g2651307
BLAST score	265
E value	4.0e-23
Match length	72
% identity	64
NCBI Description	(AC002336) putative uroporphyinogen decarboxylase [Arabidopsis thaliana]

Seq. No.	148480
Seq. ID	LIB3175-005-P1-K1-H4
Method	BLASTX
NCBI GI	g2832625
BLAST score	510
E value	8.0e-52
Match length	112
% identity	86
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	148481
Seq. ID	LIB3175-005-P1-K1-H5
Method	BLASTX
NCBI GI	g2662343
BLAST score	517
E value	9.0e-53
Match length	107
% identity	93
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]

Seq. No.	148482
Seq. ID	LIB3175-005-P1-K1-H7
Method	BLASTX
NCBI GI	g4218120
BLAST score	227
E value	6.0e-19
Match length	62
% identity	73
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	148483
Seq. ID	LIB3175-005-P1-K1-H8
Method	BLASTX
NCBI GI	g3080376
BLAST score	264
E value	3.0e-23
Match length	93
% identity	58
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	148484
Seq. ID	LIB3175-005-P1-K1-H9
Method	BLASTN
NCBI GI	g4756963

BLAST score	120
E value	6.0e-61
Match length	326
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	148485
Seq. ID	LIB3175-006-P1-K1-A1
Method	BLASTN
NCBI GI	g4691223
BLAST score	187
E value	1.0e-101
Match length	282
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	148486
Seq. ID	LIB3175-006-P1-K1-A10
Method	BLASTN
NCBI GI	g4539309
BLAST score	80
E value	2.0e-37
Match length	144
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	148487
Seq. ID	LIB3175-006-P1-K1-A11
Method	BLASTX
NCBI GI	g1817544
BLAST score	508
E value	1.0e-51
Match length	102
% identity	97
NCBI Description	(D83025) proline oxidase precursor [Arabidopsis thaliana]

Seq. No.	148488
Seq. ID	LIB3175-006-P1-K1-A12
Method	BLASTN
NCBI GI	g4159709
BLAST score	241
E value	1.0e-133
Match length	293
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	148489
Seq. ID	LIB3175-006-P1-K1-A2
Method	BLASTX
NCBI GI	g115767
BLAST score	410
E value	2.0e-40
Match length	81

% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	148490
Seq. ID	LIB3175-006-P1-K1-A3
Method	BLASTX
NCBI GI	g3249100
BLAST score	530
E value	3.0e-54
Match length	105
% identity	94
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]
Seq. No.	148491
Seq. ID	LIB3175-006-P1-K1-A5
Method	BLASTX
NCBI GI	g2501101
BLAST score	491
E value	1.0e-49
Match length	127
% identity	83
NCBI Description	SYNTAXIN HOMOLOG (PEP12 HOMOLOG) >gi_899122 (L41651) syntaxin [Arabidopsis thaliana]
Seq. No.	148492
Seq. ID	LIB3175-006-P1-K1-A6
Method	BLASTX
NCBI GI	g1705677
BLAST score	342
E value	3.0e-32
Match length	81
% identity	85
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]
Seq. No.	148493
Seq. ID	LIB3175-006-P1-K1-A8
Method	BLASTN
NCBI GI	g1877523
BLAST score	72
E value	3.0e-32
Match length	169
% identity	56
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]
Seq. No.	148494

Seq. ID	LIB3175-006-P1-K1-B1
Method	BLASTX
NCBI GI	g1518540
BLAST score	393
E value	3.0e-38
Match length	83
% identity	92
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	148495
Seq. ID	LIB3175-006-P1-K1-B2
Method	BLASTX
NCBI GI	g4505369
BLAST score	235
E value	1.0e-19
Match length	132
% identity	39
NCBI Description	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) >gi_3287881_sp_O43181_NUYM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_2655053 (AF020351) NADH:ubiquinone oxidoreductase 18 kDa IP subunit [Homo sapiens]

Seq. No.	148496
Seq. ID	LIB3175-006-P1-K1-B4
Method	BLASTX
NCBI GI	g2829891
BLAST score	530
E value	3.0e-54
Match length	118
% identity	88
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	148497
Seq. ID	LIB3175-006-P1-K1-B5
Method	BLASTX
NCBI GI	g2827712
BLAST score	351
E value	1.0e-33
Match length	70
% identity	99
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	148498
Seq. ID	LIB3175-006-P1-K1-B6
Method	BLASTX
NCBI GI	g2244750
BLAST score	551
E value	4.0e-65
Match length	136
% identity	96
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	148499
Seq. ID	LIB3175-006-P1-K1-B7
Method	BLASTN
NCBI GI	g3449334
BLAST score	155
E value	8.0e-82
Match length	277
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	148500
Seq. ID	LIB3175-006-P1-K1-B9
Method	BLASTX
NCBI GI	g1706749
BLAST score	557
E value	2.0e-57
Match length	117
% identity	96
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]

Seq. No.	148501
Seq. ID	LIB3175-006-P1-K1-C1
Method	BLASTX
NCBI GI	g1175013
BLAST score	395
E value	1.0e-38
Match length	91
% identity	86
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	148502
Seq. ID	LIB3175-006-P1-K1-C10
Method	BLASTX
NCBI GI	g940288
BLAST score	263
E value	5.0e-23
Match length	78
% identity	64
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	148503
Seq. ID	LIB3175-006-P1-K1-C11
Method	BLASTX
NCBI GI	g267073
BLAST score	613
E value	6.0e-64
Match length	113
% identity	99

NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	148504
Seq. ID	LIB3175-006-P1-K1-C12
Method	BLASTN
NCBI GI	g3659491
BLAST score	152
E value	5.0e-80
Match length	196
% identity	94
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	148505
Seq. ID	LIB3175-006-P1-K1-C3
Method	BLASTX
NCBI GI	g3786324
BLAST score	375
E value	5.0e-36
Match length	136
% identity	51
NCBI Description	(AB015139) chlorophyll a oxygenase [Chlamydomonas reinhardtii]

Seq. No.	148506
Seq. ID	LIB3175-006-P1-K1-C4
Method	BLASTX
NCBI GI	g2129559
BLAST score	171
E value	7.0e-38
Match length	96
% identity	86
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	148507
Seq. ID	LIB3175-006-P1-K1-C6
Method	BLASTX
NCBI GI	g3128228
BLAST score	57
E value	3.0e-58
Match length	131
% identity	77
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	148508
Seq. ID	LIB3175-006-P1-K1-C9
Method	BLASTX

NCBI GI	g3135254
BLAST score	142
E value	9.0e-09
Match length	129
% identity	35
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148509
Seq. ID	LIB3175-006-P1-K1-D1
Method	BLASTX
NCBI GI	g3242719
BLAST score	218
E value	4.0e-48
Match length	103
% identity	96
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	148510
Seq. ID	LIB3175-006-P1-K1-D10
Method	BLASTX
NCBI GI	g1136402
BLAST score	143
E value	7.0e-09
Match length	90
% identity	30
NCBI Description	(D79993) similar to hypothetical protein L8167.6 of Saccharomyces cerevisiae. [Homo sapiens]

Seq. No.	148511
Seq. ID	LIB3175-006-P1-K1-D12
Method	BLASTX
NCBI GI	g4455202
BLAST score	449
E value	1.0e-44
Match length	98
% identity	89
NCBI Description	(AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No.	148512
Seq. ID	LIB3175-006-P1-K1-D2
Method	BLASTX
NCBI GI	g2224931
BLAST score	510
E value	7.0e-52
Match length	105
% identity	97
NCBI Description	(AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No.	148513
Seq. ID	LIB3175-006-P1-K1-D3
Method	BLASTX
NCBI GI	g4490329
BLAST score	333
E value	4.0e-31
Match length	118

% identity	58
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	148514
Seq. ID	LIB3175-006-P1-K1-D4
Method	BLASTX
NCBI GI	g4193388
BLAST score	453
E value	3.0e-45
Match length	120
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	148515
Seq. ID	LIB3175-006-P1-K1-D5
Method	BLASTN
NCBI GI	g166611
BLAST score	69
E value	2.0e-30
Match length	223
% identity	83
NCBI Description	A.thaliana at2S3 gene encoding albumin 2S subunit 3, complete cds

Seq. No.	148516
Seq. ID	LIB3175-006-P1-K1-D9
Method	BLASTN
NCBI GI	g4314354
BLAST score	81
E value	1.0e-37
Match length	363
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148517
Seq. ID	LIB3175-006-P1-K1-E1
Method	BLASTX
NCBI GI	g267082
BLAST score	609
E value	2.0e-63
Match length	114
% identity	98
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	148518
Seq. ID	LIB3175-006-P1-K1-E10
Method	BLASTN
NCBI GI	g1669386
BLAST score	32
E value	1.0e-08
Match length	72
% identity	92
NCBI Description	Arabidopsis thaliana actin 2 (ACT2) gene, complete cds

Seq. No.	148519
Seq. ID	LIB3175-006-P1-K1-E11
Method	BLASTX
NCBI GI	g4678298
BLAST score	43
E value	4.0e-55
Match length	125
% identity	92
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	148520
Seq. ID	LIB3175-006-P1-K1-E12
Method	BLASTX
NCBI GI	g4454037
BLAST score	366
E value	3.0e-35
Match length	79
% identity	84
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	148521
Seq. ID	LIB3175-006-P1-K1-E2
Method	BLASTX
NCBI GI	g2447107
BLAST score	380
E value	1.0e-36
Match length	135
% identity	53
NCBI Description	(U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No.	148522
Seq. ID	LIB3175-006-P1-K1-E3
Method	BLASTX
NCBI GI	g127041
BLAST score	172
E value	2.0e-12
Match length	36
% identity	89
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	148523
Seq. ID	LIB3175-006-P1-K1-E5
Method	BLASTX
NCBI GI	g2244850
BLAST score	447
E value	2.0e-44
Match length	106
% identity	91
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148524

Seq. ID	LIB3175-006-P1-K1-E8
Method	BLASTN
NCBI GI	g4115930
BLAST score	37
E value	2.0e-11
Match length	61
% identity	89
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	148525
Seq. ID	LIB3175-006-P1-K1-F1
Method	BLASTN
NCBI GI	g3928074
BLAST score	151
E value	1.0e-79
Match length	198
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148526
Seq. ID	LIB3175-006-P1-K1-F2
Method	BLASTX
NCBI GI	g2829893
BLAST score	616
E value	3.0e-64
Match length	140
% identity	86
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	148527
Seq. ID	LIB3175-006-P1-K1-F3
Method	BLASTX
NCBI GI	g2160133
BLAST score	429
E value	2.0e-42
Match length	118
% identity	75
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	148528
Seq. ID	LIB3175-006-P1-K1-F4
Method	BLASTX
NCBI GI	g2244909
BLAST score	457
E value	1.0e-45
Match length	118
% identity	81
NCBI Description	(Z97339) pyruvate,orthophosphate dikinase [Arabidopsis thaliana]

Seq. No.	148529
Seq. ID	LIB3175-006-P1-K1-F7
Method	BLASTN

NCBI GI	g3985957
BLAST score	382
E value	0.0e+00
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	148530
Seq. ID	LIB3175-006-P1-K1-F9
Method	BLASTX
NCBI GI	g2129628
BLAST score	547
E value	3.0e-58
Match length	128
% identity	87
NCBI Description	ketoconazole resistent protein - Arabidopsis thaliana >gi_928938_emb_CAA61433_ (X89036) ketoconazole resistent protein [Arabidopsis thaliana]

Seq. No.	148531
Seq. ID	LIB3175-006-P1-K1-G1
Method	BLASTX
NCBI GI	g131398
BLAST score	455
E value	2.0e-45
Match length	105
% identity	86
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	148532
Seq. ID	LIB3175-006-P1-K1-G10
Method	BLASTX
NCBI GI	g3063450
BLAST score	533
E value	1.0e-54
Match length	127
% identity	93
NCBI Description	(AC003981) F22O13.12 [Arabidopsis thaliana]

Seq. No.	148533
Seq. ID	LIB3175-006-P1-K1-G11
Method	BLASTN
NCBI GI	g4559344
BLAST score	222
E value	1.0e-121
Match length	335
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic

sequence, complete sequence

Seq. No.	148534
Seq. ID	LIB3175-006-P1-K1-G3
Method	BLASTN
NCBI GI	g4220633
BLAST score	324
E value	0.0e+00
Match length	365
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	148535
Seq. ID	LIB3175-006-P1-K1-G4
Method	BLASTX
NCBI GI	g3273751
BLAST score	579
E value	5.0e-60
Match length	133
% identity	86
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	148536
Seq. ID	LIB3175-006-P1-K1-G5
Method	BLASTX
NCBI GI	g4454473
BLAST score	302
E value	1.0e-27
Match length	99
% identity	61
NCBI Description	(AC006234) putative beta-expansin protein [Arabidopsis thaliana]

Seq. No.	148537
Seq. ID	LIB3175-006-P1-K1-G6
Method	BLASTN
NCBI GI	g4220636
BLAST score	34
E value	4.0e-10
Match length	51
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	148538
Seq. ID	LIB3175-006-P1-K1-G7
Method	BLASTX
NCBI GI	g3913379
BLAST score	44
E value	4.0e-77
Match length	142
% identity	99
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	148539
Seq. ID	LIB3175-006-P1-K1-G9
Method	BLASTN
NCBI GI	g4584351
BLAST score	377
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	148540
Seq. ID	LIB3175-006-P1-K1-H1
Method	BLASTX
NCBI GI	g3063449
BLAST score	435
E value	4.0e-43
Match length	103
% identity	77
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	148541
Seq. ID	LIB3175-006-P1-K1-H10
Method	BLASTX
NCBI GI	g729470
BLAST score	424
E value	7.0e-42
Match length	123
% identity	67
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	148542
Seq. ID	LIB3175-006-P1-K1-H11
Method	BLASTX
NCBI GI	g3157924
BLAST score	196
E value	3.0e-15
Match length	37
% identity	100
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	148543
Seq. ID	LIB3175-006-P1-K1-H12
Method	BLASTN
NCBI GI	g3608126
BLAST score	234

E value	1.0e-129
Match length	289
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148544
Seq. ID	LIB3175-006-P1-K1-H3
Method	BLASTN
NCBI GI	g16228
BLAST score	55
E value	3.0e-22
Match length	193
% identity	89
NCBI Description	A.thaliana cor47 mRNA

Seq. No.	148545
Seq. ID	LIB3175-006-P1-K1-H4
Method	BLASTX
NCBI GI	g4490732
BLAST score	502
E value	7.0e-51
Match length	99
% identity	99
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	148546
Seq. ID	LIB3175-006-P1-K1-H5
Method	BLASTN
NCBI GI	g3985958
BLAST score	91
E value	1.0e-43
Match length	168
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	148547
Seq. ID	LIB3175-006-P1-K1-H7
Method	BLASTX
NCBI GI	g114335
BLAST score	564
E value	3.0e-58
Match length	123
% identity	91
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	148548
Seq. ID	LIB3175-006-P1-K1-H9
Method	BLASTX
NCBI GI	g1402904
BLAST score	626
E value	2.0e-65

Match length	125
% identity	97
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	148549
Seq. ID	LIB3175-007-P1-K1-A1
Method	BLASTN
NCBI GI	g3482964
BLAST score	136
E value	2.0e-70
Match length	386
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	148550
Seq. ID	LIB3175-007-P1-K1-A10
Method	BLASTN
NCBI GI	g4757662
BLAST score	147
E value	6.0e-77
Match length	361
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	148551
Seq. ID	LIB3175-007-P1-K1-A11
Method	BLASTN
NCBI GI	g4106339
BLAST score	345
E value	0.0e+00
Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana protein phosphatase 2A regulatory subunit isoform B' delta mRNA, complete cds

Seq. No.	148552
Seq. ID	LIB3175-007-P1-K1-A12
Method	BLASTX
NCBI GI	g2511588
BLAST score	677
E value	2.0e-71
Match length	133
% identity	100
NCBI Description	(Y13691) multicatalytic endopeptidase complex, proteasome component, alpha subunit [Arabidopsis thaliana]

Seq. No.	148553
Seq. ID	LIB3175-007-P1-K1-A2
Method	BLASTX
NCBI GI	g4406780
BLAST score	485
E value	5.0e-49
Match length	98
% identity	90
NCBI Description	(AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No.	148554
Seq. ID	LIB3175-007-P1-K1-A3
Method	BLASTN
NCBI GI	g3702736
BLAST score	43
E value	7.0e-15
Match length	203
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	148555
Seq. ID	LIB3175-007-P1-K1-A5
Method	BLASTX
NCBI GI	g2829903
BLAST score	68
E value	6.0e-62
Match length	136
% identity	91
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	148556
Seq. ID	LIB3175-007-P1-K1-A7
Method	BLASTN
NCBI GI	g4159710
BLAST score	297
E value	1.0e-166
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	148557
Seq. ID	LIB3175-007-P1-K1-A9
Method	BLASTN
NCBI GI	g2264307
BLAST score	291
E value	1.0e-163
Match length	382
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	148558
Seq. ID	LIB3175-007-P1-K1-B1
Method	BLASTX
NCBI GI	g4538963
BLAST score	626
E value	2.0e-65
Match length	146
% identity	65
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	148559
Seq. ID	LIB3175-007-P1-K1-B10
Method	BLASTX
NCBI GI	g4185153
BLAST score	251
E value	2.0e-21
Match length	101
% identity	54
NCBI Description	(AC005724) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148560
Seq. ID	LIB3175-007-P1-K1-B11
Method	BLASTX
NCBI GI	g4454478
BLAST score	641
E value	3.0e-67
Match length	144
% identity	87
NCBI Description	(AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148561
Seq. ID	LIB3175-007-P1-K1-B12
Method	BLASTX
NCBI GI	g2501056
BLAST score	541
E value	1.0e-55
Match length	112
% identity	97
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	148562
Seq. ID	LIB3175-007-P1-K1-B3
Method	BLASTX
NCBI GI	g4589396
BLAST score	249
E value	3.0e-21
Match length	100
% identity	47
NCBI Description	(D89971) asparaginyl endopeptidase (VmPE-1) [Vigna mungo]

Seq. No.	148563
Seq. ID	LIB3175-007-P1-K1-B4
Method	BLASTX
NCBI GI	g3928150
BLAST score	391
E value	7.0e-38
Match length	135
% identity	58
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	148564
Seq. ID	LIB3175-007-P1-K1-B5
Method	BLASTN
NCBI GI	g2924728

BLAST score	168
E value	2.0e-89
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	148565
Seq. ID	LIB3175-007-P1-K1-B6
Method	BLASTX
NCBI GI	g728904
BLAST score	236
E value	1.0e-19
Match length	111
% identity	48
NCBI Description	CALCIUM-TRANSPORTING ATPASE 2 (VACUOLAR CA2+-ATPASE) >gi_1077041_pir__S48877 Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) >gi_454003 (U03060) calcium ATPase [Saccharomyces cerevisiae] >gi_1322457_emb_CAA96706_ (Z72528) ORF YGL006w [Saccharomyces cerevisiae]

Seq. No.	148566
Seq. ID	LIB3175-007-P1-K1-B7
Method	BLASTX
NCBI GI	g2879811
BLAST score	522
E value	3.0e-53
Match length	112
% identity	87
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	148567
Seq. ID	LIB3175-007-P1-K1-B8
Method	BLASTN
NCBI GI	g2351061
BLAST score	228
E value	1.0e-125
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	148568
Seq. ID	LIB3175-007-P1-K1-B9
Method	BLASTX
NCBI GI	g1352347
BLAST score	511
E value	5.0e-52
Match length	122
% identity	84
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	148569
Seq. ID	LIB3175-007-P1-K1-C11
Method	BLASTX
NCBI GI	g2738248
BLAST score	485
E value	5.0e-49
Match length	119
% identity	82
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	148570
Seq. ID	LIB3175-007-P1-K1-C2
Method	BLASTX
NCBI GI	g4127456
BLAST score	124
E value	2.0e-27
Match length	89
% identity	60
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	148571
Seq. ID	LIB3175-007-P1-K1-C3
Method	BLASTX
NCBI GI	g1518540
BLAST score	545
E value	6.0e-56
Match length	117
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	148572
Seq. ID	LIB3175-007-P1-K1-C4
Method	BLASTX
NCBI GI	g1705677
BLAST score	729
E value	2.0e-77
Match length	144
% identity	59
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	148573
Seq. ID	LIB3175-007-P1-K1-C5
Method	BLASTX
NCBI GI	g3461838
BLAST score	456
E value	2.0e-45
Match length	142
% identity	58
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	148574
Seq. ID	LIB3175-007-P1-K1-C6

Method	BLASTX
NCBI GI	g1402916
BLAST score	384
E value	4.0e-37
Match length	121
% identity	64
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	148575
Seq. ID	LIB3175-007-P1-K1-C7
Method	BLASTX
NCBI GI	g2160133
BLAST score	380
E value	1.0e-36
Match length	89
% identity	88
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	148576
Seq. ID	LIB3175-007-P1-K1-C8
Method	BLASTN
NCBI GI	g4544461
BLAST score	333
E value	0.0e+00
Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F23E6 genomic sequence, complete sequence

Seq. No.	148577
Seq. ID	LIB3175-007-P1-K1-C9
Method	BLASTX
NCBI GI	g4427003
BLAST score	406
E value	1.0e-39
Match length	123
% identity	63
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	148578
Seq. ID	LIB3175-007-P1-K1-D1
Method	BLASTX
NCBI GI	g4539292
BLAST score	494
E value	6.0e-50
Match length	96
% identity	97
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	148579
Seq. ID	LIB3175-007-P1-K1-D10

Method	BLASTX
NCBI GI	g113782
BLAST score	535
E value	7.0e-55
Match length	104
% identity	99
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	148580
Seq. ID	LIB3175-007-P1-K1-D11
Method	BLASTN
NCBI GI	g2924505
BLAST score	333
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	148581
Seq. ID	LIB3175-007-P1-K1-D12
Method	BLASTN
NCBI GI	g4455339
BLAST score	58
E value	5.0e-24
Match length	141
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	148582
Seq. ID	LIB3175-007-P1-K1-D2
Method	BLASTX
NCBI GI	g166834
BLAST score	408
E value	6.0e-40
Match length	81
% identity	96
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	148583
Seq. ID	LIB3175-007-P1-K1-D3
Method	BLASTX
NCBI GI	g4584548
BLAST score	601
E value	2.0e-62
Match length	115
% identity	100
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	148584

Seq. ID	LIB3175-007-P1-K1-D4
Method	BLASTN
NCBI GI	g3449326
BLAST score	250
E value	1.0e-138
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	148585
Seq. ID	LIB3175-007-P1-K1-D5
Method	BLASTX
NCBI GI	g584892
BLAST score	390
E value	7.0e-38
Match length	97
% identity	66
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	148586
Seq. ID	LIB3175-007-P1-K1-D6
Method	BLASTX
NCBI GI	g1246019
BLAST score	670
E value	1.0e-70
Match length	128
% identity	100
NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No.	148587
Seq. ID	LIB3175-007-P1-K1-D7
Method	BLASTX
NCBI GI	g4586265
BLAST score	469
E value	4.0e-47
Match length	111
% identity	78
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148588
Seq. ID	LIB3175-007-P1-K1-D9
Method	BLASTX
NCBI GI	g2459417
BLAST score	383
E value	4.0e-37
Match length	84
% identity	85
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	148589
Seq. ID	LIB3175-007-P1-K1-E1

Method	BLASTX
NCBI GI	g4262228
BLAST score	386
E value	2.0e-37
Match length	76
% identity	97
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	148590
Seq. ID	LIB3175-007-P1-K1-E10
Method	BLASTX
NCBI GI	g112681
BLAST score	594
E value	9.0e-62
Match length	125
% identity	92
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148591
Seq. ID	LIB3175-007-P1-K1-E11
Method	BLASTN
NCBI GI	g2494106
BLAST score	250
E value	1.0e-138
Match length	430
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148592
Seq. ID	LIB3175-007-P1-K1-E12
Method	BLASTX
NCBI GI	g3318611
BLAST score	289
E value	6.0e-26
Match length	68
% identity	82
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	148593
Seq. ID	LIB3175-007-P1-K1-E2
Method	BLASTX
NCBI GI	g2119846
BLAST score	630
E value	5.0e-66
Match length	119
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem

II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	148594
Seq. ID	LIB3175-007-P1-K1-E3
Method	BLASTN
NCBI GI	g3004543
BLAST score	66
E value	1.0e-28
Match length	214
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148595
Seq. ID	LIB3175-007-P1-K1-E5
Method	BLASTN
NCBI GI	g4531433
BLAST score	432
E value	0.0e+00
Match length	447
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	148596
Seq. ID	LIB3175-007-P1-K1-E6
Method	BLASTN
NCBI GI	g4049332
BLAST score	303
E value	1.0e-170
Match length	391
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	148597
Seq. ID	LIB3175-007-P1-K1-E8
Method	BLASTX
NCBI GI	g1346263
BLAST score	440
E value	1.0e-43
Match length	100
% identity	98
NCBI Description	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor - Arabidopsis thaliana >gi_1049057 (U27118) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	148598
Seq. ID	LIB3175-007-P1-K1-E9
Method	BLASTX
NCBI GI	g2623962
BLAST score	376
E value	2.0e-36
Match length	78

% identity	94
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	148599
Seq. ID	LIB3175-007-P1-K1-F1
Method	BLASTX
NCBI GI	g4538947
BLAST score	463
E value	2.0e-46
Match length	95
% identity	49
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	148600
Seq. ID	LIB3175-007-P1-K1-F12
Method	BLASTN
NCBI GI	g2160155
BLAST score	231
E value	1.0e-127
Match length	422
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	148601
Seq. ID	LIB3175-007-P1-K1-F2
Method	BLASTX
NCBI GI	g1174851
BLAST score	61
E value	6.0e-48
Match length	124
% identity	77
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 3 (UBIQUITIN-PROTEIN LIGASE 6) (UBIQUITIN CARRIER PROTEIN 6)

Seq. No.	148602
Seq. ID	LIB3175-007-P1-K1-F3
Method	BLASTX
NCBI GI	g3641837
BLAST score	475
E value	9.0e-48
Match length	95
% identity	98
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	148603
Seq. ID	LIB3175-007-P1-K1-F4
Method	BLASTX
NCBI GI	g1170191
BLAST score	621
E value	7.0e-65
Match length	132
% identity	94
NCBI Description	HOMEOBOX PROTEIN HD1 >gi_1076449_pir__S47535

homeodomain-containing protein - rape
>gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing protein [Brassica napus] >gi_1090522_prf__2019252A homeobox protein [Brassica napus]

Seq. No.	148604
Seq. ID	LIB3175-007-P1-K1-F6
Method	BLASTN
NCBI GI	g3608126
BLAST score	172
E value	8.0e-92
Match length	394
% identity	79
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148605
Seq. ID	LIB3175-007-P1-K1-F7
Method	BLASTX
NCBI GI	g2369714
BLAST score	481
E value	1.0e-48
Match length	102
% identity	91
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	148606
Seq. ID	LIB3175-007-P1-K1-F8
Method	BLASTX
NCBI GI	g112681
BLAST score	489
E value	2.0e-49
Match length	118
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148607
Seq. ID	LIB3175-007-P1-K1-F9
Method	BLASTX
NCBI GI	g3128168
BLAST score	573
E value	3.0e-59
Match length	124
% identity	89
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	148608
Seq. ID	LIB3175-007-P1-K1-G1
Method	BLASTX
NCBI GI	g629541
BLAST score	627
E value	1.0e-65

Match length	134
% identity	93
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	148609
Seq. ID	LIB3175-007-P1-K1-G10
Method	BLASTX
NCBI GI	g3169182
BLAST score	394
E value	3.0e-38
Match length	75
% identity	100
NCBI Description	(AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.	148610
Seq. ID	LIB3175-007-P1-K1-G11
Method	BLASTN
NCBI GI	g166927
BLAST score	296
E value	1.0e-166
Match length	300
% identity	100
NCBI Description	Arabidopsis thaliana unidentified mRNA sequence, complete cds

Seq. No.	148611
Seq. ID	LIB3175-007-P1-K1-G2
Method	BLASTX
NCBI GI	g1174779
BLAST score	649
E value	4.0e-68
Match length	142
% identity	89
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] >gi_4490703_emb_CAB38837.1_ (AL035680) tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana]

Seq. No.	148612
Seq. ID	LIB3175-007-P1-K1-G3
Method	BLASTX
NCBI GI	g3021506
BLAST score	396
E value	2.0e-38
Match length	122
% identity	66
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	148613
Seq. ID	LIB3175-007-P1-K1-G4
Method	BLASTN
NCBI GI	g2618602
BLAST score	59
E value	2.0e-24

Match length	192
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	148614
Seq. ID	LIB3175-007-P1-K1-G5
Method	BLASTN
NCBI GI	g2244950
BLAST score	340
E value	0.0e+00
Match length	359
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	148615
Seq. ID	LIB3175-007-P1-K1-G6
Method	BLASTX
NCBI GI	g3152600
BLAST score	473
E value	1.0e-48
Match length	106
% identity	94
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. ESTs gb_H37409, gb_AA395290, and gb_T43907 come from this gene. [Arabidopsis thaliana]

Seq. No.	148616
Seq. ID	LIB3175-007-P1-K1-G7
Method	BLASTX
NCBI GI	g3386611
BLAST score	747
E value	1.0e-79
Match length	144
% identity	99
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	148617
Seq. ID	LIB3175-007-P1-K1-G8
Method	BLASTX
NCBI GI	g4432867
BLAST score	192
E value	1.0e-14
Match length	59
% identity	61
NCBI Description	(AC006300) putative dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	148618
Seq. ID	LIB3175-007-P1-K1-G9
Method	BLASTX
NCBI GI	g1769968
BLAST score	317
E value	3.0e-29
Match length	134

% identity	51
NCBI Description	(Y10156) myrosinase-associated protein [Brassica napus]

Seq. No.	148619
Seq. ID	LIB3175-007-P1-K1-H1
Method	BLASTX
NCBI GI	g548847
BLAST score	337
E value	8.0e-32
Match length	75
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_1086182_pir__S39501 ribosomal protein S12 - curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal protein S12 [Nicotiana tabacum]

Seq. No.	148620
Seq. ID	LIB3175-007-P1-K1-H11
Method	BLASTX
NCBI GI	g3549670
BLAST score	423
E value	1.0e-41
Match length	83
% identity	100
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	148621
Seq. ID	LIB3175-007-P1-K1-H12
Method	BLASTN
NCBI GI	g1469225
BLAST score	88
E value	9.0e-42
Match length	168
% identity	89
NCBI Description	B.oleracea mRNA for putative major latex protein

Seq. No.	148622
Seq. ID	LIB3175-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2979555
BLAST score	750
E value	5.0e-80
Match length	142
% identity	99
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	148623
Seq. ID	LIB3175-007-P1-K1-H4
Method	BLASTX
NCBI GI	g3785983
BLAST score	317
E value	3.0e-29
Match length	99
% identity	58
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148624

Seq. ID	LIB3175-007-P1-K1-H5
Method	BLASTN
NCBI GI	g3860243
BLAST score	266
E value	1.0e-148
Match length	323
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148625
Seq. ID	LIB3175-007-P1-K1-H6
Method	BLASTX
NCBI GI	g3128176
BLAST score	306
E value	7.0e-28
Match length	108
% identity	48
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	148626
Seq. ID	LIB3175-007-P1-K1-H7
Method	BLASTX
NCBI GI	g1864017
BLAST score	548
E value	2.0e-56
Match length	104
% identity	100
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	148627
Seq. ID	LIB3175-007-P1-K1-H8
Method	BLASTN
NCBI GI	g2656031
BLAST score	90
E value	4.0e-43
Match length	303
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	148628
Seq. ID	LIB3175-007-P1-K1-H9
Method	BLASTX
NCBI GI	g2661422
BLAST score	293
E value	9.0e-27
Match length	68
% identity	85
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	148629
Seq. ID	LIB3175-009-P1-K1-A12
Method	BLASTX

NCBI GI	g1408471
BLAST score	159
E value	3.0e-11
Match length	36
% identity	92
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	148630
Seq. ID	LIB3175-009-P1-K1-A8
Method	BLASTN
NCBI GI	g396217
BLAST score	39
E value	1.0e-12
Match length	110
% identity	86
NCBI Description	A.thaliana mRNA for transmembrane protein TMP-B

Seq. No.	148631
Seq. ID	LIB3175-009-P1-K1-B2
Method	BLASTN
NCBI GI	g4741953
BLAST score	54
E value	1.0e-21
Match length	122
% identity	82
NCBI Description	Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA, complete cds

Seq. No.	148632
Seq. ID	LIB3175-009-P1-K1-B3
Method	BLASTN
NCBI GI	g2264304
BLAST score	40
E value	3.0e-13
Match length	153
% identity	77
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	148633
Seq. ID	LIB3175-009-P1-K1-B7
Method	BLASTX
NCBI GI	g4580392
BLAST score	433
E value	5.0e-43
Match length	99
% identity	87
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148634
Seq. ID	LIB3175-009-P1-K1-D10
Method	BLASTN
NCBI GI	g3688161
BLAST score	34
E value	6.0e-10

Match length	56
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for centrin

Seq. No.	148635
Seq. ID	LIB3175-009-P1-K1-D3
Method	BLASTN
NCBI GI	g4510360
BLAST score	111
E value	1.0e-55
Match length	234
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	148636
Seq. ID	LIB3175-009-P1-K1-D7
Method	BLASTN
NCBI GI	g1592684
BLAST score	50
E value	1.0e-19
Match length	86
% identity	90
NCBI Description	A.thaliana mRNA for oleosin type3 protein

Seq. No.	148637
Seq. ID	LIB3175-009-P1-K1-E11
Method	BLASTN
NCBI GI	g2656028
BLAST score	42
E value	1.0e-14
Match length	125
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	148638
Seq. ID	LIB3175-009-P1-K1-E2
Method	BLASTX
NCBI GI	g4263525
BLAST score	407
E value	7.0e-40
Match length	119
% identity	70
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	148639
Seq. ID	LIB3175-009-P1-K1-E5
Method	BLASTX
NCBI GI	g3176668
BLAST score	295
E value	5.0e-27
Match length	80
% identity	76
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and

gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	148640
Seq. ID	LIB3175-009-P1-K1-F10
Method	BLASTN
NCBI GI	g4371278
BLAST score	62
E value	1.0e-26
Match length	137
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148641
Seq. ID	LIB3175-009-P1-K1-F2
Method	BLASTN
NCBI GI	g3241926
BLAST score	55
E value	2.0e-22
Match length	111
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	148642
Seq. ID	LIB3175-009-P1-K1-F5
Method	BLASTN
NCBI GI	g4309719
BLAST score	74
E value	1.0e-33
Match length	179
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148643
Seq. ID	LIB3175-009-P1-K1-F9
Method	BLASTN
NCBI GI	g16185
BLAST score	39
E value	5.0e-13
Match length	74
% identity	86
NCBI Description	A.thaliana atpgp1 gene for P-glycoprotein, homologous to mammalian mdr genes

Seq. No.	148644
Seq. ID	LIB3175-009-P1-K1-G3
Method	BLASTN
NCBI GI	g1402909
BLAST score	47
E value	1.0e-17
Match length	163
% identity	79
NCBI Description	A.thaliana mRNA for peroxidase, prxr4

Seq. No. 148645

Seq. ID	LIB3175-009-P1-K1-G4
Method	BLASTX
NCBI GI	g1076414
BLAST score	476
E value	4.0e-48
Match length	101
% identity	92
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	148646
Seq. ID	LIB3175-009-P1-K1-G7
Method	BLASTN
NCBI GI	g1359496
BLAST score	33
E value	4.0e-09
Match length	268
% identity	45
NCBI Description	A.thaliana mRNA for seryl-tRNA synthetase

Seq. No.	148647
Seq. ID	LIB3175-009-P1-K1-H8
Method	BLASTN
NCBI GI	g2244991
BLAST score	20
E value	9.1e-02
Match length	99
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	148648
Seq. ID	LIB3175-009-P1-K1-H9
Method	BLASTX
NCBI GI	g1168748
BLAST score	584
E value	2.0e-60
Match length	121
% identity	58
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	148649
Seq. ID	LIB3175-015-P1-K1-A10
Method	BLASTN
NCBI GI	g4220643
BLAST score	240
E value	1.0e-132
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	148650
Seq. ID	LIB3175-015-P1-K1-A11

Method	BLASTX
NCBI GI	g2655420
BLAST score	556
E value	3.0e-57
Match length	114
% identity	92
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica napus]

Seq. No.	148651
Seq. ID	LIB3175-015-P1-K1-A12
Method	BLASTX
NCBI GI	g2226202
BLAST score	175
E value	1.0e-12
Match length	102
% identity	42
NCBI Description	(Y14082) hypothetical protein [Bacillus subtilis] >gi_2633281_emb_CAB12785_ (Z99109) similar to amino acid transporter [Bacillus subtilis]

Seq. No.	148652
Seq. ID	LIB3175-015-P1-K1-A3
Method	BLASTN
NCBI GI	g2264315
BLAST score	85
E value	3.0e-40
Match length	168
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	148653
Seq. ID	LIB3175-015-P1-K1-A5
Method	BLASTX
NCBI GI	g535780
BLAST score	683
E value	3.0e-72
Match length	133
% identity	98
NCBI Description	(D26609) transmembrane protein [Arabidopsis thaliana]

Seq. No.	148654
Seq. ID	LIB3175-015-P1-K1-A6
Method	BLASTN
NCBI GI	g3449327
BLAST score	275
E value	1.0e-153
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	148655
Seq. ID	LIB3175-015-P1-K1-A7
Method	BLASTX
NCBI GI	g4128133

BLAST score	184
E value	1.0e-13
Match length	60
% identity	55
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	148656
Seq. ID	LIB3175-015-P1-K1-A8
Method	BLASTX
NCBI GI	g3738320
BLAST score	358
E value	4.0e-34
Match length	108
% identity	64
NCBI Description	(AC005170) putative cinnamoyl CoA reductase [Arabidopsis thaliana]

Seq. No.	148657
Seq. ID	LIB3175-015-P1-K1-A9
Method	BLASTN
NCBI GI	g3046854
BLAST score	37
E value	2.0e-11
Match length	53
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	148658
Seq. ID	LIB3175-015-P1-K1-B1
Method	BLASTX
NCBI GI	g4826972
BLAST score	159
E value	9.0e-11
Match length	66
% identity	53
NCBI Description	RNA binding motif protein 8 >gi_4455129_gb_AAD21089.1_ (AF127761) ribonucleoprotein RBM8 [Homo sapiens]

Seq. No.	148659
Seq. ID	LIB3175-015-P1-K1-B10
Method	BLASTX
NCBI GI	g4185511
BLAST score	527
E value	7.0e-54
Match length	102
% identity	99
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	148660
Seq. ID	LIB3175-015-P1-K1-B11
Method	BLASTX
NCBI GI	g1170939
BLAST score	646
E value	7.0e-68
Match length	132

% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	148661
Seq. ID	LIB3175-015-P1-K1-B12
Method	BLASTX
NCBI GI	g4741948
BLAST score	628
E value	9.0e-66
Match length	118
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	148662
Seq. ID	LIB3175-015-P1-K1-B2
Method	BLASTX
NCBI GI	g4539376
BLAST score	171
E value	4.0e-12
Match length	81
% identity	56
NCBI Description	(AL049525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148663
Seq. ID	LIB3175-015-P1-K1-B4
Method	BLASTN
NCBI GI	g4159706
BLAST score	405
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	148664
Seq. ID	LIB3175-015-P1-K1-B5
Method	BLASTX
NCBI GI	g4063739
BLAST score	509
E value	9.0e-52
Match length	133
% identity	75
NCBI Description	(AC005851) putative copper/zinc superoxide dismutase [Arabidopsis thaliana]

Seq. No.	148665
Seq. ID	LIB3175-015-P1-K1-B6
Method	BLASTX
NCBI GI	g114339
BLAST score	200
E value	1.0e-21
Match length	102

% identity	70
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]

Seq. No.	148666
Seq. ID	LIB3175-015-P1-K1-B7
Method	BLASTX
NCBI GI	g4741952
BLAST score	207
E value	2.0e-43
Match length	92
% identity	98
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	148667
Seq. ID	LIB3175-015-P1-K1-B8
Method	BLASTX
NCBI GI	g2462935
BLAST score	530
E value	3.0e-54
Match length	131
% identity	73
NCBI Description	(Y12321) open reading frame 1 [Brassica oleracea]

Seq. No.	148668
Seq. ID	LIB3175-015-P1-K1-B9
Method	BLASTX
NCBI GI	g3021336
BLAST score	646
E value	7.0e-68
Match length	126
% identity	99
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	148669
Seq. ID	LIB3175-015-P1-K1-C1
Method	BLASTN
NCBI GI	g2832639
BLAST score	380
E value	0.0e+00
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	148670
Seq. ID	LIB3175-015-P1-K1-C10
Method	BLASTX
NCBI GI	g2129577
BLAST score	426
E value	5.0e-42
Match length	81
% identity	100
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	148671
Seq. ID	LIB3175-015-P1-K1-C11
Method	BLASTN
NCBI GI	g4468801
BLAST score	46
E value	7.0e-17
Match length	193
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	148672
Seq. ID	LIB3175-015-P1-K1-C12
Method	BLASTX
NCBI GI	g4406816
BLAST score	671
E value	9.0e-71
Match length	127
% identity	100
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	148673
Seq. ID	LIB3175-015-P1-K1-C2
Method	BLASTX
NCBI GI	g4193388
BLAST score	403
E value	2.0e-39
Match length	110
% identity	72
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	148674
Seq. ID	LIB3175-015-P1-K1-C3
Method	BLASTN
NCBI GI	g4557061
BLAST score	386
E value	0.0e+00
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	148675
Seq. ID	LIB3175-015-P1-K1-C4
Method	BLASTX
NCBI GI	g2224931
BLAST score	425
E value	6.0e-42
Match length	88
% identity	98
NCBI Description	(AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No.	148676
Seq. ID	LIB3175-015-P1-K1-C5

Method	BLASTN
NCBI GI	g3341671
BLAST score	131
E value	2.0e-67
Match length	410
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148677
Seq. ID	LIB3175-015-P1-K1-C6
Method	BLASTX
NCBI GI	g2213592
BLAST score	329
E value	1.0e-30
Match length	134
% identity	26
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	148678
Seq. ID	LIB3175-015-P1-K1-C7
Method	BLASTN
NCBI GI	g3241917
BLAST score	136
E value	2.0e-70
Match length	349
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	148679
Seq. ID	LIB3175-015-P1-K1-D10
Method	BLASTX
NCBI GI	g4581156
BLAST score	211
E value	7.0e-17
Match length	40
% identity	100
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No.	148680
Seq. ID	LIB3175-015-P1-K1-D11
Method	BLASTX
NCBI GI	g2160133
BLAST score	386
E value	2.0e-37
Match length	91
% identity	87
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	148681
Seq. ID	LIB3175-015-P1-K1-D12
Method	BLASTX
NCBI GI	g974294

BLAST score	164
E value	2.0e-11
Match length	70
% identity	53
NCBI Description	(U31309) LP6 [Pinus taeda]

Seq. No.	148682
Seq. ID	LIB3175-015-P1-K1-D2
Method	BLASTX
NCBI GI	g4773885
BLAST score	555
E value	3.0e-57
Match length	121
% identity	87
NCBI Description	(AF076243) putative aspartic protease [Arabidopsis thaliana]

Seq. No.	148683
Seq. ID	LIB3175-015-P1-K1-D3
Method	BLASTX
NCBI GI	g2492519
BLAST score	503
E value	4.0e-51
Match length	113
% identity	86
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	148684
Seq. ID	LIB3175-015-P1-K1-D6
Method	BLASTX
NCBI GI	g4539459
BLAST score	411
E value	3.0e-40
Match length	135
% identity	62
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	148685
Seq. ID	LIB3175-015-P1-K1-D7
Method	BLASTN
NCBI GI	g4662640
BLAST score	367
E value	0.0e+00
Match length	387
% identity	34
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	148686
Seq. ID	LIB3175-015-P1-K1-D8
Method	BLASTX
NCBI GI	g1169598
BLAST score	388
E value	1.0e-37
Match length	85

% identity	86
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]
Seq. No.	148687
Seq. ID	LIB3175-015-P1-K1-E10
Method	BLASTN
NCBI GI	g3047074
BLAST score	389
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21E10
Seq. No.	148688
Seq. ID	LIB3175-015-P1-K1-E11
Method	BLASTX
NCBI GI	g1076416
BLAST score	696
E value	1.0e-73
Match length	133
% identity	100
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]
Seq. No.	148689
Seq. ID	LIB3175-015-P1-K1-E12
Method	BLASTN
NCBI GI	g2191126
BLAST score	395
E value	0.0e+00
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01
Seq. No.	148690
Seq. ID	LIB3175-015-P1-K1-E3
Method	BLASTN
NCBI GI	g4760411
BLAST score	340
E value	0.0e+00
Match length	408
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence
Seq. No.	148691
Seq. ID	LIB3175-015-P1-K1-E4
Method	BLASTX
NCBI GI	g2921094
BLAST score	604
E value	6.0e-63
Match length	129

% identity	90
NCBI Description	(AF018174) thioredoxin-f [Brassica napus]

Seq. No.	148692
Seq. ID	LIB3175-015-P1-K1-E6
Method	BLASTX
NCBI GI	g3434969
BLAST score	165
E value	2.0e-11
Match length	37
% identity	76
NCBI Description	(AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]

Seq. No.	148693
Seq. ID	LIB3175-015-P1-K1-E7
Method	BLASTX
NCBI GI	g2407800
BLAST score	349
E value	4.0e-33
Match length	71
% identity	100
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	148694
Seq. ID	LIB3175-015-P1-K1-E8
Method	BLASTX
NCBI GI	g3924615
BLAST score	157
E value	2.0e-10
Match length	95
% identity	33
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148695
Seq. ID	LIB3175-015-P1-K1-E9
Method	BLASTN
NCBI GI	g2760172
BLAST score	387
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	148696
Seq. ID	LIB3175-015-P1-K1-F1
Method	BLASTN
NCBI GI	g4584531
BLAST score	102
E value	4.0e-50
Match length	404
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	148697

Seq. ID	LIB3175-015-P1-K1-F10
Method	BLASTX
NCBI GI	g2118220
BLAST score	334
E value	2.0e-31
Match length	86
% identity	51
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	148698
Seq. ID	LIB3175-015-P1-K1-F11
Method	BLASTN
NCBI GI	g3063438
BLAST score	400
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	148699
Seq. ID	LIB3175-015-P1-K1-F2
Method	BLASTX
NCBI GI	g3123745
BLAST score	390
E value	8.0e-38
Match length	96
% identity	82
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	148700
Seq. ID	LIB3175-015-P1-K1-F3
Method	BLASTN
NCBI GI	g4335744
BLAST score	335
E value	0.0e+00
Match length	359
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148701
Seq. ID	LIB3175-015-P1-K1-F4
Method	BLASTX
NCBI GI	g4678226
BLAST score	480
E value	2.0e-48

Match length	97
% identity	98
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	148702
Seq. ID	LIB3175-015-P1-K1-F6
Method	BLASTX
NCBI GI	g99752
BLAST score	507
E value	2.0e-51
Match length	125
% identity	86
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	148703
Seq. ID	LIB3175-015-P1-K1-F7
Method	BLASTX
NCBI GI	g4586265
BLAST score	510
E value	7.0e-52
Match length	135
% identity	74
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148704
Seq. ID	LIB3175-015-P1-K1-F8
Method	BLASTN
NCBI GI	g4678266
BLAST score	309
E value	1.0e-173
Match length	350
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	148705
Seq. ID	LIB3175-015-P1-K1-F9
Method	BLASTX
NCBI GI	g4678288
BLAST score	231
E value	3.0e-19
Match length	132
% identity	46
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	148706
Seq. ID	LIB3175-015-P1-K1-G10
Method	BLASTN
NCBI GI	g556473
BLAST score	223
E value	1.0e-122
Match length	377
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ERD14 protein, complete cds

Seq. No.	148707
Seq. ID	LIB3175-015-P1-K1-G11
Method	BLASTX
NCBI GI	g112681
BLAST score	567
E value	1.0e-58
Match length	131
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148708
Seq. ID	LIB3175-015-P1-K1-G2
Method	BLASTX
NCBI GI	g1773330
BLAST score	543
E value	8.0e-56
Match length	125
% identity	84
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	148709
Seq. ID	LIB3175-015-P1-K1-G3
Method	BLASTN
NCBI GI	g807576
BLAST score	236
E value	1.0e-130
Match length	272
% identity	98
NCBI Description	Arabidopsis thaliana GTP-binding protein mRNA, complete cds

Seq. No.	148710
Seq. ID	LIB3175-015-P1-K1-G5
Method	BLASTX
NCBI GI	g132102
BLAST score	151
E value	6.0e-10
Match length	41
% identity	71
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	148711
Seq. ID	LIB3175-015-P1-K1-G6
Method	BLASTN
NCBI GI	g16244
BLAST score	55
E value	2.0e-22
Match length	87
% identity	91

NCBI Description	Arabidopsis thaliana Csr 1.2 gene for acetolactate synthase (EC 4.1.3.18)
Seq. No.	148712
Seq. ID	LIB3175-015-P1-K1-G7
Method	BLASTX
NCBI GI	g2145356
BLAST score	423
E value	1.0e-41
Match length	81
% identity	99
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.	148713
Seq. ID	LIB3175-015-P1-K1-G8
Method	BLASTN
NCBI GI	g1209241
BLAST score	387
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence
Seq. No.	148714
Seq. ID	LIB3175-015-P1-K1-G9
Method	BLASTX
NCBI GI	g3176668
BLAST score	665
E value	4.0e-70
Match length	131
% identity	98
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]
Seq. No.	148715
Seq. ID	LIB3175-015-P1-K1-H1
Method	BLASTN
NCBI GI	g3927822
BLAST score	286
E value	1.0e-160
Match length	405
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	148716
Seq. ID	LIB3175-015-P1-K1-H11
Method	BLASTX
NCBI GI	g1769905
BLAST score	396
E value	2.0e-38
Match length	118
% identity	67
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	148717
Seq. ID	LIB3175-015-P1-K1-H2
Method	BLASTN
NCBI GI	g1143391
BLAST score	106
E value	2.0e-52
Match length	265
% identity	88
NCBI Description	A.thaliana mRNA for uridine diphosphate glucose epimerase

Seq. No.	148718
Seq. ID	LIB3175-015-P1-K1-H4
Method	BLASTX
NCBI GI	g913445
BLAST score	501
E value	7.0e-51
Match length	134
% identity	74
NCBI Description	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No.	148719
Seq. ID	LIB3175-015-P1-K1-H7
Method	BLASTN
NCBI GI	g3492855
BLAST score	390
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	148720
Seq. ID	LIB3175-015-P1-K1-H8
Method	BLASTX
NCBI GI	g1799787
BLAST score	281
E value	5.0e-25
Match length	122
% identity	48
NCBI Description	(D90868) OXALYL-COA DECARBOXYLASE (EC 4.1.1.8). [Escherichia coli]

Seq. No.	148721
Seq. ID	LIB3175-015-P1-K1-H9
Method	BLASTN
NCBI GI	g4263694
BLAST score	398
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 148722

Seq. ID	LIB3175-016-P1-K1-A10
Method	BLASTX
NCBI GI	g2642159
BLAST score	463
E value	1.0e-46
Match length	101
% identity	93
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	148723
Seq. ID	LIB3175-016-P1-K1-A11
Method	BLASTX
NCBI GI	g2642159
BLAST score	262
E value	2.0e-23
Match length	52
% identity	98
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	148724
Seq. ID	LIB3175-016-P1-K1-A12
Method	BLASTX
NCBI GI	g2642159
BLAST score	703
E value	2.0e-74
Match length	139
% identity	99
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	148725
Seq. ID	LIB3175-016-P1-K1-A5
Method	BLASTN
NCBI GI	g16472
BLAST score	314
E value	1.0e-176
Match length	388
% identity	95
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	148726
Seq. ID	LIB3175-016-P1-K1-A6
Method	BLASTN
NCBI GI	g2564044
BLAST score	276
E value	1.0e-154
Match length	413
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	148727
Seq. ID	LIB3175-016-P1-K1-A7
Method	BLASTX
NCBI GI	g1710581
BLAST score	579
E value	5.0e-60
Match length	118
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	148728
Seq. ID	LIB3175-016-P1-K1-A8
Method	BLASTX
NCBI GI	g3834309
BLAST score	664
E value	6.0e-70
Match length	134
% identity	98
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	148729
Seq. ID	LIB3175-016-P1-K1-B1
Method	BLASTN
NCBI GI	g3763944
BLAST score	199
E value	1.0e-108
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	148730
Seq. ID	LIB3175-016-P1-K1-B10
Method	BLASTX
NCBI GI	g2642159
BLAST score	696
E value	1.0e-73
Match length	137
% identity	100
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	148731
Seq. ID	LIB3175-016-P1-K1-B11
Method	BLASTN
NCBI GI	g3282170
BLAST score	48
E value	6.0e-18

Match length	144
% identity	83
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148732
Seq. ID	LIB3175-016-P1-K1-B12
Method	BLASTX
NCBI GI	g4490329
BLAST score	531
E value	2.0e-54
Match length	120
% identity	84
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	148733
Seq. ID	LIB3175-016-P1-K1-B2
Method	BLASTX
NCBI GI	g2275202
BLAST score	296
E value	7.0e-27
Match length	59
% identity	98
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	148734
Seq. ID	LIB3175-016-P1-K1-B3
Method	BLASTX
NCBI GI	g4827050
BLAST score	339
E value	8.0e-32
Match length	117
% identity	56
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No.	148735
Seq. ID	LIB3175-016-P1-K1-B4
Method	BLASTN
NCBI GI	g3510346
BLAST score	387
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	148736
Seq. ID	LIB3175-016-P1-K1-B5
Method	BLASTX
NCBI GI	g1944518
BLAST score	235
E value	1.0e-19

Match length	47
% identity	98
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	148737
Seq. ID	LIB3175-016-P1-K1-B6
Method	BLASTX
NCBI GI	g3953473
BLAST score	637
E value	9.0e-67
Match length	128
% identity	100
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	148738
Seq. ID	LIB3175-016-P1-K1-B7
Method	BLASTX
NCBI GI	g416922
BLAST score	292
E value	2.0e-26
Match length	84
% identity	68
NCBI Description	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE) (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP pyrophosphatase (EC 3.6.1.23) - tomato >gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase, dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No.	148739
Seq. ID	LIB3175-016-P1-K1-B8
Method	BLASTN
NCBI GI	g972918
BLAST score	62
E value	1.0e-26
Match length	186
% identity	83
NCBI Description	Arabidopsis thaliana IAA8 (IAA8) gene complete cds

Seq. No.	148740
Seq. ID	LIB3175-016-P1-K1-B9
Method	BLASTN
NCBI GI	g4191760
BLAST score	43
E value	7.0e-15
Match length	306
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	148741
Seq. ID	LIB3175-016-P1-K1-C1
Method	BLASTX
NCBI GI	g4662641
BLAST score	282

E value	4.0e-25
Match length	71
% identity	79
NCBI Description	(AC006429) putative auxin down-regulated protein [Arabidopsis thaliana]

Seq. No.	148742
Seq. ID	LIB3175-016-P1-K1-C10
Method	BLASTX
NCBI GI	g585350
BLAST score	362
E value	2.0e-34
Match length	92
% identity	77
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 2 (CK II) >gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA2) - Arabidopsis thaliana >gi_391605_dbj_BAA01091_ (D10247) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	148743
Seq. ID	LIB3175-016-P1-K1-C11
Method	BLASTX
NCBI GI	g115767
BLAST score	622
E value	4.0e-65
Match length	118
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	148744
Seq. ID	LIB3175-016-P1-K1-C12
Method	BLASTX
NCBI GI	g4538959
BLAST score	593
E value	1.0e-61
Match length	110
% identity	100
NCBI Description	(AL049488) putative protein [Arabidopsis thaliana]

Seq. No.	148745
Seq. ID	LIB3175-016-P1-K1-C2
Method	BLASTX
NCBI GI	g4454036
BLAST score	695
E value	1.0e-73
Match length	127
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	148746
Seq. ID	LIB3175-016-P1-K1-C3
Method	BLASTX
NCBI GI	g2829899
BLAST score	405
E value	1.0e-39
Match length	116
% identity	66
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	148747
Seq. ID	LIB3175-016-P1-K1-C4
Method	BLASTN
NCBI GI	g2342717
BLAST score	141
E value	2.0e-73
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148748
Seq. ID	LIB3175-016-P1-K1-C5
Method	BLASTX
NCBI GI	g2979555
BLAST score	371
E value	1.0e-35
Match length	138
% identity	53
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana]

Seq. No.	148749
Seq. ID	LIB3175-016-P1-K1-C6
Method	BLASTN
NCBI GI	g4220633
BLAST score	336
E value	0.0e+00
Match length	384
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	148750
Seq. ID	LIB3175-016-P1-K1-C7
Method	BLASTN
NCBI GI	g928809
BLAST score	66
E value	2.0e-29
Match length	89
% identity	100
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq3) gene

Seq. No.	148751
Seq. ID	LIB3175-016-P1-K1-C8
Method	BLASTX

NCBI GI	g2507421
BLAST score	554
E value	5.0e-57
Match length	113
% identity	96
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	148752
Seq. ID	LIB3175-016-P1-K1-C9
Method	BLASTX
NCBI GI	g267073
BLAST score	487
E value	3.0e-49
Match length	89
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	148753
Seq. ID	LIB3175-016-P1-K1-D1
Method	BLASTN
NCBI GI	g3510339
BLAST score	44
E value	1.0e-15
Match length	90
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	148754
Seq. ID	LIB3175-016-P1-K1-D10
Method	BLASTX
NCBI GI	g2529229
BLAST score	524
E value	2.0e-53
Match length	112
% identity	89
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	148755
Seq. ID	LIB3175-016-P1-K1-D11
Method	BLASTX
NCBI GI	g1644427
BLAST score	500
E value	1.0e-50
Match length	109
% identity	91
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	148756
Seq. ID	LIB3175-016-P1-K1-D12
Method	BLASTX

NCBI GI g4584255
BLAST score 238
E value 5.0e-20
Match length 56
% identity 79
NCBI Description (Y18471) SINA1p [Vitis vinifera]

Seq. No. 148757
Seq. ID LIB3175-016-P1-K1-D2
Method BLASTX
NCBI GI g974294
BLAST score 244
E value 1.0e-20
Match length 92
% identity 54
NCBI Description (U31309) LP6 [Pinus taeda]

Seq. No. 148758
Seq. ID LIB3175-016-P1-K1-D3
Method BLASTX
NCBI GI g1946367
BLAST score 155
E value 3.0e-10
Match length 70
% identity 47
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 148759
Seq. ID LIB3175-016-P1-K1-D4
Method BLASTX
NCBI GI g4314363
BLAST score 725
E value 4.0e-77
Match length 140
% identity 100
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 148760
Seq. ID LIB3175-016-P1-K1-D5
Method BLASTX
NCBI GI g2501056
BLAST score 661
E value 1.0e-69
Match length 132
% identity 100
NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No. 148761
Seq. ID LIB3175-016-P1-K1-D6
Method BLASTX
NCBI GI g4586249
BLAST score 718
E value 3.0e-76
Match length 140

% identity	100
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No.	148762
Seq. ID	LIB3175-016-P1-K1-D7
Method	BLASTX
NCBI GI	g4371282
BLAST score	604
E value	6.0e-63
Match length	121
% identity	100
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	148763
Seq. ID	LIB3175-016-P1-K1-D8
Method	BLASTX
NCBI GI	g231586
BLAST score	289
E value	6.0e-26
Match length	118
% identity	56
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	148764
Seq. ID	LIB3175-016-P1-K1-D9
Method	BLASTX
NCBI GI	g4689386
BLAST score	549
E value	2.0e-56
Match length	117
% identity	85
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	148765
Seq. ID	LIB3175-016-P1-K1-E1
Method	BLASTX
NCBI GI	g730864
BLAST score	162
E value	4.0e-11
Match length	130
% identity	32
NCBI Description	SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN SPX19) >gi_2117442_pir__S50729 sporulation protein SPS19 - yeast (Saccharomyces cerevisiae) >gi_600063_emb_CAA55506_ (X78898) N1362 [Saccharomyces cerevisiae] >gi_1302205_emb_CAA96103_ (Z71479) ORF YNL202w [Saccharomyces cerevisiae]

Seq. No.	148766
Seq. ID	LIB3175-016-P1-K1-E10

Method	BLASTX
NCBI GI	g2829899
BLAST score	410
E value	4.0e-40
Match length	118
% identity	65
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	148767
Seq. ID	LIB3175-016-P1-K1-E12
Method	BLASTX
NCBI GI	g4006915
BLAST score	234
E value	2.0e-19
Match length	119
% identity	45
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148768
Seq. ID	LIB3175-016-P1-K1-E2
Method	BLASTX
NCBI GI	g4467148
BLAST score	691
E value	4.0e-73
Match length	138
% identity	100
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	148769
Seq. ID	LIB3175-016-P1-K1-E4
Method	BLASTN
NCBI GI	g1657620
BLAST score	387
E value	0.0e+00
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No.	148770
Seq. ID	LIB3175-016-P1-K1-E5
Method	BLASTX
NCBI GI	g3402692
BLAST score	305
E value	7.0e-28
Match length	77
% identity	75
NCBI Description	(AC004697) putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Arabidopsis thaliana]

Seq. No.	148771
Seq. ID	LIB3175-016-P1-K1-E6
Method	BLASTN
NCBI GI	g3236234

BLAST score	337
E value	0.0e+00
Match length	393
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148772
Seq. ID	LIB3175-016-P1-K1-E7
Method	BLASTN
NCBI GI	g1931636
BLAST score	265
E value	1.0e-147
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	148773
Seq. ID	LIB3175-016-P1-K1-E8
Method	BLASTX
NCBI GI	g4567268
BLAST score	586
E value	8.0e-61
Match length	124
% identity	99
NCBI Description	(AC006841) putative fructose biphosphate aldolase [Arabidopsis thaliana]

Seq. No.	148774
Seq. ID	LIB3175-016-P1-K1-F1
Method	BLASTX
NCBI GI	g2225877
BLAST score	368
E value	3.0e-35
Match length	99
% identity	70
NCBI Description	(AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694) Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_ (AB001581) DNA helicase p50 [Rattus norvegicus]

Seq. No.	148775
Seq. ID	LIB3175-016-P1-K1-F10
Method	BLASTX
NCBI GI	g4432856
BLAST score	410
E value	2.0e-40
Match length	84
% identity	95
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	148776
Seq. ID	LIB3175-016-P1-K1-F11
Method	BLASTX
NCBI GI	g4512675
BLAST score	699
E value	5.0e-74
Match length	138

% identity	99
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	148777
Seq. ID	LIB3175-016-P1-K1-F12
Method	BLASTX
NCBI GI	g119143
BLAST score	730
E value	1.0e-77
Match length	138
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	148778
Seq. ID	LIB3175-016-P1-K1-F2
Method	BLASTX
NCBI GI	g3445416
BLAST score	168
E value	9.0e-12
Match length	39
% identity	92
NCBI Description	(Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]

Seq. No.	148779
Seq. ID	LIB3175-016-P1-K1-F3
Method	BLASTX
NCBI GI	g1172599
BLAST score	598
E value	3.0e-62
Match length	118
% identity	97
NCBI Description	PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5) (TAS-F22/FAFP98) >gi_600387_emb_CAA47753_ (X67338) proteosome subunit [Arabidopsis thaliana]

Seq. No.	148780
Seq. ID	LIB3175-016-P1-K1-F4
Method	BLASTX
NCBI GI	g112681
BLAST score	739
E value	1.0e-78
Match length	138
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.	148781
Seq. ID	LIB3175-016-P1-K1-F6
Method	BLASTX
NCBI GI	g3236248
BLAST score	530
E value	3.0e-54
Match length	133
% identity	80
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	148782
Seq. ID	LIB3175-016-P1-K1-F7
Method	BLASTX
NCBI GI	g113334
BLAST score	419
E value	3.0e-41
Match length	131
% identity	60
NCBI Description	ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) >gi_90291_pir__A30111 alpha-adaptin A - mouse >gi_49878_emb_CAA33096_ (X14971) alpha-adaptin (A) (AA 1-977) [Mus musculus]

Seq. No.	148783
Seq. ID	LIB3175-016-P1-K1-F8
Method	BLASTX
NCBI GI	g3522946
BLAST score	501
E value	8.0e-51
Match length	105
% identity	90
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148784
Seq. ID	LIB3175-016-P1-K1-F9
Method	BLASTN
NCBI GI	g3201608
BLAST score	228
E value	1.0e-125
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148785
Seq. ID	LIB3175-016-P1-K1-G1
Method	BLASTN
NCBI GI	g3319365
BLAST score	113
E value	1.0e-56
Match length	349
% identity	98
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	148786
Seq. ID	LIB3175-016-P1-K1-G10
Method	BLASTX
NCBI GI	g4580384
BLAST score	246
E value	7.0e-21
Match length	138
% identity	52
NCBI Description	(AC007184) putative histone H2B [Arabidopsis thaliana]

Seq. No.	148787
Seq. ID	LIB3175-016-P1-K1-G12
Method	BLASTX
NCBI GI	g4587552
BLAST score	512
E value	4.0e-52
Match length	99
% identity	100
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	148788
Seq. ID	LIB3175-016-P1-K1-G2
Method	BLASTN
NCBI GI	g3421122
BLAST score	141
E value	9.0e-74
Match length	181
% identity	94
NCBI Description	Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA, complete cds

Seq. No.	148789
Seq. ID	LIB3175-016-P1-K1-G3
Method	BLASTX
NCBI GI	g3834310
BLAST score	522
E value	3.0e-53
Match length	99
% identity	100
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	148790
Seq. ID	LIB3175-016-P1-K1-G4
Method	BLASTX
NCBI GI	g541858
BLAST score	495
E value	3.0e-50
Match length	100
% identity	95
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana

>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	148791
Seq. ID	LIB3175-016-P1-K1-G5
Method	BLASTN
NCBI GI	g1297184
BLAST score	222
E value	1.0e-121
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	148792
Seq. ID	LIB3175-016-P1-K1-G6
Method	BLASTX
NCBI GI	g3600059
BLAST score	726
E value	3.0e-77
Match length	139
% identity	100
NCBI Description	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]

Seq. No.	148793
Seq. ID	LIB3175-016-P1-K1-G8
Method	BLASTX
NCBI GI	g1172873
BLAST score	672
E value	7.0e-71
Match length	133
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	148794
Seq. ID	LIB3175-016-P1-K1-H10
Method	BLASTX
NCBI GI	g2909781
BLAST score	270
E value	2.0e-24
Match length	53
% identity	100
NCBI Description	(AF020288) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	148795
Seq. ID	LIB3175-016-P1-K1-H11
Method	BLASTX
NCBI GI	g4689386

BLAST score	318
E value	2.0e-29
Match length	143
% identity	52
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	148796
Seq. ID	LIB3175-016-P1-K1-H12
Method	BLASTX
NCBI GI	g4753651
BLAST score	638
E value	7.0e-67
Match length	129
% identity	94
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	148797
Seq. ID	LIB3175-016-P1-K1-H2
Method	BLASTX
NCBI GI	g132074
BLAST score	733
E value	5.0e-78
Match length	136
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	148798
Seq. ID	LIB3175-016-P1-K1-H4
Method	BLASTX
NCBI GI	g112681
BLAST score	102
E value	2.0e-35
Match length	122
% identity	70
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	148799
Seq. ID	LIB3175-016-P1-K1-H5
Method	BLASTX
NCBI GI	g2129550
BLAST score	308
E value	3.0e-28
Match length	134
% identity	57
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi_836944 (U20625)
calcium-dependent protein kinase [Arabidopsis thaliana]
>gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent
protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	148800
Seq. ID	LIB3175-016-P1-K1-H6
Method	BLASTX
NCBI GI	g4753651
BLAST score	306
E value	4.0e-28
Match length	81
% identity	73
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	148801
Seq. ID	LIB3175-016-P1-K1-H7
Method	BLASTX
NCBI GI	g3184082
BLAST score	287
E value	1.0e-25
Match length	95
% identity	52
NCBI Description	(AL023781) N-terminal acetyltransferase 1 [Schizosaccharomyces pombe]

Seq. No.	148802
Seq. ID	LIB3175-016-P1-K1-H8
Method	BLASTX
NCBI GI	g4454467
BLAST score	218
E value	1.0e-17
Match length	135
% identity	33
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	148803
Seq. ID	LIB3175-016-P1-K1-H9
Method	BLASTN
NCBI GI	g4106339
BLAST score	387
E value	0.0e+00
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana protein phosphatase 2A regulatory subunit isoform B' delta mRNA, complete cds

Seq. No.	148804
Seq. ID	LIB3175-017-P1-K1-A1
Method	BLASTN
NCBI GI	g4263753
BLAST score	170
E value	1.0e-90
Match length	353
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No.	148805
Seq. ID	LIB3175-017-P1-K1-A10
Method	BLASTX
NCBI GI	g2795803
BLAST score	425
E value	6.0e-42
Match length	124
% identity	63
NCBI Description	(AC003674) putative beta-1,3-endoglucanase [Arabidopsis thaliana] >gi_3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	148806
Seq. ID	LIB3175-017-P1-K1-A12
Method	BLASTN
NCBI GI	g4662640
BLAST score	172
E value	7.0e-92
Match length	410
% identity	31
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	148807
Seq. ID	LIB3175-017-P1-K1-A2
Method	BLASTX
NCBI GI	g3834312
BLAST score	681
E value	5.0e-72
Match length	126
% identity	100
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an

Seq. No.	148808
Seq. ID	LIB3175-017-P1-K1-A4
Method	BLASTX
NCBI GI	g2497539
BLAST score	155
E value	2.0e-10
Match length	39
% identity	85
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	148809
Seq. ID	LIB3175-017-P1-K1-A5
Method	BLASTX
NCBI GI	g2129608
BLAST score	705
E value	1.0e-74
Match length	142

% identity	99
NCBI Description	GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]
Seq. No.	148810
Seq. ID	LIB3175-017-P1-K1-A6
Method	BLASTX
NCBI GI	g2894612
BLAST score	213
E value	1.0e-19
Match length	95
% identity	54
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	148811
Seq. ID	LIB3175-017-P1-K1-A8
Method	BLASTX
NCBI GI	g4220612
BLAST score	531
E value	2.0e-54
Match length	114
% identity	89
NCBI Description	(AB021934) nicotianamine synthase [Arabidopsis thaliana]
Seq. No.	148812
Seq. ID	LIB3175-017-P1-K1-A9
Method	BLASTX
NCBI GI	g4544458
BLAST score	193
E value	8.0e-15
Match length	123
% identity	41
NCBI Description	(AC006592) unknown protein [Arabidopsis thaliana]
Seq. No.	148813
Seq. ID	LIB3175-017-P1-K1-B2
Method	BLASTN
NCBI GI	g4510360
BLAST score	405
E value	0.0e+00
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence
Seq. No.	148814
Seq. ID	LIB3175-017-P1-K1-B3
Method	BLASTX
NCBI GI	g542157
BLAST score	559
E value	1.0e-57
Match length	128
% identity	82
NCBI Description	ribosomal 5S RNA-binding protein - Rice
Seq. No.	148815
Seq. ID	LIB3175-017-P1-K1-B4

Method	BLASTX
NCBI GI	g2398679
BLAST score	184
E value	1.0e-13
Match length	119
% identity	44
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	148816
Seq. ID	LIB3175-017-P1-K1-B5
Method	BLASTN
NCBI GI	g4454447
BLAST score	345
E value	0.0e+00
Match length	425
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148817
Seq. ID	LIB3175-017-P1-K1-B6
Method	BLASTX
NCBI GI	g115767
BLAST score	662
E value	1.0e-69
Match length	126
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	148818
Seq. ID	LIB3175-017-P1-K1-B7
Method	BLASTX
NCBI GI	g2829911
BLAST score	402
E value	3.0e-39
Match length	115
% identity	68
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	148819
Seq. ID	LIB3175-017-P1-K1-B8
Method	BLASTX
NCBI GI	g2454184
BLAST score	546
E value	3.0e-56
Match length	110
% identity	100
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	148820
Seq. ID	LIB3175-017-P1-K1-B9
Method	BLASTX
NCBI GI	g166867
BLAST score	602
E value	1.0e-62
Match length	133
% identity	87
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	148821
Seq. ID	LIB3175-017-P1-K1-C1
Method	BLASTX
NCBI GI	g126962
BLAST score	576
E value	1.0e-59
Match length	116
% identity	100
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7 >gi_99747_pir__S13718 probable membrane channel protein - Arabidopsis thaliana >gi_16492_emb_CAA38633_ (X54854) possible membrane channel protein [Arabidopsis thaliana]

Seq. No.	148822
Seq. ID	LIB3175-017-P1-K1-C11
Method	BLASTX
NCBI GI	g2245093
BLAST score	485
E value	5.0e-49
Match length	117
% identity	51
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	148823
Seq. ID	LIB3175-017-P1-K1-C12
Method	BLASTN
NCBI GI	g4567237
BLAST score	108
E value	1.0e-53
Match length	329
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	148824
Seq. ID	LIB3175-017-P1-K1-C2
Method	BLASTN
NCBI GI	g4589446
BLAST score	241
E value	1.0e-133
Match length	286
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	148825

Seq. ID	LIB3175-017-P1-K1-C5
Method	BLASTX
NCBI GI	g2842477
BLAST score	589
E value	4.0e-61
Match length	122
% identity	89
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	148826
Seq. ID	LIB3175-017-P1-K1-C6
Method	BLASTX
NCBI GI	g1161926
BLAST score	559
E value	1.0e-57
Match length	136
% identity	79
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	148827
Seq. ID	LIB3175-017-P1-K1-C7
Method	BLASTX
NCBI GI	g115385
BLAST score	686
E value	1.0e-72
Match length	132
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	148828
Seq. ID	LIB3175-017-P1-K1-D1
Method	BLASTX
NCBI GI	g1710780
BLAST score	453
E value	3.0e-45
Match length	121
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	148829
Seq. ID	LIB3175-017-P1-K1-D2
Method	BLASTX
NCBI GI	g4454032
BLAST score	303
E value	1.0e-27
Match length	110
% identity	56
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	148830
Seq. ID	LIB3175-017-P1-K1-D4

Method	BLASTN
NCBI GI	g3046855
BLAST score	231
E value	1.0e-127
Match length	380
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	148831
Seq. ID	LIB3175-017-P1-K1-D5
Method	BLASTX
NCBI GI	g100490
BLAST score	583
E value	2.0e-60
Match length	117
% identity	28
NCBI Description	polyubiquitin - garden snapdragon (fragment) >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No.	148832
Seq. ID	LIB3175-017-P1-K1-D6
Method	BLASTN
NCBI GI	g3128142
BLAST score	393
E value	0.0e+00
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	148833
Seq. ID	LIB3175-017-P1-K1-D7
Method	BLASTN
NCBI GI	g4314354
BLAST score	113
E value	1.0e-56
Match length	357
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148834
Seq. ID	LIB3175-017-P1-K1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	148835
Seq. ID	LIB3175-017-P1-K1-E1

Method	BLASTX
NCBI GI	g1173103
BLAST score	506
E value	2.0e-51
Match length	87
% identity	99
NCBI Description	RIBONUCLEASE 1 PRECURSOR >gi_561998 (U05206) ribonuclease [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease, RNS1 [Arabidopsis thaliana]

Seq. No.	148836
Seq. ID	LIB3175-017-P1-K1-E10
Method	BLASTX
NCBI GI	g2244750
BLAST score	429
E value	3.0e-45
Match length	116
% identity	78
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	148837
Seq. ID	LIB3175-017-P1-K1-E11
Method	BLASTX
NCBI GI	g1717949
BLAST score	355
E value	7.0e-34
Match length	72
% identity	85
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) >gi_100375_pir__B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) >gi_170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]

Seq. No.	148838
Seq. ID	LIB3175-017-P1-K1-E12
Method	BLASTX
NCBI GI	g4544419
BLAST score	443
E value	5.0e-44
Match length	118
% identity	79
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	148839
Seq. ID	LIB3175-017-P1-K1-E2
Method	BLASTX
NCBI GI	g3660469
BLAST score	558
E value	2.0e-57
Match length	113
% identity	99
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	148840
Seq. ID	LIB3175-017-P1-K1-E3
Method	BLASTX
NCBI GI	g1617013
BLAST score	334
E value	3.0e-31
Match length	67
% identity	100
NCBI Description	(Y07745) histone H2B like protein [Arabidopsis thaliana]

Seq. No.	148841
Seq. ID	LIB3175-017-P1-K1-E4
Method	BLASTN
NCBI GI	g4263774
BLAST score	278
E value	1.0e-155
Match length	366
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148842
Seq. ID	LIB3175-017-P1-K1-E6
Method	BLASTX
NCBI GI	g2129473
BLAST score	295
E value	1.0e-26
Match length	92
% identity	60
NCBI Description	arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No.	148843
Seq. ID	LIB3175-017-P1-K1-E8
Method	BLASTX
NCBI GI	g4741940
BLAST score	516
E value	1.0e-52
Match length	95
% identity	64
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	148844
Seq. ID	LIB3175-017-P1-K1-E9
Method	BLASTX
NCBI GI	g2129543
BLAST score	706
E value	7.0e-75
Match length	130
% identity	100
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana (fragment) >gi_1183868_emb_CAA64781_ (X95537) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	148845

Seq. ID	LIB3175-017-P1-K1-F10
Method	BLASTX
NCBI GI	g1709825
BLAST score	590
E value	3.0e-61
Match length	123
% identity	99
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	148846
Seq. ID	LIB3175-017-P1-K1-F12
Method	BLASTX
NCBI GI	g4432856
BLAST score	358
E value	5.0e-34
Match length	71
% identity	99
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	148847
Seq. ID	LIB3175-017-P1-K1-F3
Method	BLASTN
NCBI GI	g2760170
BLAST score	250
E value	1.0e-138
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	148848
Seq. ID	LIB3175-017-P1-K1-F4
Method	BLASTX
NCBI GI	g1561730
BLAST score	153
E value	5.0e-10
Match length	58
% identity	47
NCBI Description	(U65491) Dreg-3 protein [Drosophila melanogaster]

Seq. No.	148849
Seq. ID	LIB3175-017-P1-K1-F6
Method	BLASTN
NCBI GI	g3449329
BLAST score	23
E value	6.0e-03
Match length	409
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	148850
Seq. ID	LIB3175-017-P1-K1-F7
Method	BLASTN
NCBI GI	g2088638
BLAST score	34

E value	6.0e-10
Match length	70
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148851
Seq. ID	LIB3175-017-P1-K1-F8
Method	BLASTX
NCBI GI	g3511285
BLAST score	609
E value	2.0e-63
Match length	125
% identity	88
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	148852
Seq. ID	LIB3175-017-P1-K1-G1
Method	BLASTN
NCBI GI	g3319365
BLAST score	307
E value	1.0e-172
Match length	410
% identity	94
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	148853
Seq. ID	LIB3175-017-P1-K1-G11
Method	BLASTX
NCBI GI	g132074
BLAST score	668
E value	2.0e-70
Match length	124
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	148854
Seq. ID	LIB3175-017-P1-K1-G12
Method	BLASTX
NCBI GI	g2506443
BLAST score	476
E value	6.0e-48
Match length	124
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	148855
Seq. ID	LIB3175-017-P1-K1-G2
Method	BLASTX
NCBI GI	g2605769
BLAST score	237
E value	4.0e-20
Match length	87
% identity	60
NCBI Description	(AF027288) NADH dehydrogenase [Olea europaea]

Seq. No.	148856
Seq. ID	LIB3175-017-P1-K1-G3
Method	BLASTX
NCBI GI	g3859606
BLAST score	460
E value	5.0e-46
Match length	111
% identity	84
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	148857
Seq. ID	LIB3175-017-P1-K1-G4
Method	BLASTX
NCBI GI	g3075394
BLAST score	656
E value	5.0e-69
Match length	130
% identity	98
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	148858
Seq. ID	LIB3175-017-P1-K1-G5
Method	BLASTX
NCBI GI	g544242
BLAST score	332
E value	5.0e-36
Match length	123
% identity	69
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	148859
Seq. ID	LIB3175-017-P1-K1-G7
Method	BLASTX
NCBI GI	g125576
BLAST score	338
E value	9.0e-32
Match length	92
% identity	76
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC

2.7.1.19) precursor - Arabidopsis thaliana
>gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate
kinase [Arabidopsis thaliana]

Seq. No.	148860
Seq. ID	LIB3175-017-P1-K1-G8
Method	BLASTN
NCBI GI	g3449334
BLAST score	98
E value	8.0e-48
Match length	228
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	148861
Seq. ID	LIB3175-017-P1-K1-H1
Method	BLASTX
NCBI GI	g3157928
BLAST score	559
E value	1.0e-57
Match length	115
% identity	99
NCBI Description	(AC002131) Similar to fumarylacetoacetate hydrolase, gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No.	148862
Seq. ID	LIB3175-017-P1-K1-H3
Method	BLASTX
NCBI GI	g82677
BLAST score	254
E value	8.0e-29
Match length	81
% identity	75
NCBI Description	catalase (EC 1.11.1.6) chain 1 - maize >gi_22232_emb_CAA31056_ (X12538) catalase-1 (AA 1-492) [Zea mays]

Seq. No.	148863
Seq. ID	LIB3175-017-P1-K1-H5
Method	BLASTX
NCBI GI	g2924777
BLAST score	201
E value	1.0e-15
Match length	132
% identity	2
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	148864
Seq. ID	LIB3175-017-P1-K1-H7
Method	BLASTX
NCBI GI	g131211
BLAST score	176
E value	9.0e-13
Match length	36
% identity	94

NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J) >gi_1363533_pir__S58571 photosystem I protein psaJ - maize chloroplast >gi_552734 (J04502) ORF42 [Zea mays] >gi_902241_emb_CAA60305_ (X86563) psaJ [Zea mays]

Seq. No.	148865
Seq. ID	LIB3175-017-P1-K1-H9
Method	BLASTN
NCBI GI	g3176695
BLAST score	364
E value	0.0e+00
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	148866
Seq. ID	LIB3175-018-P1-K1-A1
Method	BLASTX
NCBI GI	g1350680
BLAST score	611
E value	1.0e-63
Match length	123
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	148867
Seq. ID	LIB3175-018-P1-K1-A10
Method	BLASTX
NCBI GI	g3522945
BLAST score	689
E value	7.0e-73
Match length	133
% identity	100
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148868
Seq. ID	LIB3175-018-P1-K1-A11
Method	BLASTX
NCBI GI	g3522945
BLAST score	659
E value	2.0e-69
Match length	129
% identity	98
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148869
Seq. ID	LIB3175-018-P1-K1-A12
Method	BLASTX
NCBI GI	g3522945
BLAST score	593
E value	1.0e-61
Match length	114
% identity	99
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148870
Seq. ID	LIB3175-018-P1-K1-A2
Method	BLASTX
NCBI GI	g322571
BLAST score	303
E value	1.0e-27
Match length	77
% identity	79
NCBI Description	proteinase inhibitor II - Arabidopsis thaliana >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II [Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	148871
Seq. ID	LIB3175-018-P1-K1-A3
Method	BLASTX
NCBI GI	g2781354
BLAST score	615
E value	3.0e-64
Match length	118
% identity	97
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	148872
Seq. ID	LIB3175-018-P1-K1-A4
Method	BLASTX
NCBI GI	g1172872
BLAST score	281
E value	4.0e-25
Match length	82
% identity	70
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	148873
Seq. ID	LIB3175-018-P1-K1-A6
Method	BLASTX
NCBI GI	g1710530
BLAST score	145
E value	4.0e-74
Match length	140
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	148874
Seq. ID	LIB3175-018-P1-K1-A7
Method	BLASTX
NCBI GI	g4220446
BLAST score	547
E value	2.0e-56

Match length	111
% identity	98
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	148875
Seq. ID	LIB3175-018-P1-K1-A8
Method	BLASTX
NCBI GI	g1710581
BLAST score	594
E value	9.0e-62
Match length	123
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	148876
Seq. ID	LIB3175-018-P1-K1-A9
Method	BLASTX
NCBI GI	g1914683
BLAST score	223
E value	3.0e-18
Match length	73
% identity	67
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	148877
Seq. ID	LIB3175-018-P1-K1-B1
Method	BLASTX
NCBI GI	g417381
BLAST score	585
E value	9.0e-61
Match length	114
% identity	99
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	148878
Seq. ID	LIB3175-018-P1-K1-B10
Method	BLASTX
NCBI GI	g2493122
BLAST score	180
E value	2.0e-13
Match length	73
% identity	55
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) (TONOPLAST ATPASE 70 KD SUBUNIT) (BN59) >gi_1362024_pir__S57790 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 70K chain (clone BN59) - rape >gi_558479 (U15604) tonoplast ATPase 70 kDa subunit [Brassica napus]

Seq. No.	148879
Seq. ID	LIB3175-018-P1-K1-B12
Method	BLASTX
NCBI GI	g3522945
BLAST score	653
E value	1.0e-68
Match length	127
% identity	98
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148880
Seq. ID	LIB3175-018-P1-K1-B3
Method	BLASTX
NCBI GI	g899608
BLAST score	591
E value	2.0e-61
Match length	120
% identity	21
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	148881
Seq. ID	LIB3175-018-P1-K1-B7
Method	BLASTX
NCBI GI	g1755162
BLAST score	209
E value	9.0e-55
Match length	108
% identity	90
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	148882
Seq. ID	LIB3175-018-P1-K1-B8
Method	BLASTN
NCBI GI	g4678705
BLAST score	384
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	148883
Seq. ID	LIB3175-018-P1-K1-B9
Method	BLASTX
NCBI GI	g3522945
BLAST score	487
E value	3.0e-49
Match length	117
% identity	84
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148884
Seq. ID	LIB3175-018-P1-K1-C1
Method	BLASTN
NCBI GI	g2618677
BLAST score	428
E value	0.0e+00

Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	148885
Seq. ID	LIB3175-018-P1-K1-C10
Method	BLASTX
NCBI GI	g2244879
BLAST score	456
E value	1.0e-45
Match length	103
% identity	88
NCBI Description	(Z97338) Nucleotide sequence of a cDNA clone encoding a beta-amylase from Arabidopsis thaliana

Seq. No.	148886
Seq. ID	LIB3175-018-P1-K1-C11
Method	BLASTX
NCBI GI	g1175014
BLAST score	567
E value	1.0e-58
Match length	125
% identity	90
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi_629543_pir__S44085 plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic protein 2b [Arabidopsis thaliana]

Seq. No.	148887
Seq. ID	LIB3175-018-P1-K1-C3
Method	BLASTX
NCBI GI	g3080435
BLAST score	298
E value	4.0e-27
Match length	78
% identity	63
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	148888
Seq. ID	LIB3175-018-P1-K1-C4
Method	BLASTN
NCBI GI	g3695372
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Arabidopsis thaliana BAC F1104

Seq. No.	148889
Seq. ID	LIB3175-018-P1-K1-C5
Method	BLASTX
NCBI GI	g4559346
BLAST score	594
E value	1.0e-61
Match length	112
% identity	100

NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]

Seq. No. 148890
Seq. ID LIB3175-018-P1-K1-C6
Method BLASTX
NCBI GI g113782
BLAST score 718
E value 3.0e-76
Match length 136
% identity 100
NCBI Description BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No. 148891
Seq. ID LIB3175-018-P1-K1-C7
Method BLASTX
NCBI GI g112741
BLAST score 626
E value 1.0e-65
Match length 118
% identity 99
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 148892
Seq. ID LIB3175-018-P1-K1-C8
Method BLASTX
NCBI GI g2462824
BLAST score 409
E value 4.0e-40
Match length 81
% identity 98
NCBI Description (AF000657) similar to Jun activation domain binding protein [Arabidopsis thaliana] >gi_2791885 (AF042334) JAB1 [Arabidopsis thaliana]

Seq. No. 148893
Seq. ID LIB3175-018-P1-K1-C9
Method BLASTN
NCBI GI g4417264
BLAST score 324
E value 0.0e+00
Match length 421
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 148894
Seq. ID LIB3175-018-P1-K1-D10

Method	BLASTX
NCBI GI	g3738335
BLAST score	312
E value	1.0e-28
Match length	113
% identity	58
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	148895
Seq. ID	LIB3175-018-P1-K1-D11
Method	BLASTX
NCBI GI	g464621
BLAST score	602
E value	1.0e-62
Match length	140
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	148896
Seq. ID	LIB3175-018-P1-K1-D12
Method	BLASTX
NCBI GI	g3522945
BLAST score	582
E value	2.0e-60
Match length	111
% identity	100
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148897
Seq. ID	LIB3175-018-P1-K1-D2
Method	BLASTX
NCBI GI	g1619300
BLAST score	310
E value	2.0e-28
Match length	67
% identity	84
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	148898
Seq. ID	LIB3175-018-P1-K1-D3
Method	BLASTX
NCBI GI	g4185505
BLAST score	356
E value	8.0e-34
Match length	103
% identity	67
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	148899
Seq. ID	LIB3175-018-P1-K1-D4
Method	BLASTX
NCBI GI	g126985
BLAST score	551

E value	1.0e-56
Match length	115
% identity	94
NCBI Description	MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis thaliana]

Seq. No.	148900
Seq. ID	LIB3175-018-P1-K1-D5
Method	BLASTX
NCBI GI	g231586
BLAST score	248
E value	3.0e-21
Match length	127
% identity	50
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	148901
Seq. ID	LIB3175-018-P1-K1-D6
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	148902
Seq. ID	LIB3175-018-P1-K1-D7
Method	BLASTX
NCBI GI	g1346113
BLAST score	488
E value	2.0e-49
Match length	103
% identity	90
NCBI Description	GTP CYCLOHYDROLASE II >gi_1084339_pir__JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana >gi_940383_dbj_BAA08113_ (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]

Seq. No.	148903
Seq. ID	LIB3175-018-P1-K1-D9
Method	BLASTX
NCBI GI	g1169598
BLAST score	461
E value	4.0e-46
Match length	98
% identity	87
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	148904

Seq. ID	LIB3175-018-P1-K1-E1
Method	BLASTX
NCBI GI	g1209756
BLAST score	159
E value	8.0e-11
Match length	35
% identity	86
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	148905
Seq. ID	LIB3175-018-P1-K1-E2
Method	BLASTN
NCBI GI	g4519195
BLAST score	366
E value	0.0e+00
Match length	404
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	148906
Seq. ID	LIB3175-018-P1-K1-E3
Method	BLASTX
NCBI GI	g4185515
BLAST score	422
E value	1.0e-41
Match length	81
% identity	100
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	148907
Seq. ID	LIB3175-018-P1-K1-E5
Method	BLASTX
NCBI GI	g2565009
BLAST score	495
E value	4.0e-50
Match length	124
% identity	70
NCBI Description	(AC002983) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	148908
Seq. ID	LIB3175-018-P1-K1-E6
Method	BLASTN
NCBI GI	g2739359
BLAST score	364
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148909
Seq. ID	LIB3175-018-P1-K1-E7
Method	BLASTX
NCBI GI	g2494320

BLAST score	450
E value	7.0e-45
Match length	107
% identity	80
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	148910
Seq. ID	LIB3175-018-P1-K1-E8
Method	BLASTX
NCBI GI	g2924779
BLAST score	615
E value	3.0e-64
Match length	123
% identity	99
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	148911
Seq. ID	LIB3175-018-P1-K1-E9
Method	BLASTN
NCBI GI	g4220644
BLAST score	271
E value	1.0e-151
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	148912
Seq. ID	LIB3175-018-P1-K1-F1
Method	BLASTN
NCBI GI	g4567237
BLAST score	33
E value	6.0e-09
Match length	295
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	148913
Seq. ID	LIB3175-018-P1-K1-F10
Method	BLASTX
NCBI GI	g1346263
BLAST score	398
E value	8.0e-39
Match length	81
% identity	99
NCBI Description	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor - Arabidopsis thaliana >gi_1049057 (U27118) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	148914
Seq. ID	LIB3175-018-P1-K1-F11
Method	BLASTN
NCBI GI	g4584841
BLAST score	157
E value	6.0e-83
Match length	416
% identity	66
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	148915
Seq. ID	LIB3175-018-P1-K1-F2
Method	BLASTX
NCBI GI	g1864017
BLAST score	210
E value	3.0e-17
Match length	43
% identity	93
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	148916
Seq. ID	LIB3175-018-P1-K1-F4
Method	BLASTX
NCBI GI	g3413716
BLAST score	581
E value	3.0e-60
Match length	139
% identity	57
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana] >gi_3643589 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	148917
Seq. ID	LIB3175-018-P1-K1-F5
Method	BLASTX
NCBI GI	g119350
BLAST score	657
E value	4.0e-69
Match length	130
% identity	99
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	148918
Seq. ID	LIB3175-018-P1-K1-F6
Method	BLASTX
NCBI GI	g2129759
BLAST score	543
E value	9.0e-56
Match length	110

% identity	98
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	148919
Seq. ID	LIB3175-018-P1-K1-F8
Method	BLASTX
NCBI GI	g2894574
BLAST score	616
E value	2.0e-64
Match length	118
% identity	99
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	148920
Seq. ID	LIB3175-018-P1-K1-G1
Method	BLASTN
NCBI GI	g3426057
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for IB1P8-4 protein

Seq. No.	148921
Seq. ID	LIB3175-018-P1-K1-G11
Method	BLASTX
NCBI GI	g3522945
BLAST score	624
E value	3.0e-65
Match length	120
% identity	99
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148922
Seq. ID	LIB3175-018-P1-K1-G12
Method	BLASTX
NCBI GI	g3522945
BLAST score	637
E value	8.0e-67
Match length	122
% identity	100
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	148923
Seq. ID	LIB3175-018-P1-K1-G2
Method	BLASTX
NCBI GI	g4586265
BLAST score	512
E value	4.0e-52
Match length	117
% identity	81
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	148924
Seq. ID	LIB3175-018-P1-K1-G3
Method	BLASTX
NCBI GI	g1304227
BLAST score	290
E value	4.0e-26
Match length	107
% identity	50
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	148925
Seq. ID	LIB3175-018-P1-K1-G4
Method	BLASTX
NCBI GI	g4741923
BLAST score	368
E value	3.0e-35
Match length	92
% identity	71
NCBI Description	(AF130849) PIT1 [Arabidopsis thaliana]

Seq. No.	148926
Seq. ID	LIB3175-018-P1-K1-G5
Method	BLASTX
NCBI GI	g4680661
BLAST score	149
E value	2.0e-09
Match length	107
% identity	27
NCBI Description	(AF132945) CGI-11 protein [Homo sapiens]

Seq. No.	148927
Seq. ID	LIB3175-018-P1-K1-G6
Method	BLASTN
NCBI GI	g972937
BLAST score	223
E value	1.0e-122
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana putative chlorophyll synthetase (G4) gene, complete cds

Seq. No.	148928
Seq. ID	LIB3175-018-P1-K1-G7
Method	BLASTX
NCBI GI	g2129769
BLAST score	669
E value	2.0e-70
Match length	122
% identity	99
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	148929
Seq. ID	LIB3175-018-P1-K1-G8

Method	BLASTN
NCBI GI	g3449329
BLAST score	353
E value	0.0e+00
Match length	377
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	148930
Seq. ID	LIB3175-018-P1-K1-G9
Method	BLASTX
NCBI GI	g4115387
BLAST score	393
E value	4.0e-38
Match length	78
% identity	99
NCBI Description	(AC005967) putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	148931
Seq. ID	LIB3175-018-P1-K1-H1
Method	BLASTX
NCBI GI	g584998
BLAST score	265
E value	4.0e-23
Match length	96
% identity	50
NCBI Description	FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450 LXXVA2) (P-450EG1) >gi_629713_pir__S43342 flavonoid hydroxylase cytochrome P450 - eggplant >gi_395261_emb_CAA50155_ (X70824) flavonoid hydroxylase (P450) [Solanum melongena]

Seq. No.	148932
Seq. ID	LIB3175-018-P1-K1-H10
Method	BLASTX
NCBI GI	g2914700
BLAST score	563
E value	4.0e-58
Match length	111
% identity	100
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	148933
Seq. ID	LIB3175-018-P1-K1-H12
Method	BLASTX
NCBI GI	g3522945
BLAST score	672
E value	8.0e-71
Match length	137
% identity	96
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 148934

Seq. ID	LIB3175-018-P1-K1-H2
Method	BLASTX
NCBI GI	g2832629
BLAST score	164
E value	2.0e-11
Match length	104
% identity	37
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	148935
Seq. ID	LIB3175-018-P1-K1-H3
Method	BLASTN
NCBI GI	g3449330
BLAST score	321
E value	0.0e+00
Match length	400
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	148936
Seq. ID	LIB3175-018-P1-K1-H5
Method	BLASTX
NCBI GI	g282865
BLAST score	638
E value	6.0e-67
Match length	133
% identity	69
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	148937
Seq. ID	LIB3175-018-P1-K1-H7
Method	BLASTX
NCBI GI	g4006899
BLAST score	375
E value	5.0e-36
Match length	121
% identity	56
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	148938
Seq. ID	LIB3175-018-P1-K1-H9
Method	BLASTX
NCBI GI	g4585882
BLAST score	496
E value	3.0e-50
Match length	95
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	148939
Seq. ID	LIB3175-019-P1-K1-A10
Method	BLASTN
NCBI GI	g4415905
BLAST score	184
E value	5.0e-99
Match length	451
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148940
Seq. ID	LIB3175-019-P1-K1-A12
Method	BLASTX
NCBI GI	g119723
BLAST score	800
E value	8.0e-86
Match length	153
% identity	100
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	148941
Seq. ID	LIB3175-019-P1-K1-A2
Method	BLASTX
NCBI GI	g1542941
BLAST score	288
E value	2.0e-26
Match length	61
% identity	90
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	148942
Seq. ID	LIB3175-019-P1-K1-A6
Method	BLASTX
NCBI GI	g1076389
BLAST score	540
E value	2.0e-55
Match length	125
% identity	86
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	148943
Seq. ID	LIB3175-019-P1-K1-A7
Method	BLASTX
NCBI GI	g1402904
BLAST score	513
E value	2.0e-52
Match length	100
% identity	98
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	148944
Seq. ID	LIB3175-019-P1-K1-A8
Method	BLASTX
NCBI GI	g4206206
BLAST score	305
E value	7.0e-28
Match length	74
% identity	85
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	148945
Seq. ID	LIB3175-019-P1-K1-A9
Method	BLASTX
NCBI GI	g2583126
BLAST score	527
E value	9.0e-54
Match length	109
% identity	95
NCBI Description	(AC002387) putative DNA repair protein (RAD57) [Arabidopsis thaliana]

Seq. No.	148946
Seq. ID	LIB3175-019-P1-K1-B10
Method	BLASTX
NCBI GI	g2829899
BLAST score	468
E value	7.0e-47
Match length	136
% identity	65
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	148947
Seq. ID	LIB3175-019-P1-K1-B12
Method	BLASTN
NCBI GI	g2828278
BLAST score	66
E value	9.0e-29
Match length	118
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	148948
Seq. ID	LIB3175-019-P1-K1-B2
Method	BLASTX
NCBI GI	g1173187
BLAST score	579
E value	6.0e-60
Match length	121
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden

strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	148949
Seq. ID	LIB3175-019-P1-K1-B3
Method	BLASTX
NCBI GI	g4200165
BLAST score	342
E value	4.0e-32
Match length	130
% identity	62
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	148950
Seq. ID	LIB3175-019-P1-K1-B8
Method	BLASTX
NCBI GI	g584892
BLAST score	506
E value	2.0e-51
Match length	145
% identity	63
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) >gi_629805_pir__S43516 serine carboxypeptidase I - rice >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I [Oryza sativa]

Seq. No.	148951
Seq. ID	LIB3175-019-P1-K1-B9
Method	BLASTN
NCBI GI	g4753195
BLAST score	54
E value	2.0e-21
Match length	360
% identity	84
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	148952
Seq. ID	LIB3175-019-P1-K1-C10
Method	BLASTN
NCBI GI	g2564049
BLAST score	171
E value	3.0e-91
Match length	210
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	148953
Seq. ID	LIB3175-019-P1-K1-C11
Method	BLASTX
NCBI GI	g127041
BLAST score	445
E value	2.0e-44
Match length	86
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	148954
Seq. ID	LIB3175-019-P1-K1-C12
Method	BLASTX
NCBI GI	g2645971
BLAST score	697
E value	8.0e-74
Match length	130
% identity	99
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	148955
Seq. ID	LIB3175-019-P1-K1-C4
Method	BLASTN
NCBI GI	g2828278
BLAST score	278
E value	1.0e-155
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	148956
Seq. ID	LIB3175-019-P1-K1-C6
Method	BLASTX
NCBI GI	g2645971
BLAST score	305
E value	5.0e-28
Match length	61
% identity	93
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	148957
Seq. ID	LIB3175-019-P1-K1-C7
Method	BLASTX
NCBI GI	g4538963
BLAST score	362
E value	1.0e-34
Match length	100
% identity	72
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	148958
Seq. ID	LIB3175-019-P1-K1-C9
Method	BLASTX
NCBI GI	g2213590
BLAST score	184
E value	1.0e-13
Match length	82

% identity	43
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	148959
Seq. ID	LIB3175-019-P1-K1-D1
Method	BLASTX
NCBI GI	g4204300
BLAST score	615
E value	4.0e-64
Match length	120
% identity	100
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	148960
Seq. ID	LIB3175-019-P1-K1-D10
Method	BLASTN
NCBI GI	g3548797
BLAST score	339
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148961
Seq. ID	LIB3175-019-P1-K1-D11
Method	BLASTX
NCBI GI	g4154281
BLAST score	434
E value	6.0e-43
Match length	106
% identity	75
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	148962
Seq. ID	LIB3175-019-P1-K1-D12
Method	BLASTX
NCBI GI	g2130051
BLAST score	489
E value	2.0e-49
Match length	123
% identity	72
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No.	148963
Seq. ID	LIB3175-019-P1-K1-D2
Method	BLASTX
NCBI GI	g1172872
BLAST score	703
E value	2.0e-74
Match length	131
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A

precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	148964
Seq. ID	LIB3175-019-P1-K1-D3
Method	BLASTN
NCBI GI	g3269280
BLAST score	356
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	148965
Seq. ID	LIB3175-019-P1-K1-D4
Method	BLASTX
NCBI GI	g3858939
BLAST score	531
E value	3.0e-54
Match length	129
% identity	86
NCBI Description	(AL021636) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	148966
Seq. ID	LIB3175-019-P1-K1-D5
Method	BLASTX
NCBI GI	g2129532
BLAST score	507
E value	2.0e-51
Match length	126
% identity	79
NCBI Description	acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) - Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis thaliana]

Seq. No.	148967
Seq. ID	LIB3175-019-P1-K1-D6
Method	BLASTX
NCBI GI	g2129675
BLAST score	686
E value	2.0e-72
Match length	158
% identity	84
NCBI Description	probable chlorophyll synthetase G4 - Arabidopsis thaliana >gi_972938 (U19382) putative chlorophyll synthetase [Arabidopsis thaliana] >gi_3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]

Seq. No.	148968
Seq. ID	LIB3175-019-P1-K1-D8
Method	BLASTN
NCBI GI	g4757400

BLAST score	173
E value	2.0e-92
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20, complete sequence

Seq. No.	148969
Seq. ID	LIB3175-019-P1-K1-D9
Method	BLASTX
NCBI GI	g4406753
BLAST score	495
E value	5.0e-50
Match length	106
% identity	94
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No.	148970
Seq. ID	LIB3175-019-P1-K1-E1
Method	BLASTX
NCBI GI	g3309170
BLAST score	245
E value	1.0e-20
Match length	133
% identity	42
NCBI Description	(AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No.	148971
Seq. ID	LIB3175-019-P1-K1-E11
Method	BLASTN
NCBI GI	g4757411
BLAST score	243
E value	1.0e-134
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	148972
Seq. ID	LIB3175-019-P1-K1-E12
Method	BLASTX
NCBI GI	g4158221
BLAST score	630
E value	7.0e-66
Match length	139
% identity	80
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	148973
Seq. ID	LIB3175-019-P1-K1-E2
Method	BLASTN
NCBI GI	g2160132
BLAST score	165
E value	1.0e-87
Match length	921
% identity	56
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome

1, complete sequence [Arabidopsis thaliana]

Seq. No.	148974
Seq. ID	LIB3175-019-P1-K1-E3
Method	BLASTX
NCBI GI	g3859591
BLAST score	330
E value	7.0e-31
Match length	108
% identity	55
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	148975
Seq. ID	LIB3175-019-P1-K1-E5
Method	BLASTX
NCBI GI	g3892712
BLAST score	500
E value	1.0e-50
Match length	97
% identity	100
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	148976
Seq. ID	LIB3175-019-P1-K1-E6
Method	BLASTX
NCBI GI	g2244759
BLAST score	771
E value	2.0e-82
Match length	157
% identity	92
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	148977
Seq. ID	LIB3175-019-P1-K1-E7
Method	BLASTN
NCBI GI	g4734003
BLAST score	377
E value	0.0e+00
Match length	381
% identity	68
NCBI Description	Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No.	148978
Seq. ID	LIB3175-019-P1-K1-E8
Method	BLASTX
NCBI GI	g3123745
BLAST score	510
E value	7.0e-52
Match length	107
% identity	94
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	148979
Seq. ID	LIB3175-019-P1-K1-E9
Method	BLASTN

NCBI GI	g4220633
BLAST score	41
E value	1.0e-13
Match length	287
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	148980
Seq. ID	LIB3175-019-P1-K1-F1
Method	BLASTN
NCBI GI	g3449326
BLAST score	377
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	148981
Seq. ID	LIB3175-019-P1-K1-F11
Method	BLASTX
NCBI GI	g1169278
BLAST score	283
E value	3.0e-25
Match length	71
% identity	83
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	148982
Seq. ID	LIB3175-019-P1-K1-F12
Method	BLASTX
NCBI GI	g3157924
BLAST score	309
E value	3.0e-28
Match length	80
% identity	76
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	148983
Seq. ID	LIB3175-019-P1-K1-F2
Method	BLASTX
NCBI GI	g2827699
BLAST score	457
E value	1.0e-45
Match length	159
% identity	63
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	148984
Seq. ID	LIB3175-019-P1-K1-F3

Method	BLASTN
NCBI GI	g3449322
BLAST score	438
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	148985
Seq. ID	LIB3175-019-P1-K1-F4
Method	BLASTX
NCBI GI	g4589396
BLAST score	330
E value	1.0e-30
Match length	146
% identity	46
NCBI Description	(D89971) asparaginyl endopeptidase (VmPE-1) [Vigna mungo]

Seq. No.	148986
Seq. ID	LIB3175-019-P1-K1-F5
Method	BLASTX
NCBI GI	g2196466
BLAST score	443
E value	4.0e-44
Match length	104
% identity	90
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	148987
Seq. ID	LIB3175-019-P1-K1-F6
Method	BLASTX
NCBI GI	g2244750
BLAST score	799
E value	1.0e-85
Match length	155
% identity	99
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	148988
Seq. ID	LIB3175-019-P1-K1-F7
Method	BLASTX
NCBI GI	g3600053
BLAST score	337
E value	1.0e-31
Match length	116
% identity	65
NCBI Description	(AF080120) contains similarity to HMG (high mobility group) box (Pfam: HMG_box.hmm, scores: 70.67, 53.09 and 80.15) [Arabidopsis thaliana]

Seq. No.	148989
Seq. ID	LIB3175-019-P1-K1-F8
Method	BLASTN

NCBI GI	g3426033
BLAST score	123
E value	1.0e-62
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	148990
Seq. ID	LIB3175-019-P1-K1-F9
Method	BLASTX
NCBI GI	g1706368
BLAST score	773
E value	1.0e-82
Match length	148
% identity	99
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_320557_pir__JQ1688 dihydrokaempferol 4-reductase (EC 1.1.1.219) - Arabidopsis thaliana >gi_166686 (M86359) dihydroflavonol 4-reductase [Arabidopsis thaliana]

Seq. No.	148991
Seq. ID	LIB3175-019-P1-K1-G1
Method	BLASTX
NCBI GI	g2529229
BLAST score	536
E value	7.0e-55
Match length	116
% identity	89
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	148992
Seq. ID	LIB3175-019-P1-K1-G10
Method	BLASTX
NCBI GI	g3138972
BLAST score	680
E value	9.0e-72
Match length	142
% identity	92
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	148993
Seq. ID	LIB3175-019-P1-K1-G11
Method	BLASTX
NCBI GI	g3157947
BLAST score	570
E value	6.0e-59
Match length	111
% identity	55
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	148994
Seq. ID	LIB3175-019-P1-K1-G3
Method	BLASTX
NCBI GI	g3420049
BLAST score	443
E value	6.0e-44
Match length	129
% identity	69
NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	148995
Seq. ID	LIB3175-019-P1-K1-G4
Method	BLASTN
NCBI GI	g2245031
BLAST score	141
E value	3.0e-73
Match length	495
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	148996
Seq. ID	LIB3175-019-P1-K1-G5
Method	BLASTX
NCBI GI	g2258135
BLAST score	188
E value	4.0e-14
Match length	46
% identity	67
NCBI Description	(Z83830) porin [Picea abies]

Seq. No.	148997
Seq. ID	LIB3175-019-P1-K1-G6
Method	BLASTX
NCBI GI	g1724100
BLAST score	520
E value	6.0e-53
Match length	134
% identity	74
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	148998
Seq. ID	LIB3175-019-P1-K1-G9
Method	BLASTX
NCBI GI	g132110
BLAST score	729
E value	2.0e-77
Match length	139
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	148999
Seq. ID	LIB3175-019-P1-K1-H10
Method	BLASTX
NCBI GI	g2407802
BLAST score	186
E value	7.0e-16
Match length	66
% identity	69
NCBI Description	(Y12576) histone H2B [Arabidopsis thaliana]

Seq. No.	149000
Seq. ID	LIB3175-019-P1-K1-H11
Method	BLASTX
NCBI GI	g136251
BLAST score	505
E value	2.0e-51
Match length	119
% identity	83
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	149001
Seq. ID	LIB3175-019-P1-K1-H12
Method	BLASTX
NCBI GI	g2454184
BLAST score	436
E value	3.0e-43
Match length	108
% identity	84
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	149002
Seq. ID	LIB3175-019-P1-K1-H2
Method	BLASTX
NCBI GI	g3273196
BLAST score	538
E value	3.0e-55
Match length	109
% identity	98
NCBI Description	(AB010915) responce regulator1 [Arabidopsis thaliana] >gi_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No.	149003
Seq. ID	LIB3175-019-P1-K1-H3
Method	BLASTX
NCBI GI	g3063465
BLAST score	684
E value	3.0e-72
Match length	133
% identity	100
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	149004
Seq. ID	LIB3175-019-P1-K1-H4
Method	BLASTN
NCBI GI	g2760169
BLAST score	246
E value	1.0e-136
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	149005
Seq. ID	LIB3175-019-P1-K1-H5
Method	BLASTN
NCBI GI	g2264313
BLAST score	82
E value	4.0e-38
Match length	242
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	149006
Seq. ID	LIB3175-019-P1-K1-H7
Method	BLASTX
NCBI GI	g4455302
BLAST score	438
E value	2.0e-43
Match length	122
% identity	66
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	149007
Seq. ID	LIB3175-019-P1-K1-H8
Method	BLASTX
NCBI GI	g1353163
BLAST score	237
E value	8.0e-20
Match length	75
% identity	60
NCBI Description	HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III PRECURSOR >gi_1055071 (U39851) C23G10.2 gene product [Caenorhabditis elegans]

Seq. No.	149008
Seq. ID	LIB3175-019-P1-K1-H9
Method	BLASTX
NCBI GI	g421929
BLAST score	587
E value	7.0e-63
Match length	134
% identity	15
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	149009

Seq. ID	LIB3175-020-P1-K1-A1
Method	BLASTN
NCBI GI	g3335331
BLAST score	238
E value	1.0e-131
Match length	297
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149010
Seq. ID	LIB3175-020-P1-K1-A10
Method	BLASTX
NCBI GI	g2245087
BLAST score	427
E value	3.0e-42
Match length	110
% identity	73
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149011
Seq. ID	LIB3175-020-P1-K1-A11
Method	BLASTX
NCBI GI	g2286069
BLAST score	623
E value	4.0e-65
Match length	120
% identity	98
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	149012
Seq. ID	LIB3175-020-P1-K1-A12
Method	BLASTX
NCBI GI	g2245087
BLAST score	511
E value	5.0e-52
Match length	122
% identity	79
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149013
Seq. ID	LIB3175-020-P1-K1-A2
Method	BLASTX
NCBI GI	g3643607
BLAST score	531
E value	2.0e-54
Match length	120
% identity	78
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	149014
Seq. ID	LIB3175-020-P1-K1-A3
Method	BLASTX
NCBI GI	g112741
BLAST score	526
E value	6.0e-54
Match length	97

% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	149015
Seq. ID	LIB3175-020-P1-K1-A4
Method	BLASTX
NCBI GI	g4585882
BLAST score	476
E value	7.0e-48
Match length	91
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	149016
Seq. ID	LIB3175-020-P1-K1-A5
Method	BLASTN
NCBI GI	g4510408
BLAST score	53
E value	6.0e-21
Match length	73
% identity	54
NCBI Description	Arabidopsis thaliana chromosome II BAC T1E2 genomic sequence, complete sequence

Seq. No.	149017
Seq. ID	LIB3175-020-P1-K1-A6
Method	BLASTN
NCBI GI	g4376087
BLAST score	114
E value	2.0e-57
Match length	190
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	149018
Seq. ID	LIB3175-020-P1-K1-A7
Method	BLASTX
NCBI GI	g541848
BLAST score	542
E value	1.0e-55
Match length	123
% identity	85
NCBI Description	amino acid transport protein I - Arabidopsis thaliana >gi_22641_emb_CAA47603_ (X67124) amino acid permease I [Arabidopsis thaliana] >gi_404019 (L16240) amino acid transporter [Arabidopsis thaliana]

Seq. No.	149019
Seq. ID	LIB3175-020-P1-K1-A8

Method	BLASTN
NCBI GI	g2894591
BLAST score	413
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	149020
Seq. ID	LIB3175-020-P1-K1-A9
Method	BLASTX
NCBI GI	g2245087
BLAST score	509
E value	1.0e-51
Match length	126
% identity	75
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149021
Seq. ID	LIB3175-020-P1-K1-B1
Method	BLASTX
NCBI GI	g1531758
BLAST score	388
E value	1.0e-37
Match length	84
% identity	85
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	149022
Seq. ID	LIB3175-020-P1-K1-B12
Method	BLASTX
NCBI GI	g130759
BLAST score	185
E value	2.0e-23
Match length	110
% identity	54
NCBI Description	PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_108383_pir__A37942 prolyl oligopeptidase (EC 3.4.21.26) - pig >gi_164621 (M64227) prolyl endopeptidase [Sus scrofa]

Seq. No.	149023
Seq. ID	LIB3175-020-P1-K1-B4
Method	BLASTX
NCBI GI	g2244979
BLAST score	712
E value	1.0e-75
Match length	143
% identity	100
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	149024
Seq. ID	LIB3175-020-P1-K1-B5
Method	BLASTX
NCBI GI	g3132475

BLAST score	547
E value	3.0e-56
Match length	120
% identity	87
NCBI Description	(AC003096) similar to proline-rich protein [Arabidopsis thaliana]

Seq. No.	149025
Seq. ID	LIB3175-020-P1-K1-B6
Method	BLASTX
NCBI GI	g585536
BLAST score	473
E value	1.0e-47
Match length	85
% identity	99
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	149026
Seq. ID	LIB3175-020-P1-K1-B7
Method	BLASTX
NCBI GI	g2829275
BLAST score	461
E value	4.0e-46
Match length	132
% identity	73
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	149027
Seq. ID	LIB3175-020-P1-K1-B9
Method	BLASTX
NCBI GI	g2245087
BLAST score	536
E value	7.0e-55
Match length	125
% identity	81
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149028
Seq. ID	LIB3175-020-P1-K1-C1
Method	BLASTX
NCBI GI	g2627433
BLAST score	258
E value	3.0e-22
Match length	118
% identity	45
NCBI Description	(AF012129) putative DNA methyltransferase [Mus musculus]

Seq. No. 149029

Seq. ID	LIB3175-020-P1-K1-C10
Method	BLASTX
NCBI GI	g567893
BLAST score	176
E value	8.0e-13
Match length	87
% identity	49
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No.	149030
Seq. ID	LIB3175-020-P1-K1-C11
Method	BLASTX
NCBI GI	g3043415
BLAST score	641
E value	3.0e-67
Match length	123
% identity	100
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	149031
Seq. ID	LIB3175-020-P1-K1-C12
Method	BLASTX
NCBI GI	g4454032
BLAST score	258
E value	2.0e-22
Match length	101
% identity	52
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	149032
Seq. ID	LIB3175-020-P1-K1-C2
Method	BLASTN
NCBI GI	g2150022
BLAST score	93
E value	7.0e-45
Match length	265
% identity	95
NCBI Description	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds

Seq. No.	149033
Seq. ID	LIB3175-020-P1-K1-C3
Method	BLASTN
NCBI GI	g3869075
BLAST score	260
E value	1.0e-144
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	149034
Seq. ID	LIB3175-020-P1-K1-C4
Method	BLASTN
NCBI GI	g2351065
BLAST score	243

E value	1.0e-134
Match length	255
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	149035
Seq. ID	LIB3175-020-P1-K1-C5
Method	BLASTN
NCBI GI	g2828186
BLAST score	161
E value	3.0e-85
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	149036
Seq. ID	LIB3175-020-P1-K1-C6
Method	BLASTN
NCBI GI	g2760164
BLAST score	412
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	149037
Seq. ID	LIB3175-020-P1-K1-C7
Method	BLASTX
NCBI GI	g3913871
BLAST score	756
E value	1.0e-80
Match length	146
% identity	100
NCBI Description	FERROCHELATASE, CHLOROPLAST PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) (FERROCHELATASE-II) >gi_1946377 (U93215) ferrochelatase precusor isolog [Arabidopsis thaliana] >gi_2347202 (AC002338) ferrochelatase precusor isolog [Arabidopsis thaliana]

Seq. No.	149038
Seq. ID	LIB3175-020-P1-K1-C8
Method	BLASTX
NCBI GI	g2498731
BLAST score	487
E value	3.0e-49
Match length	126
% identity	74
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	149039
Seq. ID	LIB3175-020-P1-K1-C9

Method	BLASTX
NCBI GI	g2160133
BLAST score	393
E value	4.0e-38
Match length	128
% identity	65
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	149040
Seq. ID	LIB3175-020-P1-K1-D1
Method	BLASTX
NCBI GI	g115783
BLAST score	449
E value	7.0e-45
Match length	84
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149041
Seq. ID	LIB3175-020-P1-K1-D12
Method	BLASTX
NCBI GI	g4589398
BLAST score	412
E value	2.0e-40
Match length	95
% identity	77
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	149042
Seq. ID	LIB3175-020-P1-K1-D3
Method	BLASTX
NCBI GI	g4582459
BLAST score	639
E value	6.0e-67
Match length	147
% identity	80
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	149043
Seq. ID	LIB3175-020-P1-K1-D4
Method	BLASTX
NCBI GI	g1351082
BLAST score	593
E value	1.0e-61
Match length	146
% identity	79
NCBI Description	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >gi_166700 (M55910) Fe-superoxide dismutase [Arabidopsis thaliana]

Seq. No.	149044

Seq. ID	LIB3175-020-P1-K1-D5
Method	BLASTX
NCBI GI	g115767
BLAST score	703
E value	2.0e-74
Match length	133
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	149045
Seq. ID	LIB3175-020-P1-K1-D6
Method	BLASTN
NCBI GI	g4757391
BLAST score	255
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2C19, complete sequence

Seq. No.	149046
Seq. ID	LIB3175-020-P1-K1-D8
Method	BLASTX
NCBI GI	g461550
BLAST score	403
E value	2.0e-39
Match length	115
% identity	73
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	149047
Seq. ID	LIB3175-020-P1-K1-D9
Method	BLASTX
NCBI GI	g2252825
BLAST score	649
E value	4.0e-68
Match length	124
% identity	100
NCBI Description	(AF013293) Similar to transmembrane protein; coded for by A. thaliana cDNA H37637; coded for by A. thaliana cDNA T41850; coded for by A. thaliana cDNA T13717; coded for by A. thaliana cDNA T04371; coded for by A. thaliana cDNA T43789; coded

Seq. No.	149048
Seq. ID	LIB3175-020-P1-K1-E1
Method	BLASTN

NCBI GI	g3892698
BLAST score	175
E value	6.0e-94
Match length	175
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project)

Seq. No.	149049
Seq. ID	LIB3175-020-P1-K1-E10
Method	BLASTN
NCBI GI	g886427
BLAST score	52
E value	2.0e-20
Match length	183
% identity	85
NCBI Description	A.thaliana mRNA for zeta-crystallin homologue

Seq. No.	149050
Seq. ID	LIB3175-020-P1-K1-E11
Method	BLASTN
NCBI GI	g4191771
BLAST score	157
E value	6.0e-83
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149051
Seq. ID	LIB3175-020-P1-K1-E2
Method	BLASTX
NCBI GI	g267073
BLAST score	373
E value	6.0e-36
Match length	74
% identity	93
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	149052
Seq. ID	LIB3175-020-P1-K1-E3
Method	BLASTN
NCBI GI	g4589409
BLAST score	261
E value	1.0e-145
Match length	337
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	149053
Seq. ID	LIB3175-020-P1-K1-E4
Method	BLASTX
NCBI GI	g4063749

BLAST score	176
E value	1.0e-12
Match length	85
% identity	24
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149054
Seq. ID	LIB3175-020-P1-K1-E7
Method	BLASTN
NCBI GI	g3928074
BLAST score	236
E value	1.0e-130
Match length	438
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149055
Seq. ID	LIB3175-020-P1-K1-E8
Method	BLASTX
NCBI GI	g2117612
BLAST score	803
E value	3.0e-86
Match length	143
% identity	100
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	149056
Seq. ID	LIB3175-020-P1-K1-E9
Method	BLASTX
NCBI GI	g4581207
BLAST score	488
E value	2.0e-49
Match length	93
% identity	100
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	149057
Seq. ID	LIB3175-020-P1-K1-F10
Method	BLASTN
NCBI GI	g1086460
BLAST score	188
E value	1.0e-101
Match length	316
% identity	57
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT1c) gene, complete cds

Seq. No.	149058
Seq. ID	LIB3175-020-P1-K1-F11
Method	BLASTX
NCBI GI	g267069
BLAST score	669
E value	2.0e-70
Match length	124
% identity	100

NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	149059
Seq. ID	LIB3175-020-P1-K1-F12
Method	BLASTN
NCBI GI	g495728
BLAST score	303
E value	1.0e-170
Match length	315
% identity	99
NCBI Description	Arabidopsis thaliana small Ras-like GTP-binding protein (Ran-1) mRNA, complete cds. >gi_2058277_emb_X97379_ATRRAN1 A.thaliana mRNA for AtRan1 protein

Seq. No.	149060
Seq. ID	LIB3175-020-P1-K1-F2
Method	BLASTX
NCBI GI	g2160296
BLAST score	186
E value	4.0e-14
Match length	106
% identity	42
NCBI Description	(D61395) gamma-VPE [Arabidopsis thaliana]

Seq. No.	149061
Seq. ID	LIB3175-020-P1-K1-F3
Method	BLASTN
NCBI GI	g2459406
BLAST score	99
E value	2.0e-48
Match length	312
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149062
Seq. ID	LIB3175-020-P1-K1-F4
Method	BLASTX
NCBI GI	g4835233
BLAST score	591
E value	2.0e-61
Match length	122
% identity	97
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	149063
Seq. ID	LIB3175-020-P1-K1-F6
Method	BLASTN
NCBI GI	g3869075
BLAST score	277
E value	1.0e-154
Match length	417
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.	149064
Seq. ID	LIB3175-020-P1-K1-F9
Method	BLASTX
NCBI GI	g115767
BLAST score	499
E value	8.0e-51
Match length	95
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	149065
Seq. ID	LIB3175-020-P1-K1-G10
Method	BLASTN
NCBI GI	g4589440
BLAST score	212
E value	1.0e-116
Match length	212
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence
Seq. No.	149066
Seq. ID	LIB3175-020-P1-K1-G11
Method	BLASTX
NCBI GI	g3036793
BLAST score	154
E value	4.0e-10
Match length	119
% identity	36
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805855_emb_CAA21475_ (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	149067
Seq. ID	LIB3175-020-P1-K1-G2
Method	BLASTX
NCBI GI	g4585919
BLAST score	143
E value	5.0e-09
Match length	103
% identity	41
NCBI Description	(AC007211) aSPF1 protein [Arabidopsis thaliana]
Seq. No.	149068
Seq. ID	LIB3175-020-P1-K1-G3
Method	BLASTX
NCBI GI	g3831446
BLAST score	655

E value	6.0e-69
Match length	130
% identity	98
NCBI Description	(AC005819) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	149069
Seq. ID	LIB3175-020-P1-K1-G4
Method	BLASTX
NCBI GI	g4510430
BLAST score	757
E value	8.0e-81
Match length	144
% identity	99
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	149070
Seq. ID	LIB3175-020-P1-K1-G5
Method	BLASTX
NCBI GI	g2529229
BLAST score	342
E value	5.0e-34
Match length	87
% identity	85
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	149071
Seq. ID	LIB3175-020-P1-K1-G6
Method	BLASTX
NCBI GI	g1709970
BLAST score	193
E value	1.0e-14
Match length	49
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	149072
Seq. ID	LIB3175-020-P1-K1-G9
Method	BLASTN
NCBI GI	g4519188
BLAST score	20
E value	3.7e-01
Match length	423
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	149073
Seq. ID	LIB3175-020-P1-K1-H10
Method	BLASTX
NCBI GI	g2262167
BLAST score	747
E value	1.0e-79
Match length	142
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis

thaliana]

Seq. No.	149074
Seq. ID	LIB3175-020-P1-K1-H11
Method	BLASTX
NCBI GI	g4056493
BLAST score	440
E value	1.0e-43
Match length	140
% identity	63
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	149075
Seq. ID	LIB3175-020-P1-K1-H12
Method	BLASTX
NCBI GI	g543841
BLAST score	620
E value	9.0e-65
Match length	123
% identity	98
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	149076
Seq. ID	LIB3175-020-P1-K1-H2
Method	BLASTX
NCBI GI	g112741
BLAST score	550
E value	1.0e-56
Match length	102
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	149077
Seq. ID	LIB3175-020-P1-K1-H3
Method	BLASTX
NCBI GI	g4006871
BLAST score	417
E value	3.0e-41
Match length	101
% identity	85
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	149078
Seq. ID	LIB3175-020-P1-K1-H5
Method	BLASTN
NCBI GI	g3128141

BLAST score 222
E value 1.0e-122
Match length 322
% identity 92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No. 149079
Seq. ID LIB3175-020-P1-K1-H6
Method BLASTX
NCBI GI g2864602
BLAST score 402
E value 4.0e-39
Match length 119
% identity 67
NCBI Description (Y12071) thylakoid lumen rotamase [Spinacia oleracea]

Seq. No. 149080
Seq. ID LIB3175-020-P1-K1-H7
Method BLASTX
NCBI GI g1363489
BLAST score 392
E value 6.0e-49
Match length 107
% identity 92
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No. 149081
Seq. ID LIB3175-020-P1-K1-H8
Method BLASTN
NCBI GI g2264367
BLAST score 389
E value 0.0e+00
Match length 389
% identity 100
NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No. 149082
Seq. ID LIB3175-020-P1-K1-H9
Method BLASTX
NCBI GI g132074
BLAST score 618
E value 1.0e-64
Match length 112
% identity 100
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No. 149083
Seq. ID LIB3175-021-P1-K1-A1
Method BLASTX
NCBI GI g116464

BLAST score	73
E value	8.0e-29
Match length	83
% identity	86
NCBI Description	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi_68230_pir__YKMUM citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial - Arabidopsis thaliana >gi_2652924_emb_CAA35570_ (X17528) citrate synthetase [Arabidopsis thaliana]

Seq. No.	149084
Seq. ID	LIB3175-021-P1-K1-A10
Method	BLASTX
NCBI GI	g4335750
BLAST score	493
E value	6.0e-50
Match length	90
% identity	98
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	149085
Seq. ID	LIB3175-021-P1-K1-A11
Method	BLASTX
NCBI GI	g4544399
BLAST score	439
E value	1.0e-43
Match length	101
% identity	78
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	149086
Seq. ID	LIB3175-021-P1-K1-A12
Method	BLASTX
NCBI GI	g3157931
BLAST score	689
E value	7.0e-73
Match length	133
% identity	100
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	149087
Seq. ID	LIB3175-021-P1-K1-A3
Method	BLASTX
NCBI GI	g1865681
BLAST score	651
E value	2.0e-68
Match length	133
% identity	95
NCBI Description	(Z83320) Related seqeunces: ATH1 genomic clone, acc. no. X80127; cDNA ATH1 clone, acc. no. X80126 [Arabidopsis thaliana]

Seq. No.	149088
Seq. ID	LIB3175-021-P1-K1-A4
Method	BLASTX
NCBI GI	g2645971
BLAST score	707
E value	5.0e-75
Match length	131
% identity	100
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	149089
Seq. ID	LIB3175-021-P1-K1-A5
Method	BLASTN
NCBI GI	g2979540
BLAST score	404
E value	0.0e+00
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149090
Seq. ID	LIB3175-021-P1-K1-A6
Method	BLASTX
NCBI GI	g3913410
BLAST score	589
E value	4.0e-61
Match length	134
% identity	86
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2) (SAMDC 2) >gi_2662406 (U80916) S-adenosyl-L-methionine decarboxylase [Brassica juncea]

Seq. No.	149091
Seq. ID	LIB3175-021-P1-K1-A7
Method	BLASTX
NCBI GI	g3892722
BLAST score	309
E value	1.0e-28
Match length	74
% identity	84
NCBI Description	(AL033545) putative protein [Arabidopsis thaliana]

Seq. No.	149092
Seq. ID	LIB3175-021-P1-K1-A8
Method	BLASTN
NCBI GI	g4678371
BLAST score	388
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	149093
Seq. ID	LIB3175-021-P1-K1-A9

Method	BLASTN
NCBI GI	g2618602
BLAST score	20
E value	3.3e-01
Match length	389
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	149094
Seq. ID	LIB3175-021-P1-K1-B1
Method	BLASTX
NCBI GI	g729477
BLAST score	314
E value	6.0e-29
Match length	119
% identity	55
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi_167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

Seq. No.	149095
Seq. ID	LIB3175-021-P1-K1-B10
Method	BLASTN
NCBI GI	g4519191
BLAST score	294
E value	1.0e-164
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	149096
Seq. ID	LIB3175-021-P1-K1-B11
Method	BLASTN
NCBI GI	g2264318
BLAST score	399
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	149097
Seq. ID	LIB3175-021-P1-K1-B12
Method	BLASTX
NCBI GI	g3377844
BLAST score	212
E value	6.0e-17
Match length	67
% identity	76
NCBI Description	(AF076274) contains similarity to DNA (cytosine-5-)-methyltransferases [Arabidopsis thaliana]

Seq. No.	149098
Seq. ID	LIB3175-021-P1-K1-B3
Method	BLASTX
NCBI GI	g4432856
BLAST score	205
E value	4.0e-16
Match length	89
% identity	53
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	149099
Seq. ID	LIB3175-021-P1-K1-B4
Method	BLASTN
NCBI GI	g3789706
BLAST score	229
E value	1.0e-126
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149100
Seq. ID	LIB3175-021-P1-K1-B5
Method	BLASTX
NCBI GI	g2500130
BLAST score	694
E value	2.0e-73
Match length	134
% identity	100
NCBI Description	THIOREDOXIN REDUCTASE 2 (NADPH-DEPENDENT THIOREDOXIN REDUCTASE 2) (NTR 2) >gi_1076358_pir__S44026 thioredoxin reductase (NADPH) (EC 1.6.4.5) A - Arabidopsis thaliana (fragment) >gi_468524_emb_CAA80655_ (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	149101
Seq. ID	LIB3175-021-P1-K1-B6
Method	BLASTX
NCBI GI	g3980254
BLAST score	676
E value	2.0e-71
Match length	133
% identity	100
NCBI Description	(AJ006053) peroxisomal membrane protein [Arabidopsis thaliana] >gi_4773886_gb_AAD29759.1_AF076243_6 (AF076243) pmp22 peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	149102
Seq. ID	LIB3175-021-P1-K1-B7
Method	BLASTX
NCBI GI	g1169476
BLAST score	607
E value	3.0e-63
Match length	117
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	149103
Seq. ID	LIB3175-021-P1-K1-B8
Method	BLASTX
NCBI GI	g687677
BLAST score	172
E value	3.0e-12
Match length	34
% identity	97
NCBI Description	(U19925) unknown [Arabidopsis thaliana]

Seq. No.	149104
Seq. ID	LIB3175-021-P1-K1-B9
Method	BLASTX
NCBI GI	g82200
BLAST score	309
E value	2.0e-28
Match length	121
% identity	58
NCBI Description	hypothetical protein 1244 - common tobacco chloroplast

Seq. No.	149105
Seq. ID	LIB3175-021-P1-K1-C1
Method	BLASTN
NCBI GI	g2618602
BLAST score	171
E value	3.0e-91
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	149106
Seq. ID	LIB3175-021-P1-K1-C10
Method	BLASTN
NCBI GI	g4757414
BLAST score	400
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	149107
Seq. ID	LIB3175-021-P1-K1-C11
Method	BLASTX
NCBI GI	g2828267
BLAST score	432
E value	9.0e-43
Match length	108
% identity	81
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	149108
Seq. ID	LIB3175-021-P1-K1-C12
Method	BLASTX

NCBI GI	g2828267
BLAST score	239
E value	3.0e-20
Match length	97
% identity	61
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	149109
Seq. ID	LIB3175-021-P1-K1-C2
Method	BLASTX
NCBI GI	g1362162
BLAST score	579
E value	5.0e-60
Match length	137
% identity	76
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	149110
Seq. ID	LIB3175-021-P1-K1-C3
Method	BLASTX
NCBI GI	g1362162
BLAST score	283
E value	6.0e-34
Match length	115
% identity	64
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	149111
Seq. ID	LIB3175-021-P1-K1-C4
Method	BLASTX
NCBI GI	g2738248
BLAST score	491
E value	1.0e-49
Match length	103
% identity	90
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	149112
Seq. ID	LIB3175-021-P1-K1-C5
Method	BLASTN
NCBI GI	g2618602
BLAST score	20
E value	3.5e-01
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	149113
Seq. ID	LIB3175-021-P1-K1-C6
Method	BLASTX
NCBI GI	g4415930
BLAST score	534
E value	1.0e-54

Match length	127
% identity	80
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559389_gb_AAD23049.1_AC006526_14 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	149114
Seq. ID	LIB3175-021-P1-K1-C7
Method	BLASTX
NCBI GI	g2119846
BLAST score	672
E value	7.0e-71
Match length	127
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149115
Seq. ID	LIB3175-021-P1-K1-C8
Method	BLASTX
NCBI GI	g1345592
BLAST score	681
E value	6.0e-72
Match length	136
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	149116
Seq. ID	LIB3175-021-P1-K1-C9
Method	BLASTX
NCBI GI	g3927831
BLAST score	720
E value	2.0e-76
Match length	136
% identity	67
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	149117
Seq. ID	LIB3175-021-P1-K1-D1
Method	BLASTN
NCBI GI	g4097949
BLAST score	322
E value	0.0e+00
Match length	357
% identity	100
NCBI Description	Arabidopsis thaliana plant IF-like protein mRNA, complete cds

Seq. No.	149118
Seq. ID	LIB3175-021-P1-K1-D10

Method	BLASTX
NCBI GI	g1335862
BLAST score	532
E value	2.0e-54
Match length	133
% identity	78
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	149119
Seq. ID	LIB3175-021-P1-K1-D12
Method	BLASTX
NCBI GI	g4741952
BLAST score	630
E value	6.0e-66
Match length	118
% identity	75
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	149120
Seq. ID	LIB3175-021-P1-K1-D2
Method	BLASTX
NCBI GI	g4583542
BLAST score	331
E value	7.0e-31
Match length	130
% identity	60
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	149121
Seq. ID	LIB3175-021-P1-K1-D3
Method	BLASTX
NCBI GI	g1170159
BLAST score	326
E value	3.0e-30
Match length	66
% identity	100
NCBI Description	HISTONE H2B

Seq. No.	149122
Seq. ID	LIB3175-021-P1-K1-D4
Method	BLASTX
NCBI GI	g1931639
BLAST score	244
E value	1.0e-20
Match length	106
% identity	43
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	149123
Seq. ID	LIB3175-021-P1-K1-D5
Method	BLASTX
NCBI GI	g3319349
BLAST score	646
E value	7.0e-68
Match length	126
% identity	100

NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	149124
Seq. ID	LIB3175-021-P1-K1-D6
Method	BLASTX
NCBI GI	g1169277
BLAST score	460
E value	5.0e-46
Match length	106
% identity	87
NCBI Description	DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45) >gi_2129638_pir__S60480 low temperature-induced protein lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_ (D17714) ERD10 protein [Arabidopsis thaliana] >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis thaliana]

Seq. No.	149125
Seq. ID	LIB3175-021-P1-K1-D8
Method	BLASTX
NCBI GI	g2501102
BLAST score	585
E value	1.0e-60
Match length	119
% identity	100
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf__2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	149126
Seq. ID	LIB3175-021-P1-K1-E1
Method	BLASTN
NCBI GI	g704396
BLAST score	373
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana cystathionine beta-lyase mRNA, complete cds

Seq. No.	149127
Seq. ID	LIB3175-021-P1-K1-E10
Method	BLASTX
NCBI GI	g1345595
BLAST score	598
E value	3.0e-62
Match length	122
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	149128
Seq. ID	LIB3175-021-P1-K1-E12
Method	BLASTX
NCBI GI	g2244837
BLAST score	507
E value	1.0e-51
Match length	100
% identity	100
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	149129
Seq. ID	LIB3175-021-P1-K1-E3
Method	BLASTX
NCBI GI	g4678332
BLAST score	430
E value	2.0e-42
Match length	135
% identity	66
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	149130
Seq. ID	LIB3175-021-P1-K1-E4
Method	BLASTX
NCBI GI	g1009234
BLAST score	591
E value	3.0e-64
Match length	135
% identity	93
NCBI Description	(L38829) SUP2 gene product [Nicotiana tabacum]

Seq. No.	149131
Seq. ID	LIB3175-021-P1-K1-E5
Method	BLASTX
NCBI GI	g3096935
BLAST score	221
E value	5.0e-18
Match length	85
% identity	51
NCBI Description	(AL023094) putative protein [Arabidopsis thaliana]

Seq. No.	149132
Seq. ID	LIB3175-021-P1-K1-E6
Method	BLASTN
NCBI GI	g2739359
BLAST score	404
E value	0.0e+00
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149133
Seq. ID	LIB3175-021-P1-K1-E7

Method	BLASTX
NCBI GI	g3482979
BLAST score	457
E value	1.0e-45
Match length	85
% identity	100
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana] >gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149134
Seq. ID	LIB3175-021-P1-K1-E8
Method	BLASTX
NCBI GI	g131336
BLAST score	339
E value	7.0e-32
Match length	73
% identity	93
NCBI Description	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi_72715_pir__F2NT0P photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum] >gi_225225_prf__1211235BG photosystem II 10kD phosphoprotein [Nicotiana tabacum]

Seq. No.	149135
Seq. ID	LIB3175-021-P1-K1-E9
Method	BLASTX
NCBI GI	g2275196
BLAST score	629
E value	7.0e-66
Match length	122
% identity	100
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana] >gi_4630746_gb_AAD26596.1_AC007236_1 (AC007236) water stress-induced protein [Arabidopsis thaliana]

Seq. No.	149136
Seq. ID	LIB3175-021-P1-K1-F1
Method	BLASTX
NCBI GI	g1177320
BLAST score	197
E value	3.0e-15
Match length	84
% identity	48
NCBI Description	(X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No.	149137
Seq. ID	LIB3175-021-P1-K1-F10
Method	BLASTX
NCBI GI	g132110
BLAST score	598
E value	3.0e-62
Match length	111
% identity	99

NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	149138
Seq. ID	LIB3175-021-P1-K1-F11
Method	BLASTX
NCBI GI	g2979544
BLAST score	587
E value	6.0e-61
Match length	110
% identity	100
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No.	149139
Seq. ID	LIB3175-021-P1-K1-F2
Method	BLASTX
NCBI GI	g1346106
BLAST score	589
E value	4.0e-61
Match length	128
% identity	89
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_557694 (U12232) GTP binding protein beta subunit [Arabidopsis thaliana] >gi_3096915_emb_CAA18825.1_ (AL023094) GTP binding protein beta subunit [Arabidopsis thaliana]

Seq. No.	149140
Seq. ID	LIB3175-021-P1-K1-F3
Method	BLASTX
NCBI GI	g3335333
BLAST score	488
E value	3.0e-49
Match length	124
% identity	82
NCBI Description	(AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this gene. [Arabidopsis thaliana]

Seq. No.	149141
Seq. ID	LIB3175-021-P1-K1-F4
Method	BLASTX
NCBI GI	g3201613
BLAST score	415
E value	9.0e-41
Match length	78
% identity	100
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	149142
Seq. ID	LIB3175-021-P1-K1-F5
Method	BLASTX
NCBI GI	g3183088

BLAST score	214
E value	3.0e-17
Match length	68
% identity	54
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	149143
Seq. ID	LIB3175-021-P1-K1-F6
Method	BLASTX
NCBI GI	g166834
BLAST score	521
E value	3.0e-53
Match length	116
% identity	90
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	149144
Seq. ID	LIB3175-021-P1-K1-F7
Method	BLASTX
NCBI GI	g4741940
BLAST score	567
E value	1.0e-58
Match length	103
% identity	66
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	149145
Seq. ID	LIB3175-021-P1-K1-F8
Method	BLASTX
NCBI GI	g2827627
BLAST score	538
E value	3.0e-55
Match length	101
% identity	100
NCBI Description	(AL021636) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149146
Seq. ID	LIB3175-021-P1-K1-F9
Method	BLASTN
NCBI GI	g4262221
BLAST score	323
E value	0.0e+00
Match length	323
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149147
Seq. ID	LIB3175-021-P1-K1-G1
Method	BLASTX
NCBI GI	g4688596
BLAST score	486

E value	4.0e-49
Match length	90
% identity	100
NCBI Description	(AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	149148
Seq. ID	LIB3175-021-P1-K1-G10
Method	BLASTN
NCBI GI	g2264308
BLAST score	204
E value	1.0e-111
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK22, complete sequence [Arabidopsis thaliana]

Seq. No.	149149
Seq. ID	LIB3175-021-P1-K1-G2
Method	BLASTX
NCBI GI	g4580460
BLAST score	531
E value	2.0e-54
Match length	122
% identity	86
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	149150
Seq. ID	LIB3175-021-P1-K1-G3
Method	BLASTN
NCBI GI	g3582315
BLAST score	241
E value	1.0e-133
Match length	338
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149151
Seq. ID	LIB3175-021-P1-K1-G4
Method	BLASTX
NCBI GI	g549893
BLAST score	193
E value	8.0e-15
Match length	37
% identity	100
NCBI Description	(U09342) homeobox protein [Arabidopsis thaliana]

Seq. No.	149152
Seq. ID	LIB3175-021-P1-K1-G5
Method	BLASTX
NCBI GI	g2459424
BLAST score	687
E value	1.0e-72
Match length	135
% identity	100

NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	149153
Seq. ID	LIB3175-021-P1-K1-G6
Method	BLASTX
NCBI GI	g4538943
BLAST score	496
E value	3.0e-50
Match length	122
% identity	78
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	149154
Seq. ID	LIB3175-021-P1-K1-G7
Method	BLASTX
NCBI GI	g1402906
BLAST score	402
E value	2.0e-53
Match length	127
% identity	87
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	149155
Seq. ID	LIB3175-021-P1-K1-G8
Method	BLASTX
NCBI GI	g3953473
BLAST score	545
E value	4.0e-56
Match length	110
% identity	100
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	149156
Seq. ID	LIB3175-021-P1-K1-H1
Method	BLASTX
NCBI GI	g4490732
BLAST score	358
E value	4.0e-34
Match length	90
% identity	78
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	149157
Seq. ID	LIB3175-021-P1-K1-H10
Method	BLASTX
NCBI GI	g4585882
BLAST score	442
E value	6.0e-44
Match length	86
% identity	99
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	149158
Seq. ID	LIB3175-021-P1-K1-H11
Method	BLASTX
NCBI GI	g134976
BLAST score	681
E value	6.0e-72
Match length	131
% identity	98
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	149159
Seq. ID	LIB3175-021-P1-K1-H12
Method	BLASTX
NCBI GI	g4539307
BLAST score	294
E value	1.0e-26
Match length	120
% identity	53
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	149160
Seq. ID	LIB3175-021-P1-K1-H2
Method	BLASTX
NCBI GI	g1628583
BLAST score	351
E value	2.0e-33
Match length	72
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	149161
Seq. ID	LIB3175-021-P1-K1-H3
Method	BLASTX
NCBI GI	g3941543
BLAST score	345
E value	1.0e-32
Match length	68
% identity	100
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	149162
Seq. ID	LIB3175-021-P1-K1-H5
Method	BLASTN
NCBI GI	g16519
BLAST score	66
E value	9.0e-29
Match length	66
% identity	100
NCBI Description	A.thaliana STP1 mRNA for glucose transporter

Seq. No.	149163
Seq. ID	LIB3175-021-P1-K1-H6
Method	BLASTX
NCBI GI	g267079
BLAST score	646
E value	7.0e-68
Match length	118
% identity	100
NCBI Description	TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6 chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6 tubulin [Arabidopsis thaliana]

Seq. No.	149164
Seq. ID	LIB3175-021-P1-K1-H7
Method	BLASTX
NCBI GI	g2244750
BLAST score	685
E value	2.0e-72
Match length	134
% identity	100
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	149165
Seq. ID	LIB3175-021-P1-K1-H8
Method	BLASTX
NCBI GI	g1732570
BLAST score	732
E value	6.0e-78
Match length	132
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	149166
Seq. ID	LIB3175-021-P1-K1-H9
Method	BLASTX
NCBI GI	g2244772
BLAST score	698
E value	6.0e-74
Match length	125
% identity	100
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	149167
Seq. ID	LIB3175-022-P1-K1-A1
Method	BLASTN
NCBI GI	g3059018
BLAST score	260
E value	1.0e-144
Match length	298
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	149168

Seq. ID	LIB3175-022-P1-K1-A10
Method	BLASTX
NCBI GI	g1363488
BLAST score	481
E value	2.0e-48
Match length	94
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	149169
Seq. ID	LIB3175-022-P1-K1-A11
Method	BLASTX
NCBI GI	g1172658
BLAST score	166
E value	8.0e-12
Match length	35
% identity	97
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_1262705_dbj_BAA04420.1_ (D17510) PSI P700 apoprotein A2 [Pinus thunbergii]

Seq. No.	149170
Seq. ID	LIB3175-022-P1-K1-A2
Method	BLASTN
NCBI GI	g3738275
BLAST score	347
E value	0.0e+00
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149171
Seq. ID	LIB3175-022-P1-K1-A3
Method	BLASTX
NCBI GI	g2213607
BLAST score	475
E value	9.0e-48
Match length	92
% identity	67
NCBI Description	(AC000103) F21J9.1 [Arabidopsis thaliana]

Seq. No.	149172
Seq. ID	LIB3175-022-P1-K1-A5
Method	BLASTX
NCBI GI	g4191796
BLAST score	231
E value	4.0e-19
Match length	65
% identity	60
NCBI Description	(AC005917) putative senescence-associated protein 5 [Arabidopsis thaliana]

Seq. No.	149173

Seq. ID	LIB3175-022-P1-K1-A8
Method	BLASTX
NCBI GI	g4105798
BLAST score	378
E value	2.0e-36
Match length	82
% identity	71
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	149174
Seq. ID	LIB3175-022-P1-K1-B11
Method	BLASTX
NCBI GI	g1345595
BLAST score	638
E value	7.0e-67
Match length	130
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	149175
Seq. ID	LIB3175-022-P1-K1-B2
Method	BLASTX
NCBI GI	g498038
BLAST score	474
E value	1.0e-47
Match length	143
% identity	57
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	149176
Seq. ID	LIB3175-022-P1-K1-B3
Method	BLASTX
NCBI GI	g2651314
BLAST score	384
E value	4.0e-37
Match length	110
% identity	70
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	149177
Seq. ID	LIB3175-022-P1-K1-B4
Method	BLASTX
NCBI GI	g2500082
BLAST score	600
E value	2.0e-62
Match length	120
% identity	97
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_984735_emb_CAA56907_ (X80932) photosystem II D1 protein [Vigna unguiculata]

Seq. No. 149178

Seq. ID	LIB3175-022-P1-K1-B5
Method	BLASTX
NCBI GI	g1710780
BLAST score	430
E value	1.0e-42
Match length	116
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	149179
Seq. ID	LIB3175-022-P1-K1-B6
Method	BLASTN
NCBI GI	g2618605
BLAST score	295
E value	1.0e-165
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	149180
Seq. ID	LIB3175-022-P1-K1-B8
Method	BLASTN
NCBI GI	g1402874
BLAST score	181
E value	3.0e-97
Match length	324
% identity	97
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	149181
Seq. ID	LIB3175-022-P1-K1-B9
Method	BLASTN
NCBI GI	g3510336
BLAST score	384
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	149182
Seq. ID	LIB3175-022-P1-K1-C1
Method	BLASTN
NCBI GI	g3702728
BLAST score	260
E value	1.0e-144
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	149183
Seq. ID	LIB3175-022-P1-K1-C10
Method	BLASTX

NCBI GI	g2864617
BLAST score	432
E value	1.0e-42
Match length	112
% identity	79
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	149184
Seq. ID	LIB3175-022-P1-K1-C11
Method	BLASTX
NCBI GI	g1486472
BLAST score	453
E value	3.0e-45
Match length	103
% identity	86
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	149185
Seq. ID	LIB3175-022-P1-K1-C12
Method	BLASTN
NCBI GI	g4589414
BLAST score	50
E value	3.0e-19
Match length	224
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	149186
Seq. ID	LIB3175-022-P1-K1-C2
Method	BLASTN
NCBI GI	g2760169
BLAST score	379
E value	0.0e+00
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	149187
Seq. ID	LIB3175-022-P1-K1-C3
Method	BLASTN
NCBI GI	g4589412
BLAST score	174
E value	5.0e-93
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	149188
Seq. ID	LIB3175-022-P1-K1-C4
Method	BLASTX
NCBI GI	g4651202
BLAST score	169

E value	7.0e-12
Match length	99
% identity	35
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]

Seq. No.	149189
Seq. ID	LIB3175-022-P1-K1-C5
Method	BLASTX
NCBI GI	g3935181
BLAST score	721
E value	1.0e-76
Match length	131
% identity	100
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	149190
Seq. ID	LIB3175-022-P1-K1-C6
Method	BLASTN
NCBI GI	g3335356
BLAST score	320
E value	1.0e-180
Match length	402
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149191
Seq. ID	LIB3175-022-P1-K1-C8
Method	BLASTX
NCBI GI	g1169598
BLAST score	417
E value	5.0e-41
Match length	89
% identity	87
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	149192
Seq. ID	LIB3175-022-P1-K1-C9
Method	BLASTX
NCBI GI	g1169201
BLAST score	527
E value	7.0e-54
Match length	130
% identity	84
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	149193
Seq. ID	LIB3175-022-P1-K1-D12
Method	BLASTX
NCBI GI	g4455248
BLAST score	278
E value	1.0e-24
Match length	65

% identity	92
NCBI Description	(AL035523) acyl carrier-like protein [Arabidopsis thaliana]

Seq. No.	149194
Seq. ID	LIB3175-022-P1-K1-D4
Method	BLASTX
NCBI GI	g2213610
BLAST score	271
E value	7.0e-24
Match length	115
% identity	49
NCBI Description	(AC000103) F21J9.4 [Arabidopsis thaliana]

Seq. No.	149195
Seq. ID	LIB3175-022-P1-K1-D5
Method	BLASTX
NCBI GI	g1732411
BLAST score	68
E value	7.0e-18
Match length	140
% identity	24
NCBI Description	(U47924) isopeptidase T [Homo sapiens]

Seq. No.	149196
Seq. ID	LIB3175-022-P1-K1-D6
Method	BLASTN
NCBI GI	g2558511
BLAST score	291
E value	1.0e-163
Match length	307
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for proton pump interactor, partial

Seq. No.	149197
Seq. ID	LIB3175-022-P1-K1-D7
Method	BLASTX
NCBI GI	g131289
BLAST score	749
E value	7.0e-80
Match length	141
% identity	100
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi_225285_prf__1211235W photosystem II 44kD protein [Nicotiana tabacum]

Seq. No.	149198
Seq. ID	LIB3175-022-P1-K1-D8
Method	BLASTN
NCBI GI	g1107500
BLAST score	379
E value	0.0e+00
Match length	383
% identity	100
NCBI Description	A.thaliana mRNA for unknown protein (clone YAP037)

Seq. No.	149199
Seq. ID	LIB3175-022-P1-K1-D9
Method	BLASTN
NCBI GI	g2182287
BLAST score	265
E value	1.0e-147
Match length	383
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	149200
Seq. ID	LIB3175-022-P1-K1-E10
Method	BLASTX
NCBI GI	g1399273
BLAST score	702
E value	2.0e-74
Match length	140
% identity	72
NCBI Description	(U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi_3080419_emb_CAA18738.1_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No.	149201
Seq. ID	LIB3175-022-P1-K1-E12
Method	BLASTX
NCBI GI	g3695412
BLAST score	691
E value	4.0e-73
Match length	139
% identity	100
NCBI Description	(AF096373) contains similarity to group 1 glycosyl transferases (Pfam: PF00534, E=2.1e-11) [Arabidopsis thaliana]

Seq. No.	149202
Seq. ID	LIB3175-022-P1-K1-E3
Method	BLASTX
NCBI GI	g3695023
BLAST score	319
E value	2.0e-29
Match length	113
% identity	54
NCBI Description	(AF055850) unknown [Arabidopsis thaliana]

Seq. No.	149203
Seq. ID	LIB3175-022-P1-K1-E4
Method	BLASTN
NCBI GI	g2618720
BLAST score	319
E value	1.0e-179
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana early auxin-induced (IAA16) mRNA, complete cds

Seq. No.	149204
Seq. ID	LIB3175-022-P1-K1-E6
Method	BLASTN
NCBI GI	g3319339
BLAST score	54
E value	2.0e-21
Match length	154
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	149205
Seq. ID	LIB3175-022-P1-K1-E7
Method	BLASTN
NCBI GI	g443696
BLAST score	254
E value	1.0e-141
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for ERD1 protein, complete cds

Seq. No.	149206
Seq. ID	LIB3175-022-P1-K1-E8
Method	BLASTX
NCBI GI	g2501056
BLAST score	731
E value	8.0e-78
Match length	140
% identity	100
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	149207
Seq. ID	LIB3175-022-P1-K1-E9
Method	BLASTX
NCBI GI	g2119846
BLAST score	693
E value	2.0e-73
Match length	130
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149208
Seq. ID	LIB3175-022-P1-K1-F1
Method	BLASTX
NCBI GI	g4056456
BLAST score	281
E value	5.0e-25
Match length	56

% identity	100
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No.	149209
Seq. ID	LIB3175-022-P1-K1-F10
Method	BLASTX
NCBI GI	g2342687
BLAST score	544
E value	7.0e-56
Match length	108
% identity	99
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	149210
Seq. ID	LIB3175-022-P1-K1-F11
Method	BLASTX
NCBI GI	g115783
BLAST score	601
E value	1.0e-62
Match length	113
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149211
Seq. ID	LIB3175-022-P1-K1-F12
Method	BLASTX
NCBI GI	g1737218
BLAST score	365
E value	7.0e-35
Match length	69
% identity	100
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	149212
Seq. ID	LIB3175-022-P1-K1-F2
Method	BLASTX
NCBI GI	g4580393
BLAST score	257
E value	3.0e-22
Match length	99
% identity	55
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149213
Seq. ID	LIB3175-022-P1-K1-F3
Method	BLASTX
NCBI GI	g140299
BLAST score	349

E value	5.0e-33
Match length	142
% identity	55
NCBI Description	CYTOCHROME C BIOGENESIS PROTEIN CCSA >gi_82213_pir__A05213 hypothetical protein 313 - common tobacco chloroplast >gi_1223666_emb_CAA77395_ (Z00044) c-type cytochrome synthesis protein [Nicotiana tabacum] >gi_225254_prf__1211235CN ORF 313 [Nicotiana tabacum]

Seq. No.	149214
Seq. ID	LIB3175-022-P1-K1-F4
Method	BLASTX
NCBI GI	g4586256
BLAST score	596
E value	6.0e-62
Match length	136
% identity	87
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	149215
Seq. ID	LIB3175-022-P1-K1-F6
Method	BLASTX
NCBI GI	g1575752
BLAST score	504
E value	3.0e-51
Match length	126
% identity	75
NCBI Description	(U70672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	149216
Seq. ID	LIB3175-022-P1-K1-F7
Method	BLASTX
NCBI GI	g1657621
BLAST score	720
E value	2.0e-76
Match length	140
% identity	100
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	149217
Seq. ID	LIB3175-022-P1-K1-F8
Method	BLASTX
NCBI GI	g2129932
BLAST score	549
E value	2.0e-56
Match length	99
% identity	97
NCBI Description	myb-related transcription factor TMH1 - tomato >gi_1167486_emb_CAA64615_ (X95297) transcription factor [Lycopersicon esculentum]

Seq. No.	149218
Seq. ID	LIB3175-022-P1-K1-F9
Method	BLASTN
NCBI GI	g556473

BLAST score	318
E value	1.0e-179
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ERD14 protein, complete cds

Seq. No.	149219
Seq. ID	LIB3175-022-P1-K1-G1
Method	BLASTX
NCBI GI	g267069
BLAST score	558
E value	2.0e-57
Match length	103
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	149220
Seq. ID	LIB3175-022-P1-K1-G10
Method	BLASTX
NCBI GI	g4056482
BLAST score	569
E value	7.0e-59
Match length	126
% identity	54
NCBI Description	(AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	149221
Seq. ID	LIB3175-022-P1-K1-G12
Method	BLASTN
NCBI GI	g2914688
BLAST score	319
E value	1.0e-179
Match length	405
% identity	67
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149222
Seq. ID	LIB3175-022-P1-K1-G2
Method	BLASTN
NCBI GI	g2182287
BLAST score	422
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	149223
Seq. ID	LIB3175-022-P1-K1-G4
Method	BLASTX
NCBI GI	g4033349
BLAST score	384
E value	3.0e-37

Match length	89
% identity	85
NCBI Description	(AJ223496) phosphoenolpyrovate carboxylase [Brassica juncea]

Seq. No.	149224
Seq. ID	LIB3175-022-P1-K1-G6
Method	BLASTN
NCBI GI	g3451055
BLAST score	196
E value	1.0e-106
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	149225
Seq. ID	LIB3175-022-P1-K1-H1
Method	BLASTX
NCBI GI	g4218535
BLAST score	408
E value	6.0e-40
Match length	105
% identity	66
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	149226
Seq. ID	LIB3175-022-P1-K1-H10
Method	BLASTN
NCBI GI	g3449312
BLAST score	414
E value	0.0e+00
Match length	414
% identity	35
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	149227
Seq. ID	LIB3175-022-P1-K1-H12
Method	BLASTN
NCBI GI	g3492855
BLAST score	47
E value	3.0e-17
Match length	253
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	149228
Seq. ID	LIB3175-022-P1-K1-H2
Method	BLASTX
NCBI GI	g2108252
BLAST score	668
E value	2.0e-70
Match length	139
% identity	62
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana]

	>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.	149229
Seq. ID	LIB3175-022-P1-K1-H5
Method	BLASTX
NCBI GI	g2369714
BLAST score	462
E value	3.0e-46
Match length	109
% identity	85
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	149230
Seq. ID	LIB3175-022-P1-K1-H6
Method	BLASTX
NCBI GI	g1351272
BLAST score	562
E value	5.0e-58
Match length	130
% identity	86
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]
Seq. No.	149231
Seq. ID	LIB3175-022-P1-K1-H7
Method	BLASTN
NCBI GI	g4455262
BLAST score	252
E value	1.0e-139
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)
Seq. No.	149232
Seq. ID	LIB3175-022-P1-K1-H8
Method	BLASTX
NCBI GI	g4510345
BLAST score	412
E value	2.0e-40
Match length	77
% identity	100
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.	149233
Seq. ID	LIB3175-024-P1-K1-A1
Method	BLASTN
NCBI GI	g3510342
BLAST score	379
E value	0.0e+00
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	149234
Seq. ID	LIB3175-024-P1-K1-A10
Method	BLASTN
NCBI GI	g4756963
BLAST score	316
E value	1.0e-178
Match length	376
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	149235
Seq. ID	LIB3175-024-P1-K1-A11
Method	BLASTN
NCBI GI	g3128143
BLAST score	149
E value	2.0e-78
Match length	236
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	149236
Seq. ID	LIB3175-024-P1-K1-A3
Method	BLASTX
NCBI GI	g1864017
BLAST score	562
E value	5.0e-58
Match length	108
% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	149237
Seq. ID	LIB3175-024-P1-K1-A4
Method	BLASTX
NCBI GI	g3582335
BLAST score	780
E value	2.0e-83
Match length	146
% identity	98
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	149238
Seq. ID	LIB3175-024-P1-K1-A6
Method	BLASTN
NCBI GI	g4756963
BLAST score	234
E value	1.0e-129
Match length	361
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	149239
Seq. ID	LIB3175-024-P1-K1-A7

Method	BLASTX
NCBI GI	g2245125
BLAST score	253
E value	1.0e-21
Match length	57
% identity	79
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149240
Seq. ID	LIB3175-024-P1-K1-A8
Method	BLASTX
NCBI GI	g113512
BLAST score	224
E value	2.0e-18
Match length	54
% identity	72
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL2 >gi_81610_pir__B39534 floral homeotic protein AGL2 - Arabidopsis thaliana >gi_166591 (M55551) transcription factor [Arabidopsis thaliana]

Seq. No.	149241
Seq. ID	LIB3175-024-P1-K1-A9
Method	BLASTX
NCBI GI	g544424
BLAST score	311
E value	9.0e-39
Match length	83
% identity	99
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	149242
Seq. ID	LIB3175-024-P1-K1-B1
Method	BLASTX
NCBI GI	g135467
BLAST score	576
E value	8.0e-60
Match length	114
% identity	98
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	149243
Seq. ID	LIB3175-024-P1-K1-B10
Method	BLASTX
NCBI GI	g282865
BLAST score	541
E value	1.0e-55
Match length	110
% identity	68
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana

	>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]
Seq. No.	149244
Seq. ID	LIB3175-024-P1-K1-B11
Method	BLASTN
NCBI GI	g4469002
BLAST score	129
E value	2.0e-66
Match length	318
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)
Seq. No.	149245
Seq. ID	LIB3175-024-P1-K1-B12
Method	BLASTX
NCBI GI	g2979544
BLAST score	511
E value	5.0e-52
Match length	99
% identity	98
NCBI Description	(AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.	149246
Seq. ID	LIB3175-024-P1-K1-B2
Method	BLASTX
NCBI GI	g4512712
BLAST score	345
E value	2.0e-32
Match length	92
% identity	72
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]
Seq. No.	149247
Seq. ID	LIB3175-024-P1-K1-B3
Method	BLASTX
NCBI GI	g112741
BLAST score	713
E value	1.0e-75
Match length	137
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	149248
Seq. ID	LIB3175-024-P1-K1-B4
Method	BLASTN
NCBI GI	g2828183

BLAST score	157
E value	7.0e-83
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	149249
Seq. ID	LIB3175-024-P1-K1-B5
Method	BLASTX
NCBI GI	g1709794
BLAST score	504
E value	3.0e-51
Match length	113
% identity	88
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana]

Seq. No.	149250
Seq. ID	LIB3175-024-P1-K1-B7
Method	BLASTN
NCBI GI	g4455290
BLAST score	176
E value	3.0e-94
Match length	355
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No.	149251
Seq. ID	LIB3175-024-P1-K1-B8
Method	BLASTN
NCBI GI	g3522932
BLAST score	229
E value	1.0e-126
Match length	328
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149252
Seq. ID	LIB3175-024-P1-K1-B9
Method	BLASTX
NCBI GI	g1755162
BLAST score	647
E value	4.0e-69
Match length	145
% identity	94
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	149253
Seq. ID	LIB3175-024-P1-K1-C1
Method	BLASTX
NCBI GI	g549056

BLAST score	321
E value	1.0e-29
Match length	87
% identity	74
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	149254
Seq. ID	LIB3175-024-P1-K1-C10
Method	BLASTN
NCBI GI	g2564050
BLAST score	285
E value	1.0e-159
Match length	328
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	149255
Seq. ID	LIB3175-024-P1-K1-C11
Method	BLASTX
NCBI GI	g1724100
BLAST score	466
E value	1.0e-46
Match length	133
% identity	68
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	149256
Seq. ID	LIB3175-024-P1-K1-C12
Method	BLASTN
NCBI GI	g4691223
BLAST score	216
E value	1.0e-118
Match length	348
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	149257
Seq. ID	LIB3175-024-P1-K1-C3
Method	BLASTX
NCBI GI	g4733981
BLAST score	325
E value	3.0e-30
Match length	90
% identity	72
NCBI Description	(AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	149258
Seq. ID	LIB3175-024-P1-K1-C4
Method	BLASTX
NCBI GI	g2829899
BLAST score	349

E value	4.0e-33
Match length	101
% identity	64
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	149259
Seq. ID	LIB3175-024-P1-K1-C5
Method	BLASTX
NCBI GI	g112741
BLAST score	604
E value	5.0e-63
Match length	116
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	149260
Seq. ID	LIB3175-024-P1-K1-C6
Method	BLASTX
NCBI GI	g1565225
BLAST score	364
E value	7.0e-35
Match length	67
% identity	100
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	149261
Seq. ID	LIB3175-024-P1-K1-C7
Method	BLASTX
NCBI GI	g1335862
BLAST score	563
E value	5.0e-58
Match length	148
% identity	75
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	149262
Seq. ID	LIB3175-024-P1-K1-C8
Method	BLASTX
NCBI GI	g115767
BLAST score	604
E value	6.0e-63
Match length	115
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding

protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	149263
Seq. ID	LIB3175-024-P1-K1-C9
Method	BLASTX
NCBI GI	g4583542
BLAST score	607
E value	3.0e-63
Match length	145
% identity	88
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	149264
Seq. ID	LIB3175-024-P1-K1-D1
Method	BLASTN
NCBI GI	g2618605
BLAST score	79
E value	8.0e-37
Match length	166
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	149265
Seq. ID	LIB3175-024-P1-K1-D11
Method	BLASTX
NCBI GI	g3123745
BLAST score	353
E value	1.0e-33
Match length	77
% identity	90
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	149266
Seq. ID	LIB3175-024-P1-K1-D12
Method	BLASTX
NCBI GI	g1304227
BLAST score	207
E value	6.0e-17
Match length	53
% identity	75
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	149267
Seq. ID	LIB3175-024-P1-K1-D5
Method	BLASTX
NCBI GI	g1169862
BLAST score	205
E value	3.0e-16
Match length	37
% identity	100
NCBI Description	G-BOX BINDING FACTOR 3 >gi_600863 (U17891) G-box binding factor [Arabidopsis thaliana] >gi_1262922 (U51850) G-box factor 3 [Arabidopsis thaliana]

Seq. No.	149268
Seq. ID	LIB3175-024-P1-K1-D7
Method	BLASTN
NCBI GI	g2924734
BLAST score	343
E value	0.0e+00
Match length	378
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	149269
Seq. ID	LIB3175-024-P1-K1-D8
Method	BLASTX
NCBI GI	g4371297
BLAST score	597
E value	4.0e-62
Match length	117
% identity	99
NCBI Description	(AC006260) phenylalanine ammonia-lyase 1, 3' partial [Arabidopsis thaliana]

Seq. No.	149270
Seq. ID	LIB3175-024-P1-K1-E1
Method	BLASTX
NCBI GI	g4406816
BLAST score	616
E value	2.0e-64
Match length	116
% identity	99
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	149271
Seq. ID	LIB3175-024-P1-K1-E10
Method	BLASTX
NCBI GI	g3851636
BLAST score	472
E value	2.0e-47
Match length	113
% identity	79
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	149272
Seq. ID	LIB3175-024-P1-K1-E12
Method	BLASTN
NCBI GI	g3883123
BLAST score	392
E value	0.0e+00
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA, complete cds

Seq. No.	149273
Seq. ID	LIB3175-024-P1-K1-E2

Method	BLASTX
NCBI GI	g3334123
BLAST score	398
E value	9.0e-39
Match length	101
% identity	83
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	149274
Seq. ID	LIB3175-024-P1-K1-E4
Method	BLASTN
NCBI GI	g2558511
BLAST score	261
E value	1.0e-145
Match length	296
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for proton pump interactor, partial

Seq. No.	149275
Seq. ID	LIB3175-024-P1-K1-E5
Method	BLASTN
NCBI GI	g4587641
BLAST score	282
E value	1.0e-157
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	149276
Seq. ID	LIB3175-024-P1-K1-E8
Method	BLASTX
NCBI GI	g3169569
BLAST score	542
E value	1.0e-55
Match length	114
% identity	96
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	149277
Seq. ID	LIB3175-024-P1-K1-E9
Method	BLASTX
NCBI GI	g3047101
BLAST score	258
E value	2.0e-22
Match length	105
% identity	53
NCBI Description	(AF058919) Similar to protein kinase; coded for by A. thaliana cDNA H36947; coded for by A. thaliana cDNA H37158 [Arabidopsis thaliana]

Seq. No.	149278
Seq. ID	LIB3175-024-P1-K1-F1
Method	BLASTN
NCBI GI	g4757388
BLAST score	334
E value	0.0e+00
Match length	381
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	149279
Seq. ID	LIB3175-024-P1-K1-F10
Method	BLASTX
NCBI GI	g2129577
BLAST score	463
E value	2.0e-46
Match length	98
% identity	91
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	149280
Seq. ID	LIB3175-024-P1-K1-F11
Method	BLASTN
NCBI GI	g2281648
BLAST score	266
E value	1.0e-148
Match length	270
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	149281
Seq. ID	LIB3175-024-P1-K1-F12
Method	BLASTX
NCBI GI	g3281858
BLAST score	43
E value	6.0e-54
Match length	131
% identity	85
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	149282
Seq. ID	LIB3175-024-P1-K1-F2
Method	BLASTX
NCBI GI	g4538963
BLAST score	48
E value	2.0e-44
Match length	105
% identity	89
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	149283
Seq. ID	LIB3175-024-P1-K1-F3
Method	BLASTX
NCBI GI	g4538963
BLAST score	464
E value	2.0e-46
Match length	118
% identity	77
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	149284
Seq. ID	LIB3175-024-P1-K1-F4
Method	BLASTX
NCBI GI	g1703108
BLAST score	519
E value	5.0e-53
Match length	95
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	149285
Seq. ID	LIB3175-024-P1-K1-F5
Method	BLASTX
NCBI GI	g1169476
BLAST score	613
E value	5.0e-64
Match length	117
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	149286
Seq. ID	LIB3175-024-P1-K1-F6
Method	BLASTX
NCBI GI	g4038035
BLAST score	412
E value	2.0e-40
Match length	80
% identity	100
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	149287
Seq. ID	LIB3175-024-P1-K1-F7
Method	BLASTX
NCBI GI	g4580920
BLAST score	373
E value	6.0e-36
Match length	105
% identity	70

NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	149288
Seq. ID	LIB3175-024-P1-K1-F9
Method	BLASTN
NCBI GI	g3831437
BLAST score	298
E value	1.0e-167
Match length	331
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149289
Seq. ID	LIB3175-024-P1-K1-G1
Method	BLASTN
NCBI GI	g2088638
BLAST score	127
E value	4.0e-65
Match length	377
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149290
Seq. ID	LIB3175-024-P1-K1-G10
Method	BLASTX
NCBI GI	g4510430
BLAST score	674
E value	4.0e-71
Match length	130
% identity	98
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	149291
Seq. ID	LIB3175-024-P1-K1-G2
Method	BLASTX
NCBI GI	g1172872
BLAST score	594
E value	1.0e-61
Match length	112
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	149292
Seq. ID	LIB3175-024-P1-K1-G3
Method	BLASTN
NCBI GI	g4757401
BLAST score	52
E value	3.0e-20

Match length	68
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	149293
Seq. ID	LIB3175-024-P1-K1-G4
Method	BLASTX
NCBI GI	g3983125
BLAST score	483
E value	9.0e-49
Match length	122
% identity	79
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	149294
Seq. ID	LIB3175-024-P1-K1-G5
Method	BLASTX
NCBI GI	g3688182
BLAST score	590
E value	2.0e-61
Match length	115
% identity	97
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No.	149295
Seq. ID	LIB3175-024-P1-K1-G6
Method	BLASTN
NCBI GI	g2564045
BLAST score	272
E value	1.0e-151
Match length	309
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	149296
Seq. ID	LIB3175-024-P1-K1-G7
Method	BLASTX
NCBI GI	g1351221
BLAST score	464
E value	1.0e-46
Match length	113
% identity	81
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945085 (U31096) transcription factor TFIIB [Arabidopsis thaliana] >gi_2618697 (AC002510) transcription factor TFIIB [Arabidopsis thaliana]

Seq. No.	149297
Seq. ID	LIB3175-024-P1-K1-G8
Method	BLASTX
NCBI GI	g135860
BLAST score	557
E value	2.0e-57
Match length	112

% identity	99
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	149298
Seq. ID	LIB3175-024-P1-K1-H1
Method	BLASTX
NCBI GI	g2119846
BLAST score	530
E value	2.0e-54
Match length	106
% identity	95
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149299
Seq. ID	LIB3175-024-P1-K1-H10
Method	BLASTX
NCBI GI	g4467099
BLAST score	507
E value	1.0e-51
Match length	105
% identity	94
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	149300
Seq. ID	LIB3175-024-P1-K1-H11
Method	BLASTX
NCBI GI	g3599491
BLAST score	258
E value	1.0e-22
Match length	72
% identity	67
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	149301
Seq. ID	LIB3175-024-P1-K1-H12
Method	BLASTN
NCBI GI	g4678266
BLAST score	300
E value	1.0e-168
Match length	339
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	149302
Seq. ID	LIB3175-024-P1-K1-H2
Method	BLASTX
NCBI GI	g1518540
BLAST score	545
E value	5.0e-56
Match length	114
% identity	96
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	149303
Seq. ID	LIB3175-024-P1-K1-H3
Method	BLASTN
NCBI GI	g547390
BLAST score	390
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	149304
Seq. ID	LIB3175-024-P1-K1-H4
Method	BLASTN
NCBI GI	g2760829
BLAST score	183
E value	2.0e-98
Match length	223
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149305
Seq. ID	LIB3175-024-P1-K1-H5
Method	BLASTN
NCBI GI	g3985957
BLAST score	203
E value	1.0e-110
Match length	319
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	149306
Seq. ID	LIB3175-024-P1-K1-H8
Method	BLASTX
NCBI GI	g3913651
BLAST score	238
E value	5.0e-20
Match length	120
% identity	43
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	149307
Seq. ID	LIB3175-024-P1-K1-H9

Method	BLASTN
NCBI GI	g2656026
BLAST score	270
E value	1.0e-150
Match length	333
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	149308
Seq. ID	LIB3175-025-P1-K1-A10
Method	BLASTN
NCBI GI	g336391
BLAST score	54
E value	2.0e-22
Match length	66
% identity	95
NCBI Description	A.thaliana chloroplast ribosomal protein S17 (rps17) mRNA, 3' end

Seq. No.	149309
Seq. ID	LIB3175-025-P1-K1-A2
Method	BLASTX
NCBI GI	g3858935
BLAST score	595
E value	9.0e-62
Match length	118
% identity	100
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	149310
Seq. ID	LIB3175-025-P1-K1-A4
Method	BLASTX
NCBI GI	g2511594
BLAST score	352
E value	2.0e-33
Match length	72
% identity	97
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	149311
Seq. ID	LIB3175-025-P1-K1-A5
Method	BLASTX
NCBI GI	g3548806
BLAST score	644
E value	1.0e-67
Match length	137
% identity	92
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	149312
Seq. ID	LIB3175-025-P1-K1-A6
Method	BLASTX
NCBI GI	g3885342
BLAST score	191
E value	9.0e-15
Match length	92
% identity	47
NCBI Description	(AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No.	149313
Seq. ID	LIB3175-025-P1-K1-A7
Method	BLASTX
NCBI GI	g119350
BLAST score	272
E value	2.0e-24
Match length	56
% identity	98
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	149314
Seq. ID	LIB3175-025-P1-K1-A8
Method	BLASTX
NCBI GI	g4128133
BLAST score	199
E value	2.0e-15
Match length	86
% identity	45
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	149315
Seq. ID	LIB3175-025-P1-K1-A9
Method	BLASTX
NCBI GI	g4741948
BLAST score	637
E value	9.0e-67
Match length	120
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	149316
Seq. ID	LIB3175-025-P1-K1-B1
Method	BLASTX
NCBI GI	g1084415
BLAST score	327
E value	2.0e-30
Match length	111
% identity	59
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_

(D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]

Seq. No.	149317
Seq. ID	LIB3175-025-P1-K1-B10
Method	BLASTX
NCBI GI	g1107501
BLAST score	408
E value	6.0e-40
Match length	99
% identity	84
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	149318
Seq. ID	LIB3175-025-P1-K1-B11
Method	BLASTX
NCBI GI	g4582468
BLAST score	632
E value	3.0e-66
Match length	134
% identity	96
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	149319
Seq. ID	LIB3175-025-P1-K1-B2
Method	BLASTX
NCBI GI	g4545231
BLAST score	585
E value	1.0e-60
Match length	117
% identity	95
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	149320
Seq. ID	LIB3175-025-P1-K1-B3
Method	BLASTN
NCBI GI	g4006885
BLAST score	116
E value	1.0e-58
Match length	223
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	149321
Seq. ID	LIB3175-025-P1-K1-B5
Method	BLASTX
NCBI GI	g3183088
BLAST score	214
E value	4.0e-17
Match length	68
% identity	54

NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]
Seq. No.	149322
Seq. ID	LIB3175-025-P1-K1-B7
Method	BLASTN
NCBI GI	g3293583
BLAST score	201
E value	1.0e-109
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana BAC T27D20
Seq. No.	149323
Seq. ID	LIB3175-025-P1-K1-B8
Method	BLASTX
NCBI GI	g2583125
BLAST score	377
E value	3.0e-36
Match length	110
% identity	67
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]
Seq. No.	149324
Seq. ID	LIB3175-025-P1-K1-B9
Method	BLASTX
NCBI GI	g4589398
BLAST score	394
E value	3.0e-38
Match length	86
% identity	81
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
Seq. No.	149325
Seq. ID	LIB3175-025-P1-K1-C1
Method	BLASTX
NCBI GI	g2146739
BLAST score	302
E value	2.0e-27
Match length	84
% identity	75
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.	149326
Seq. ID	LIB3175-025-P1-K1-C11
Method	BLASTX
NCBI GI	g2586127
BLAST score	276
E value	2.0e-24
Match length	109
% identity	50
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	149327
Seq. ID	LIB3175-025-P1-K1-C12
Method	BLASTX
NCBI GI	g2117612
BLAST score	496
E value	2.0e-50
Match length	96
% identity	99
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	149328
Seq. ID	LIB3175-025-P1-K1-C2
Method	BLASTX
NCBI GI	g3157944
BLAST score	727
E value	3.0e-77
Match length	141
% identity	99
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	149329
Seq. ID	LIB3175-025-P1-K1-C3
Method	BLASTN
NCBI GI	g3451055
BLAST score	218
E value	1.0e-119
Match length	468
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	149330
Seq. ID	LIB3175-025-P1-K1-C4
Method	BLASTX
NCBI GI	g3522945
BLAST score	518
E value	6.0e-53
Match length	95
% identity	100
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	149331
Seq. ID	LIB3175-025-P1-K1-C5
Method	BLASTX
NCBI GI	g584865
BLAST score	278
E value	1.0e-24
Match length	148
% identity	35
NCBI Description	CYTOCHROME P450 76A2 (CYPLXXVIA2) (P-450EG7) >gi_542073_pir__S38534 cytochrome P450 76A2 - eggplant >gi_415911_emb_CAA50648_ (X71657) P450 hydroxylase [Solanum melongena]

Seq. No.	149332
Seq. ID	LIB3175-025-P1-K1-C6
Method	BLASTX
NCBI GI	g3176874
BLAST score	177
E value	2.0e-13
Match length	47
% identity	74
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	149333
Seq. ID	LIB3175-025-P1-K1-C7
Method	BLASTX
NCBI GI	g3600031
BLAST score	766
E value	7.0e-82
Match length	148
% identity	99
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	149334
Seq. ID	LIB3175-025-P1-K1-C8
Method	BLASTX
NCBI GI	g1755162
BLAST score	635
E value	1.0e-66
Match length	126
% identity	97
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	149335
Seq. ID	LIB3175-025-P1-K1-C9
Method	BLASTX
NCBI GI	g4415907
BLAST score	520
E value	4.0e-53
Match length	101
% identity	99
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	149336
Seq. ID	LIB3175-025-P1-K1-D10
Method	BLASTX
NCBI GI	g1706772
BLAST score	317
E value	2.0e-29
Match length	63
% identity	95
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana

	>gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]
Seq. No.	149337
Seq. ID	LIB3175-025-P1-K1-D12
Method	BLASTN
NCBI GI	g2656029
BLAST score	107
E value	4.0e-53
Match length	208
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2
Seq. No.	149338
Seq. ID	LIB3175-025-P1-K1-D2
Method	BLASTN
NCBI GI	g4220638
BLAST score	360
E value	0.0e+00
Match length	458
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.	149339
Seq. ID	LIB3175-025-P1-K1-D3
Method	BLASTX
NCBI GI	g131398
BLAST score	537
E value	4.0e-55
Match length	124
% identity	88
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis
Seq. No.	149340
Seq. ID	LIB3175-025-P1-K1-D4
Method	BLASTX
NCBI GI	g3377815
BLAST score	555
E value	3.0e-57
Match length	110
% identity	96

NCBI Description	(AF076275) similar to protein kinases (Pfam: pkinase.hmm, score: 255.71) [Arabidopsis thaliana]

Seq. No.	149341
Seq. ID	LIB3175-025-P1-K1-D5
Method	BLASTX
NCBI GI	g2506443
BLAST score	595
E value	6.0e-62
Match length	117
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	149342
Seq. ID	LIB3175-025-P1-K1-D6
Method	BLASTX
NCBI GI	g115811
BLAST score	449
E value	1.0e-60
Match length	138
% identity	82
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I 37 PRECURSOR (CAB-37) (LHCP) >gi_82254_pir__A24717 chlorophyll a/b-binding protein precursor - petunia >gi_20512_emb_CAA28639_ (X04966) chlorophyll a/b binding protein [Petunia x hybrida]

Seq. No.	149343
Seq. ID	LIB3175-025-P1-K1-D7
Method	BLASTX
NCBI GI	g1550738
BLAST score	357
E value	6.0e-34
Match length	104
% identity	72
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	149344
Seq. ID	LIB3175-025-P1-K1-D8
Method	BLASTX
NCBI GI	g2384673
BLAST score	334
E value	3.0e-31
Match length	62
% identity	100
NCBI Description	(AF012658) putative potassium transporter AtKT3p [Arabidopsis thaliana]

Seq. No.	149345
Seq. ID	LIB3175-025-P1-K1-E1
Method	BLASTX
NCBI GI	g2262098
BLAST score	801
E value	6.0e-86
Match length	155
% identity	100
NCBI Description	(AC002343) HSP90 isolog [Arabidopsis thaliana]

Seq. No.	149346
Seq. ID	LIB3175-025-P1-K1-E10
Method	BLASTN
NCBI GI	g2262135
BLAST score	405
E value	0.0e+00
Match length	433
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	149347
Seq. ID	LIB3175-025-P1-K1-E11
Method	BLASTX
NCBI GI	g3550519
BLAST score	382
E value	7.0e-37
Match length	114
% identity	62
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	149348
Seq. ID	LIB3175-025-P1-K1-E12
Method	BLASTN
NCBI GI	g3241920
BLAST score	63
E value	2.0e-27
Match length	140
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	149349
Seq. ID	LIB3175-025-P1-K1-E2
Method	BLASTX
NCBI GI	g3775985
BLAST score	579
E value	6.0e-60
Match length	118
% identity	99
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	149350
Seq. ID	LIB3175-025-P1-K1-E6
Method	BLASTN
NCBI GI	g3643588

BLAST score	143
E value	1.0e-74
Match length	436
% identity	77
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149351
Seq. ID	LIB3175-025-P1-K1-E7
Method	BLASTN
NCBI GI	g4584387
BLAST score	432
E value	0.0e+00
Match length	440
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	149352
Seq. ID	LIB3175-025-P1-K1-E8
Method	BLASTN
NCBI GI	g3985931
BLAST score	209
E value	1.0e-114
Match length	229
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	149353
Seq. ID	LIB3175-025-P1-K1-E9
Method	BLASTN
NCBI GI	g4519193
BLAST score	163
E value	1.0e-86
Match length	375
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	149354
Seq. ID	LIB3175-025-P1-K1-F1
Method	BLASTX
NCBI GI	g4512687
BLAST score	330
E value	3.0e-51
Match length	125
% identity	84
NCBI Description	(AC006931) floral homeotic protein AGL5 [Arabidopsis thaliana]

Seq. No.	149355
Seq. ID	LIB3175-025-P1-K1-F10
Method	BLASTN
NCBI GI	g3264777
BLAST score	464
E value	0.0e+00

Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana H-protein promoter binding factor-1 (HPPBF-1) mRNA, complete cds

Seq. No.	149356
Seq. ID	LIB3175-025-P1-K1-F11
Method	BLASTN
NCBI GI	g4220643
BLAST score	217
E value	1.0e-118
Match length	403
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	149357
Seq. ID	LIB3175-025-P1-K1-F3
Method	BLASTX
NCBI GI	g4585935
BLAST score	733
E value	3.0e-80
Match length	150
% identity	97
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	149358
Seq. ID	LIB3175-025-P1-K1-F5
Method	BLASTX
NCBI GI	g395332
BLAST score	155
E value	3.0e-10
Match length	41
% identity	71
NCBI Description	(X69790) cytochrome P-450 [Catharanthus roseus]

Seq. No.	149359
Seq. ID	LIB3175-025-P1-K1-F6
Method	BLASTN
NCBI GI	g4455321
BLAST score	201
E value	1.0e-109
Match length	370
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	149360
Seq. ID	LIB3175-025-P1-K1-F7
Method	BLASTN
NCBI GI	g3766106
BLAST score	87
E value	3.0e-41
Match length	237
% identity	89

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149361
Seq. ID	LIB3175-025-P1-K1-F9
Method	BLASTX
NCBI GI	g3193316
BLAST score	583
E value	2.0e-60
Match length	123
% identity	91
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	149362
Seq. ID	LIB3175-025-P1-K1-G1
Method	BLASTN
NCBI GI	g2656031
BLAST score	171
E value	3.0e-91
Match length	484
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	149363
Seq. ID	LIB3175-025-P1-K1-G11
Method	BLASTX
NCBI GI	g3913651
BLAST score	161
E value	7.0e-11
Match length	104
% identity	37
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	149364
Seq. ID	LIB3175-025-P1-K1-G12
Method	BLASTX
NCBI GI	g100535
BLAST score	295
E value	1.0e-26
Match length	71
% identity	83
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	149365
Seq. ID	LIB3175-025-P1-K1-G2
Method	BLASTX
NCBI GI	g115783
BLAST score	689
E value	8.0e-73
Match length	130
% identity	99

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	149366
Seq. ID	LIB3175-025-P1-K1-G4
Method	BLASTX
NCBI GI	g120675
BLAST score	585
E value	1.0e-60
Match length	149
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]
Seq. No.	149367
Seq. ID	LIB3175-025-P1-K1-G6
Method	BLASTX
NCBI GI	g629541
BLAST score	505
E value	3.0e-51
Match length	119
% identity	86
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]
Seq. No.	149368
Seq. ID	LIB3175-025-P1-K1-G7
Method	BLASTN
NCBI GI	g2264318
BLAST score	314
E value	1.0e-176
Match length	334
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.	149369
Seq. ID	LIB3175-025-P1-K1-G8
Method	BLASTX
NCBI GI	g4586263
BLAST score	64
E value	9.0e-27
Match length	77
% identity	90
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]
Seq. No.	149370
Seq. ID	LIB3175-025-P1-K1-G9
Method	BLASTX
NCBI GI	g2384671
BLAST score	614

E value	4.0e-64
Match length	126
% identity	93
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	149371
Seq. ID	LIB3175-025-P1-K1-H1
Method	BLASTX
NCBI GI	g4581146
BLAST score	622
E value	5.0e-65
Match length	133
% identity	92
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	149372
Seq. ID	LIB3175-025-P1-K1-H10
Method	BLASTN
NCBI GI	g3449313
BLAST score	36
E value	1.0e-10
Match length	85
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	149373
Seq. ID	LIB3175-025-P1-K1-H11
Method	BLASTX
NCBI GI	g112682
BLAST score	574
E value	2.0e-59
Match length	134
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	149374
Seq. ID	LIB3175-025-P1-K1-H12
Method	BLASTX
NCBI GI	g1514443
BLAST score	141
E value	3.0e-21
Match length	58
% identity	95
NCBI Description	(X99061) blue light receptor [Arabidopsis thaliana]

Seq. No.	149375
Seq. ID	LIB3175-025-P1-K1-H2
Method	BLASTN
NCBI GI	g2760165
BLAST score	428

E value	0.0e+00
Match length	468
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	149376
Seq. ID	LIB3175-025-P1-K1-H7
Method	BLASTX
NCBI GI	g3287695
BLAST score	672
E value	6.0e-71
Match length	127
% identity	100
NCBI Description	(AC003979) Similar to hypothetical protein C34B7.2 gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana]

Seq. No.	149377
Seq. ID	LIB3175-025-P1-K1-H8
Method	BLASTX
NCBI GI	g3337356
BLAST score	160
E value	1.0e-34
Match length	84
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	149378
Seq. ID	LIB3175-025-P1-K1-H9
Method	BLASTX
NCBI GI	g2130028
BLAST score	352
E value	2.0e-33
Match length	86
% identity	73
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	149379
Seq. ID	LIB3175-026-P1-K1-A1
Method	BLASTN
NCBI GI	g4589434
BLAST score	144
E value	4.0e-75
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	149380
Seq. ID	LIB3175-026-P1-K1-A10
Method	BLASTX
NCBI GI	g2500430
BLAST score	428

E value	2.0e-42
Match length	84
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	149381
Seq. ID	LIB3175-026-P1-K1-A11
Method	BLASTX
NCBI GI	g1170028
BLAST score	457
E value	2.0e-53
Match length	127
% identity	83
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	149382
Seq. ID	LIB3175-026-P1-K1-A12
Method	BLASTX
NCBI GI	g464720
BLAST score	251
E value	1.0e-21
Match length	50
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S28 >gi_409184 (L09755) ribosomal protein S28 [Arabidopsis thaliana]

Seq. No.	149383
Seq. ID	LIB3175-026-P1-K1-A3
Method	BLASTN
NCBI GI	g4263694
BLAST score	195
E value	1.0e-105
Match length	374
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149384
Seq. ID	LIB3175-026-P1-K1-A4
Method	BLASTX
NCBI GI	g2645971
BLAST score	724
E value	2.0e-83
Match length	161
% identity	94
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	149385
Seq. ID	LIB3175-026-P1-K1-A5
Method	BLASTX
NCBI GI	g1755162
BLAST score	823

E value	2.0e-88
Match length	159
% identity	98
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	149386
Seq. ID	LIB3175-026-P1-K1-A7
Method	BLASTX
NCBI GI	g4586263
BLAST score	323
E value	3.0e-34
Match length	112
% identity	64
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149387
Seq. ID	LIB3175-026-P1-K1-A8
Method	BLASTX
NCBI GI	g3273743
BLAST score	601
E value	2.0e-62
Match length	118
% identity	97
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	149388
Seq. ID	LIB3175-026-P1-K1-A9
Method	BLASTX
NCBI GI	g3024500
BLAST score	486
E value	4.0e-49
Match length	104
% identity	91
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177_ (Z73949) RAB11A [Lotus japonicus]

Seq. No.	149389
Seq. ID	LIB3175-026-P1-K1-B10
Method	BLASTN
NCBI GI	g3449313
BLAST score	324
E value	0.0e+00
Match length	365
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	149390
Seq. ID	LIB3175-026-P1-K1-B11
Method	BLASTN
NCBI GI	g4335744
BLAST score	229
E value	1.0e-126
Match length	487
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149391
Seq. ID	LIB3175-026-P1-K1-B12
Method	BLASTX
NCBI GI	g4753651
BLAST score	639
E value	5.0e-67
Match length	132
% identity	92
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	149392
Seq. ID	LIB3175-026-P1-K1-B2
Method	BLASTX
NCBI GI	g4468813
BLAST score	686
E value	2.0e-72
Match length	137
% identity	97
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	149393
Seq. ID	LIB3175-026-P1-K1-B3
Method	BLASTX
NCBI GI	g2129594
BLAST score	310
E value	1.0e-28
Match length	93
% identity	70
NCBI Description	germin type 2 - Arabidopsis thaliana >gi_1107491_emb_CAA63023_ (X91957) germin type2 [Arabidopsis thaliana]

Seq. No.	149394
Seq. ID	LIB3175-026-P1-K1-B4
Method	BLASTN
NCBI GI	g3298610
BLAST score	57
E value	2.0e-23
Match length	141
% identity	85
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	149395
Seq. ID	LIB3175-026-P1-K1-B5
Method	BLASTN
NCBI GI	g3402745
BLAST score	110
E value	5.0e-55
Match length	291
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	149396
Seq. ID	LIB3175-026-P1-K1-B6
Method	BLASTX
NCBI GI	g99735
BLAST score	692
E value	3.0e-73
Match length	134
% identity	97
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	149397
Seq. ID	LIB3175-026-P1-K1-B7
Method	BLASTX
NCBI GI	g3329294
BLAST score	191
E value	2.0e-14
Match length	142
% identity	35
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	149398
Seq. ID	LIB3175-026-P1-K1-B8
Method	BLASTX
NCBI GI	g2104536
BLAST score	648
E value	5.0e-68
Match length	151
% identity	77
NCBI Description	(AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

Seq. No.	149399
Seq. ID	LIB3175-026-P1-K1-B9
Method	BLASTX
NCBI GI	g4583542
BLAST score	392
E value	6.0e-38
Match length	100
% identity	77
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	149400
Seq. ID	LIB3175-026-P1-K1-C11
Method	BLASTX
NCBI GI	g4158221
BLAST score	586
E value	1.0e-60
Match length	132
% identity	80
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	149401
Seq. ID	LIB3175-026-P1-K1-C12
Method	BLASTN

NCBI GI	g3449327
BLAST score	122
E value	6.0e-62
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	149402
Seq. ID	LIB3175-026-P1-K1-C2
Method	BLASTN
NCBI GI	g2623294
BLAST score	365
E value	0.0e+00
Match length	493
% identity	79
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149403
Seq. ID	LIB3175-026-P1-K1-C3
Method	BLASTX
NCBI GI	g2244911
BLAST score	596
E value	7.0e-62
Match length	135
% identity	84
NCBI Description	(Z97339) similar to indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	149404
Seq. ID	LIB3175-026-P1-K1-C4
Method	BLASTX
NCBI GI	g1724100
BLAST score	211
E value	5.0e-17
Match length	71
% identity	59
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	149405
Seq. ID	LIB3175-026-P1-K1-C5
Method	BLASTX
NCBI GI	g2341034
BLAST score	405
E value	9.0e-40
Match length	81
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	149406
Seq. ID	LIB3175-026-P1-K1-C6
Method	BLASTX
NCBI GI	g81615
BLAST score	388
E value	3.0e-69
Match length	160

% identity	87
NCBI Description	G-box-binding factor 1 - Arabidopsis thaliana >gi_16286_emb_CAA45356_ (X63894) G-box binding factor 1 [Arabidopsis thaliana]

Seq. No.	149407
Seq. ID	LIB3175-026-P1-K1-C8
Method	BLASTX
NCBI GI	g4056467
BLAST score	669
E value	2.0e-70
Match length	130
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	149408
Seq. ID	LIB3175-026-P1-K1-C9
Method	BLASTX
NCBI GI	g1170373
BLAST score	624
E value	3.0e-65
Match length	123
% identity	97
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	149409
Seq. ID	LIB3175-026-P1-K1-D10
Method	BLASTX
NCBI GI	g3126967
BLAST score	430
E value	1.0e-42
Match length	96
% identity	16
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No.	149410
Seq. ID	LIB3175-026-P1-K1-D11
Method	BLASTX
NCBI GI	g99696
BLAST score	691
E value	3.0e-73
Match length	124
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	149411

Seq. ID	LIB3175-026-P1-K1-D12
Method	BLASTX
NCBI GI	g464720
BLAST score	248
E value	4.0e-21
Match length	50
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S28 >gi_409184 (L09755) ribosomal protein S28 [Arabidopsis thaliana]

Seq. No.	149412
Seq. ID	LIB3175-026-P1-K1-D2
Method	BLASTX
NCBI GI	g4006834
BLAST score	752
E value	3.0e-80
Match length	148
% identity	99
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	149413
Seq. ID	LIB3175-026-P1-K1-D3
Method	BLASTX
NCBI GI	g320558
BLAST score	557
E value	3.0e-57
Match length	141
% identity	82
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	149414
Seq. ID	LIB3175-026-P1-K1-D4
Method	BLASTX
NCBI GI	g119143
BLAST score	318
E value	9.0e-30
Match length	69
% identity	91
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	149415
Seq. ID	LIB3175-026-P1-K1-D5
Method	BLASTX
NCBI GI	g119350
BLAST score	621
E value	7.0e-65

Match length	127
% identity	96
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	149416
Seq. ID	LIB3175-026-P1-K1-D7
Method	BLASTN
NCBI GI	g4376087
BLAST score	316
E value	1.0e-178
Match length	423
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	149417
Seq. ID	LIB3175-026-P1-K1-D8
Method	BLASTX
NCBI GI	g132794
BLAST score	378
E value	2.0e-36
Match length	99
% identity	79
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi_71288_pir__R5NT22 ribosomal protein L22 - common tobacco chloroplast >gi_11866_emb_CAA77382_ (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi_225236_prf__1211235BU ribosomal protein L22 [Nicotiana tabacum]

Seq. No.	149418
Seq. ID	LIB3175-026-P1-K1-D9
Method	BLASTX
NCBI GI	g2160133
BLAST score	408
E value	7.0e-40
Match length	142
% identity	61
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	149419
Seq. ID	LIB3175-026-P1-K1-E10
Method	BLASTX
NCBI GI	g115783
BLAST score	538
E value	3.0e-55
Match length	110
% identity	94

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149420
Seq. ID	LIB3175-026-P1-K1-E11
Method	BLASTN
NCBI GI	g1490552
BLAST score	320
E value	1.0e-180
Match length	354
% identity	98
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	149421
Seq. ID	LIB3175-026-P1-K1-E12
Method	BLASTX
NCBI GI	g4455253
BLAST score	616
E value	3.0e-64
Match length	146
% identity	80
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	149422
Seq. ID	LIB3175-026-P1-K1-E2
Method	BLASTX
NCBI GI	g3860277
BLAST score	46
E value	5.0e-58
Match length	142
% identity	77
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	149423
Seq. ID	LIB3175-026-P1-K1-E3
Method	BLASTX
NCBI GI	g3522945
BLAST score	543
E value	5.0e-75
Match length	152
% identity	95
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	149424
Seq. ID	LIB3175-026-P1-K1-E5
Method	BLASTN
NCBI GI	g1109698
BLAST score	131
E value	1.0e-67
Match length	231
% identity	90

NCBI Description	A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
Seq. No.	149425
Seq. ID	LIB3175-026-P1-K1-E7
Method	BLASTN
NCBI GI	g3450888
BLAST score	429
E value	0.0e+00
Match length	457
% identity	99
NCBI Description	Arabidopsis thaliana 19S proteosome subunit 9 mRNA, complete cds
Seq. No.	149426
Seq. ID	LIB3175-026-P1-K1-E8
Method	BLASTX
NCBI GI	g1351017
BLAST score	267
E value	2.0e-23
Match length	76
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S4) >gi_629697_pir__S45375 ribosomal protein S4 - common tobacco (fragment) >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4 [Nicotiana tabacum]
Seq. No.	149427
Seq. ID	LIB3175-026-P1-K1-F10
Method	BLASTN
NCBI GI	g16557
BLAST score	349
E value	0.0e+00
Match length	380
% identity	98
NCBI Description	A.thaliana TOP1 mRNA for topoisomerase I
Seq. No.	149428
Seq. ID	LIB3175-026-P1-K1-F11
Method	BLASTX
NCBI GI	g4468993
BLAST score	621
E value	6.0e-65
Match length	117
% identity	100
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]
Seq. No.	149429
Seq. ID	LIB3175-026-P1-K1-F12
Method	BLASTX
NCBI GI	g2500082
BLAST score	765
E value	1.0e-81
Match length	148
% identity	97
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_984735_emb_CAA56907_ (X80932) photosystem II D1 protein [Vigna unguiculata]

Seq. No.	149430
Seq. ID	LIB3175-026-P1-K1-F2
Method	BLASTX
NCBI GI	g1922937
BLAST score	479
E value	2.0e-48
Match length	102
% identity	92
NCBI Description	(AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs gb_H76869,gb_T21700,gb_ATTS5089 come from this gene. [Arabidopsis thaliana]

Seq. No.	149431
Seq. ID	LIB3175-026-P1-K1-F3
Method	BLASTX
NCBI GI	g2924779
BLAST score	727
E value	3.0e-77
Match length	149
% identity	98
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	149432
Seq. ID	LIB3175-026-P1-K1-F4
Method	BLASTN
NCBI GI	g1550737
BLAST score	186
E value	1.0e-100
Match length	273
% identity	92
NCBI Description	A.thaliana mRNA for endomembrane-associated protein

Seq. No.	149433
Seq. ID	LIB3175-026-P1-K1-F6
Method	BLASTX
NCBI GI	g421929
BLAST score	501
E value	1.0e-57
Match length	139
% identity	13
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	149434
Seq. ID	LIB3175-026-P1-K1-F7
Method	BLASTX
NCBI GI	g4741944
BLAST score	661
E value	1.0e-69
Match length	123
% identity	99
NCBI Description	(AF134122) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	149435
Seq. ID	LIB3175-026-P1-K1-F8
Method	BLASTX
NCBI GI	g2565275
BLAST score	675
E value	4.0e-71
Match length	142
% identity	85
NCBI Description	(AF023611) Dim1p homolog [Homo sapiens]

Seq. No.	149436
Seq. ID	LIB3175-026-P1-K1-F9
Method	BLASTN
NCBI GI	g4580745
BLAST score	291
E value	1.0e-163
Match length	337
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	149437
Seq. ID	LIB3175-026-P1-K1-G11
Method	BLASTN
NCBI GI	g1550737
BLAST score	54
E value	1.0e-21
Match length	194
% identity	82
NCBI Description	A.thaliana mRNA for endomembrane-associated protein

Seq. No.	149438
Seq. ID	LIB3175-026-P1-K1-G5
Method	BLASTX
NCBI GI	g1550738
BLAST score	321
E value	8.0e-30
Match length	79
% identity	82
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	149439
Seq. ID	LIB3175-026-P1-K1-G7
Method	BLASTX
NCBI GI	g3510256
BLAST score	177
E value	9.0e-13
Match length	63
% identity	49
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	149440
Seq. ID	LIB3175-026-P1-K1-H1
Method	BLASTX

NCBI GI	g3150402
BLAST score	199
E value	2.0e-27
Match length	98
% identity	71
NCBI Description	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]

Seq. No.	149441
Seq. ID	LIB3175-026-P1-K1-H10
Method	BLASTX
NCBI GI	g4584548
BLAST score	575
E value	1.0e-59
Match length	116
% identity	92
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	149442
Seq. ID	LIB3175-026-P1-K1-H11
Method	BLASTX
NCBI GI	g4371282
BLAST score	224
E value	4.0e-63
Match length	141
% identity	85
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	149443
Seq. ID	LIB3175-026-P1-K1-H12
Method	BLASTX
NCBI GI	g2494130
BLAST score	448
E value	3.0e-52
Match length	110
% identity	96
NCBI Description	(AC002376) Contains similarity to Glycine SRC2 (gb_AB000130). [Arabidopsis thaliana]

Seq. No.	149444
Seq. ID	LIB3175-026-P1-K1-H3
Method	BLASTX
NCBI GI	g4544399
BLAST score	331
E value	8.0e-31
Match length	131
% identity	46
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	149445
Seq. ID	LIB3175-026-P1-K1-H5
Method	BLASTX
NCBI GI	g4185505
BLAST score	268
E value	9.0e-24

Match length	80
% identity	68
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	149446
Seq. ID	LIB3175-026-P1-K1-H8
Method	BLASTX
NCBI GI	g2494113
BLAST score	714
E value	9.0e-76
Match length	128
% identity	100
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	149447
Seq. ID	LIB3175-026-P1-K1-H9
Method	BLASTN
NCBI GI	g4519192
BLAST score	26
E value	7.0e-05
Match length	273
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	149448
Seq. ID	LIB3175-027-P1-K1-A10
Method	BLASTN
NCBI GI	g2828183
BLAST score	258
E value	1.0e-143
Match length	437
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	149449
Seq. ID	LIB3175-027-P1-K1-A11
Method	BLASTX
NCBI GI	g131372
BLAST score	161
E value	3.0e-11
Match length	34
% identity	100
NCBI Description	PHOTOSYSTEM II REACTION CENTRE M PROTEIN >gi_72719_pir__F2RZM photosystem II protein psbM - rice chloroplast >gi_11969_emb_CAA33984_ (X15901) PSII low MW protein [Oryza sativa] >gi_2924261_emb_CAA77413_ (Z00044) PSII M-protein [Nicotiana tabacum] >gi_226687_prf__1603356M photosystem II low MW protein [Oryza sativa]

Seq. No.	149450
Seq. ID	LIB3175-027-P1-K1-A2
Method	BLASTX

NCBI GI	g2226202
BLAST score	146
E value	4.0e-09
Match length	90
% identity	41
NCBI Description	(Y14082) hypothetical protein [Bacillus subtilis] >gi_2633281_emb_CAB12785_ (Z99109) similar to amino acid transporter [Bacillus subtilis]

Seq. No.	149451
Seq. ID	LIB3175-027-P1-K1-A4
Method	BLASTX
NCBI GI	g3914666
BLAST score	319
E value	1.0e-29
Match length	100
% identity	73
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565) ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	149452
Seq. ID	LIB3175-027-P1-K1-A5
Method	BLASTN
NCBI GI	g3985933
BLAST score	204
E value	1.0e-111
Match length	208
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9E15, complete sequence [Arabidopsis thaliana]

Seq. No.	149453
Seq. ID	LIB3175-027-P1-K1-A6
Method	BLASTX
NCBI GI	g4335761
BLAST score	402
E value	3.0e-39
Match length	77
% identity	97
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	149454
Seq. ID	LIB3175-027-P1-K1-A7
Method	BLASTX
NCBI GI	g2129538
BLAST score	715
E value	7.0e-76
Match length	143
% identity	97
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	149455
Seq. ID	LIB3175-027-P1-K1-B10
Method	BLASTN

NCBI GI	g529643
BLAST score	34
E value	3.0e-10
Match length	62
% identity	89
NCBI Description	Pinus thunbergii chloroplast DNA, complete sequence

Seq. No.	149456
Seq. ID	LIB3175-027-P1-K1-B12
Method	BLASTX
NCBI GI	g4325282
BLAST score	406
E value	7.0e-40
Match length	99
% identity	79
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	149457
Seq. ID	LIB3175-027-P1-K1-B3
Method	BLASTX
NCBI GI	g1575130
BLAST score	69
E value	5.0e-09
Match length	55
% identity	57
NCBI Description	(U58209) lumenal binding protein cBiPe3 [Zea mays]

Seq. No.	149458
Seq. ID	LIB3175-027-P1-K1-B4
Method	BLASTX
NCBI GI	g4539327
BLAST score	95
E value	7.0e-16
Match length	70
% identity	66
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	149459
Seq. ID	LIB3175-027-P1-K1-B5
Method	BLASTN
NCBI GI	g2160155
BLAST score	223
E value	1.0e-122
Match length	423
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	149460
Seq. ID	LIB3175-027-P1-K1-B6
Method	BLASTX
NCBI GI	g3337356
BLAST score	226
E value	3.0e-19
Match length	45

% identity	98
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	149461
Seq. ID	LIB3175-027-P1-K1-B7
Method	BLASTX
NCBI GI	g1703108
BLAST score	442
E value	7.0e-44
Match length	104
% identity	85
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	149462
Seq. ID	LIB3175-027-P1-K1-B9
Method	BLASTX
NCBI GI	g4469023
BLAST score	436
E value	4.0e-43
Match length	133
% identity	66
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	149463
Seq. ID	LIB3175-027-P1-K1-C1
Method	BLASTN
NCBI GI	g2264319
BLAST score	45
E value	4.0e-16
Match length	97
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	149464
Seq. ID	LIB3175-027-P1-K1-C11
Method	BLASTN
NCBI GI	g4519192
BLAST score	143
E value	5.0e-75
Match length	151
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	149465
Seq. ID	LIB3175-027-P1-K1-C12
Method	BLASTN
NCBI GI	g3449315
BLAST score	62
E value	1.0e-26
Match length	110

% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	149466
Seq. ID	LIB3175-027-P1-K1-C3
Method	BLASTX
NCBI GI	g3242075
BLAST score	669
E value	2.0e-70
Match length	139
% identity	93
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	149467
Seq. ID	LIB3175-027-P1-K1-C4
Method	BLASTN
NCBI GI	g3046847
BLAST score	101
E value	2.0e-49
Match length	353
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	149468
Seq. ID	LIB3175-027-P1-K1-C5
Method	BLASTX
NCBI GI	g2262167
BLAST score	660
E value	2.0e-69
Match length	127
% identity	99
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	149469
Seq. ID	LIB3175-027-P1-K1-C7
Method	BLASTX
NCBI GI	g4586265
BLAST score	523
E value	2.0e-53
Match length	137
% identity	75
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149470
Seq. ID	LIB3175-027-P1-K1-C8
Method	BLASTX
NCBI GI	g2623962
BLAST score	430
E value	2.0e-42
Match length	90
% identity	92
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	149471
Seq. ID	LIB3175-027-P1-K1-D1
Method	BLASTX
NCBI GI	g1709002
BLAST score	141
E value	5.0e-21
Match length	72
% identity	74
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_1033190 (U38186) S-adenosyl methionine synthetase [Pinus banksiana]

Seq. No.	149472
Seq. ID	LIB3175-027-P1-K1-D11
Method	BLASTX
NCBI GI	g115783
BLAST score	721
E value	1.0e-76
Match length	140
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149473
Seq. ID	LIB3175-027-P1-K1-D2
Method	BLASTN
NCBI GI	g3510337
BLAST score	301
E value	1.0e-169
Match length	454
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	149474
Seq. ID	LIB3175-027-P1-K1-D3
Method	BLASTX
NCBI GI	g1076316
BLAST score	545
E value	5.0e-56
Match length	106
% identity	98
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	149475
Seq. ID	LIB3175-027-P1-K1-D5
Method	BLASTX
NCBI GI	g3738335
BLAST score	333
E value	4.0e-31
Match length	152
% identity	52

NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.	149476
Seq. ID	LIB3175-027-P1-K1-D6
Method	BLASTN
NCBI GI	g4757392
BLAST score	223
E value	1.0e-122
Match length	255
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence
Seq. No.	149477
Seq. ID	LIB3175-027-P1-K1-D7
Method	BLASTX
NCBI GI	g2052383
BLAST score	654
E value	3.0e-69
Match length	140
% identity	93
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]
Seq. No.	149478
Seq. ID	LIB3175-027-P1-K1-D8
Method	BLASTX
NCBI GI	g112739
BLAST score	408
E value	6.0e-40
Match length	119
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	149479
Seq. ID	LIB3175-027-P1-K1-D9
Method	BLASTX
NCBI GI	g1911774
BLAST score	173
E value	2.0e-12
Match length	71
% identity	39
NCBI Description	(S83364) putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]
Seq. No.	149480
Seq. ID	LIB3175-027-P1-K1-E10
Method	BLASTX
NCBI GI	g4741960
BLAST score	763
E value	1.0e-81
Match length	140

% identity	99
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	149481
Seq. ID	LIB3175-027-P1-K1-E11
Method	BLASTX
NCBI GI	g3063465
BLAST score	473
E value	1.0e-47
Match length	95
% identity	99
NCBI Description	(AC003981) F22O13.27 [Arabidopsis thaliana]

Seq. No.	149482
Seq. ID	LIB3175-027-P1-K1-E2
Method	BLASTX
NCBI GI	g3319457
BLAST score	163
E value	3.0e-11
Match length	98
% identity	39
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	149483
Seq. ID	LIB3175-027-P1-K1-E3
Method	BLASTN
NCBI GI	g3355463
BLAST score	200
E value	1.0e-108
Match length	284
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149484
Seq. ID	LIB3175-027-P1-K1-E4
Method	BLASTN
NCBI GI	g3242700
BLAST score	39
E value	1.0e-12
Match length	153
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149485
Seq. ID	LIB3175-027-P1-K1-E5
Method	BLASTX
NCBI GI	g4406814
BLAST score	493
E value	8.0e-50
Match length	98
% identity	100
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	149486
Seq. ID	LIB3175-027-P1-K1-E6
Method	BLASTX
NCBI GI	g2829275
BLAST score	323
E value	4.0e-30
Match length	60
% identity	100
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	149487
Seq. ID	LIB3175-027-P1-K1-E7
Method	BLASTX
NCBI GI	g1705677
BLAST score	674
E value	4.0e-76
Match length	148
% identity	66
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	149488
Seq. ID	LIB3175-027-P1-K1-E9
Method	BLASTN
NCBI GI	g3668174
BLAST score	42
E value	2.0e-14
Match length	50
% identity	96
NCBI Description	Arabidopsis thaliana Vsp2 gene for vegetative storage protein, complete cds

Seq. No.	149489
Seq. ID	LIB3175-027-P1-K1-F1
Method	BLASTX
NCBI GI	g1657855
BLAST score	174
E value	1.0e-12
Match length	77
% identity	45
NCBI Description	(U73216) cold acclimation protein WCOR413 [Triticum aestivum]

Seq. No.	149490
Seq. ID	LIB3175-027-P1-K1-F10
Method	BLASTX
NCBI GI	g899608
BLAST score	641
E value	3.0e-67
Match length	130

% identity	22
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	149491
Seq. ID	LIB3175-027-P1-K1-F11
Method	BLASTN
NCBI GI	g3643588
BLAST score	283
E value	1.0e-158
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149492
Seq. ID	LIB3175-027-P1-K1-F12
Method	BLASTX
NCBI GI	g1644388
BLAST score	328
E value	2.0e-30
Match length	145
% identity	41
NCBI Description	(U72654) flavonoid 3'5'-hydroxylase [Eustoma grandiflorum]

Seq. No.	149493
Seq. ID	LIB3175-027-P1-K1-F3
Method	BLASTN
NCBI GI	g3985949
BLAST score	105
E value	2.0e-52
Match length	141
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	149494
Seq. ID	LIB3175-027-P1-K1-F4
Method	BLASTX
NCBI GI	g3786017
BLAST score	507
E value	2.0e-51
Match length	104
% identity	95
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	149495
Seq. ID	LIB3175-027-P1-K1-F6
Method	BLASTN
NCBI GI	g2623294
BLAST score	66
E value	1.0e-28
Match length	157
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149496
Seq. ID	LIB3175-027-P1-K1-F7
Method	BLASTN
NCBI GI	g4757395
BLAST score	185
E value	1.0e-99
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	149497
Seq. ID	LIB3175-027-P1-K1-F8
Method	BLASTX
NCBI GI	g135406
BLAST score	626
E value	2.0e-65
Match length	118
% identity	99
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	149498
Seq. ID	LIB3175-027-P1-K1-G10
Method	BLASTN
NCBI GI	g2828185
BLAST score	324
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	149499
Seq. ID	LIB3175-027-P1-K1-G12
Method	BLASTX
NCBI GI	g4158221
BLAST score	133
E value	4.0e-61
Match length	139
% identity	85
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	149500
Seq. ID	LIB3175-027-P1-K1-G2
Method	BLASTX
NCBI GI	g131398
BLAST score	471
E value	2.0e-47
Match length	113
% identity	84
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]

>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	149501
Seq. ID	LIB3175-027-P1-K1-G4
Method	BLASTN
NCBI GI	g4469002
BLAST score	304
E value	1.0e-170
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	149502
Seq. ID	LIB3175-027-P1-K1-G5
Method	BLASTX
NCBI GI	g4589398
BLAST score	438
E value	2.0e-43
Match length	105
% identity	74
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	149503
Seq. ID	LIB3175-027-P1-K1-G6
Method	BLASTX
NCBI GI	g3024697
BLAST score	569
E value	9.0e-59
Match length	115
% identity	100
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	149504
Seq. ID	LIB3175-027-P1-K1-G7
Method	BLASTX
NCBI GI	g3983125
BLAST score	624
E value	3.0e-65
Match length	145
% identity	83
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	149505
Seq. ID	LIB3175-027-P1-K1-G8
Method	BLASTN
NCBI GI	g2584827
BLAST score	180
E value	1.0e-96
Match length	329

% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149506
Seq. ID	LIB3175-027-P1-K1-G9
Method	BLASTX
NCBI GI	g2811226
BLAST score	460
E value	5.0e-46
Match length	91
% identity	99
NCBI Description	(AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No.	149507
Seq. ID	LIB3175-027-P1-K1-H10
Method	BLASTX
NCBI GI	g2645971
BLAST score	470
E value	3.0e-47
Match length	100
% identity	84
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	149508
Seq. ID	LIB3175-027-P1-K1-H2
Method	BLASTX
NCBI GI	g4586265
BLAST score	254
E value	2.0e-49
Match length	130
% identity	76
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149509
Seq. ID	LIB3175-027-P1-K1-H3
Method	BLASTN
NCBI GI	g4220636
BLAST score	35
E value	2.0e-10
Match length	123
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	149510
Seq. ID	LIB3175-027-P1-K1-H4
Method	BLASTX
NCBI GI	g1172872
BLAST score	594
E value	1.0e-61
Match length	114
% identity	98
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A

precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	149511
Seq. ID	LIB3175-027-P1-K1-H5
Method	BLASTX
NCBI GI	g4335719
BLAST score	638
E value	5.0e-67
Match length	118
% identity	100
NCBI Description	(AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana]

Seq. No.	149512
Seq. ID	LIB3175-027-P1-K1-H7
Method	BLASTX
NCBI GI	g4741952
BLAST score	700
E value	4.0e-74
Match length	130
% identity	76
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	149513
Seq. ID	LIB3175-028-P1-K1-A1
Method	BLASTX
NCBI GI	g421929
BLAST score	413
E value	1.0e-40
Match length	86
% identity	14
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	149514
Seq. ID	LIB3175-028-P1-K1-A10
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	149515
Seq. ID	LIB3175-028-P1-K1-A11
Method	BLASTX
NCBI GI	g417103
BLAST score	226
E value	7.0e-19
Match length	68
% identity	69
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	149516
Seq. ID	LIB3175-028-P1-K1-A2
Method	BLASTX
NCBI GI	g3786005
BLAST score	504
E value	3.0e-51
Match length	106
% identity	93
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	149517
Seq. ID	LIB3175-028-P1-K1-A3
Method	BLASTX
NCBI GI	g1209756
BLAST score	449
E value	8.0e-45
Match length	126
% identity	71
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	149518
Seq. ID	LIB3175-028-P1-K1-A8
Method	BLASTN
NCBI GI	g3868723
BLAST score	271
E value	1.0e-151
Match length	330
% identity	96
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	149519
Seq. ID	LIB3175-028-P1-K1-A9
Method	BLASTX
NCBI GI	g4741952
BLAST score	514
E value	2.0e-52

Match length	95
% identity	70
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	149520
Seq. ID	LIB3175-028-P1-K1-B1
Method	BLASTX
NCBI GI	g2435522
BLAST score	503
E value	4.0e-51
Match length	126
% identity	71
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	149521
Seq. ID	LIB3175-028-P1-K1-B10
Method	BLASTN
NCBI GI	g4309719
BLAST score	202
E value	1.0e-110
Match length	266
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149522
Seq. ID	LIB3175-028-P1-K1-B11
Method	BLASTX
NCBI GI	g3915826
BLAST score	502
E value	5.0e-51
Match length	119
% identity	80
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	149523
Seq. ID	LIB3175-028-P1-K1-B2
Method	BLASTX
NCBI GI	g231586
BLAST score	223
E value	3.0e-18
Match length	100
% identity	54
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	149524
Seq. ID	LIB3175-028-P1-K1-B5
Method	BLASTX
NCBI GI	g464621
BLAST score	217
E value	9.0e-18
Match length	94

% identity	49
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
Seq. No.	149525
Seq. ID	LIB3175-028-P1-K1-B6
Method	BLASTX
NCBI GI	g1363489
BLAST score	841
E value	1.0e-90
Match length	154
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]
Seq. No.	149526
Seq. ID	LIB3175-028-P1-K1-B7
Method	BLASTX
NCBI GI	g2132124
BLAST score	279
E value	8.0e-25
Match length	102
% identity	54
NCBI Description	hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae) >gi_1420671_emb_CAA99622_ (Z75212) ORF YOR304w [Saccharomyces cerevisiae]
Seq. No.	149527
Seq. ID	LIB3175-028-P1-K1-B8
Method	BLASTX
NCBI GI	g1619300
BLAST score	309
E value	2.0e-28
Match length	66
% identity	85
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]
Seq. No.	149528
Seq. ID	LIB3175-028-P1-K1-C1
Method	BLASTX
NCBI GI	g119350
BLAST score	579
E value	5.0e-60
Match length	112
% identity	99
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	149529
Seq. ID	LIB3175-028-P1-K1-C11
Method	BLASTN
NCBI GI	g2351069
BLAST score	172
E value	7.0e-92
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	149530
Seq. ID	LIB3175-028-P1-K1-C12
Method	BLASTN
NCBI GI	g3643588
BLAST score	207
E value	1.0e-113
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149531
Seq. ID	LIB3175-028-P1-K1-C2
Method	BLASTX
NCBI GI	g3033384
BLAST score	108
E value	3.0e-42
Match length	141
% identity	63
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	149532
Seq. ID	LIB3175-028-P1-K1-C3
Method	BLASTX
NCBI GI	g1888557
BLAST score	331
E value	8.0e-31
Match length	81
% identity	74
NCBI Description	(U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase [Lupinus angustifolius]

Seq. No.	149533
Seq. ID	LIB3175-028-P1-K1-C5
Method	BLASTX
NCBI GI	g345829
BLAST score	315
E value	6.0e-29
Match length	96
% identity	64
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	149534
Seq. ID	LIB3175-028-P1-K1-C6
Method	BLASTX
NCBI GI	g2191132

BLAST score	453
E value	4.0e-45
Match length	140
% identity	74
NCBI Description	(AF007269) contains weak similarity to nebulin [Arabidopsis thaliana]

Seq. No.	149535
Seq. ID	LIB3175-028-P1-K1-C7
Method	BLASTX
NCBI GI	g3450842
BLAST score	284
E value	3.0e-27
Match length	112
% identity	61
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	149536
Seq. ID	LIB3175-028-P1-K1-C8
Method	BLASTX
NCBI GI	g2191184
BLAST score	630
E value	6.0e-66
Match length	142
% identity	90
NCBI Description	(AF007271) Similar to sodium/hydrogen exchanger; coded for by A. thaliana cDNA T75860 [Arabidopsis thaliana]

Seq. No.	149537
Seq. ID	LIB3175-028-P1-K1-C9
Method	BLASTX
NCBI GI	g2369714
BLAST score	402
E value	2.0e-39
Match length	85
% identity	95
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	149538
Seq. ID	LIB3175-028-P1-K1-D1
Method	BLASTX
NCBI GI	g2062161
BLAST score	64
E value	2.0e-55
Match length	126
% identity	60
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	149539
Seq. ID	LIB3175-028-P1-K1-D10
Method	BLASTX
NCBI GI	g2244750
BLAST score	718
E value	3.0e-76
Match length	147

% identity	90
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	149540
Seq. ID	LIB3175-028-P1-K1-D11
Method	BLASTN
NCBI GI	g4220510
BLAST score	259
E value	1.0e-144
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	149541
Seq. ID	LIB3175-028-P1-K1-D12
Method	BLASTN
NCBI GI	g2351062
BLAST score	197
E value	1.0e-107
Match length	329
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	149542
Seq. ID	LIB3175-028-P1-K1-D6
Method	BLASTN
NCBI GI	g2281648
BLAST score	234
E value	1.0e-129
Match length	238
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	149543
Seq. ID	LIB3175-028-P1-K1-D7
Method	BLASTX
NCBI GI	g3158376
BLAST score	405
E value	1.0e-39
Match length	120
% identity	68
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	149544
Seq. ID	LIB3175-028-P1-K1-E1
Method	BLASTX
NCBI GI	g4467099
BLAST score	603
E value	7.0e-63
Match length	118
% identity	99
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein

[Arabidopsis thaliana]

Seq. No.	149545
Seq. ID	LIB3175-028-P1-K1-E10
Method	BLASTX
NCBI GI	g1710151
BLAST score	702
E value	2.0e-74
Match length	135
% identity	98
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No.	149546
Seq. ID	LIB3175-028-P1-K1-E12
Method	BLASTN
NCBI GI	g2435510
BLAST score	217
E value	1.0e-118
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	149547
Seq. ID	LIB3175-028-P1-K1-E2
Method	BLASTN
NCBI GI	g3449329
BLAST score	262
E value	1.0e-145
Match length	379
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	149548
Seq. ID	LIB3175-028-P1-K1-E3
Method	BLASTN
NCBI GI	g3176701
BLAST score	181
E value	2.0e-97
Match length	235
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149549
Seq. ID	LIB3175-028-P1-K1-E4
Method	BLASTN
NCBI GI	g4741939
BLAST score	167
E value	4.0e-89
Match length	239
% identity	93
NCBI Description	Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds

Seq. No.	149550
Seq. ID	LIB3175-028-P1-K1-E5

Method	BLASTX
NCBI GI	g4741940
BLAST score	593
E value	1.0e-61
Match length	108
% identity	67
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	149551
Seq. ID	LIB3175-028-P1-K1-E6
Method	BLASTX
NCBI GI	g99698
BLAST score	667
E value	3.0e-70
Match length	150
% identity	85
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgskb6) - Arabidopsis thaliana

Seq. No.	149552
Seq. ID	LIB3175-028-P1-K1-E7
Method	BLASTX
NCBI GI	g4539408
BLAST score	145
E value	1.0e-10
Match length	65
% identity	63
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	149553
Seq. ID	LIB3175-028-P1-K1-E9
Method	BLASTX
NCBI GI	g3024697
BLAST score	379
E value	1.0e-36
Match length	76
% identity	100
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	149554
Seq. ID	LIB3175-028-P1-K1-F10
Method	BLASTX
NCBI GI	g1518540
BLAST score	368
E value	2.0e-44
Match length	107
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	149555
Seq. ID	LIB3175-028-P1-K1-F12
Method	BLASTX
NCBI GI	g4741940
BLAST score	311
E value	7.0e-29

Match length	57
% identity	100
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	149556
Seq. ID	LIB3175-028-P1-K1-F2
Method	BLASTX
NCBI GI	g2894574
BLAST score	679
E value	9.0e-72
Match length	127
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	149557
Seq. ID	LIB3175-028-P1-K1-F3
Method	BLASTN
NCBI GI	g2842474
BLAST score	39
E value	5.0e-13
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	149558
Seq. ID	LIB3175-028-P1-K1-F4
Method	BLASTX
NCBI GI	g3929649
BLAST score	138
E value	7.0e-09
Match length	40
% identity	68
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	149559
Seq. ID	LIB3175-028-P1-K1-F6
Method	BLASTX
NCBI GI	g2317729
BLAST score	744
E value	3.0e-79
Match length	141
% identity	98
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	149560
Seq. ID	LIB3175-028-P1-K1-F7
Method	BLASTX
NCBI GI	g2317729
BLAST score	266
E value	6.0e-42
Match length	98
% identity	90

NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	149561
Seq. ID	LIB3175-028-P1-K1-F8
Method	BLASTX
NCBI GI	g1170503
BLAST score	506
E value	1.0e-51
Match length	100
% identity	99
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	149562
Seq. ID	LIB3175-028-P1-K1-F9
Method	BLASTX
NCBI GI	g3914442
BLAST score	443
E value	4.0e-44
Match length	126
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi_1916350 (U92504) PSI-H subunit [Brassica rapa]

Seq. No.	149563
Seq. ID	LIB3175-028-P1-K1-G1
Method	BLASTN
NCBI GI	g1490552
BLAST score	126
E value	1.0e-64
Match length	134
% identity	99
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	149564
Seq. ID	LIB3175-028-P1-K1-G10
Method	BLASTN
NCBI GI	g16316
BLAST score	216
E value	1.0e-118
Match length	272
% identity	99
NCBI Description	A.thaliana gene for histone H1-1

Seq. No.	149565
Seq. ID	LIB3175-028-P1-K1-G11
Method	BLASTX
NCBI GI	g2960364
BLAST score	442
E value	5.0e-44
Match length	106

% identity	76
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	149566
Seq. ID	LIB3175-028-P1-K1-G2
Method	BLASTN
NCBI GI	g1209241
BLAST score	64
E value	5.0e-28
Match length	108
% identity	90
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	149567
Seq. ID	LIB3175-028-P1-K1-G4
Method	BLASTN
NCBI GI	g2459406
BLAST score	139
E value	2.0e-72
Match length	271
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149568
Seq. ID	LIB3175-028-P1-K1-G5
Method	BLASTX
NCBI GI	g416681
BLAST score	239
E value	5.0e-20
Match length	109
% identity	41
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	149569
Seq. ID	LIB3175-028-P1-K1-G6
Method	BLASTX
NCBI GI	g1061040
BLAST score	569
E value	7.0e-59
Match length	108
% identity	98
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	149570
Seq. ID	LIB3175-028-P1-K1-G8
Method	BLASTX
NCBI GI	g4388726
BLAST score	727
E value	3.0e-77

Match length	145
% identity	98
NCBI Description	(AC006413) putative 12-oxophytodienoate-10,11-reductase [Arabidopsis thaliana]

Seq. No.	149571
Seq. ID	LIB3175-028-P1-K1-H10
Method	BLASTX
NCBI GI	g266731
BLAST score	157
E value	5.0e-42
Match length	130
% identity	74
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	149572
Seq. ID	LIB3175-028-P1-K1-H11
Method	BLASTN
NCBI GI	g1402874
BLAST score	325
E value	0.0e+00
Match length	376
% identity	99
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	149573
Seq. ID	LIB3175-028-P1-K1-H3
Method	BLASTX
NCBI GI	g832876
BLAST score	277
E value	6.0e-25
Match length	59
% identity	86
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	149574
Seq. ID	LIB3175-028-P1-K1-H4
Method	BLASTN
NCBI GI	g3068806
BLAST score	146
E value	8.0e-77
Match length	158
% identity	98
NCBI Description	Arabidopsis thaliana Skp1 homolog (SKP1a) mRNA, complete cds

Seq. No.	149575
Seq. ID	LIB3175-028-P1-K1-H7
Method	BLASTN
NCBI GI	g4468103
BLAST score	339

E value	0.0e+00
Match length	351
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	149576
Seq. ID	LIB3175-028-P1-K1-H8
Method	BLASTN
NCBI GI	g3228389
BLAST score	189
E value	1.0e-102
Match length	460
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	149577
Seq. ID	LIB3175-028-P1-K1-H9
Method	BLASTX
NCBI GI	g2129769
BLAST score	182
E value	2.0e-13
Match length	98
% identity	52
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	149578
Seq. ID	LIB3175-029-P1-K1-A1
Method	BLASTX
NCBI GI	g4090884
BLAST score	527
E value	6.0e-54
Match length	104
% identity	97
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	149579
Seq. ID	LIB3175-029-P1-K1-A10
Method	BLASTX
NCBI GI	g4337175
BLAST score	290
E value	2.0e-47
Match length	127
% identity	77
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	149580
Seq. ID	LIB3175-029-P1-K1-A11
Method	BLASTN
NCBI GI	g4206766

BLAST score	235
E value	1.0e-129
Match length	267
% identity	97
NCBI Description	Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S) mRNA, complete cds

Seq. No.	149581
Seq. ID	LIB3175-029-P1-K1-A2
Method	BLASTX
NCBI GI	g1669387
BLAST score	513
E value	3.0e-52
Match length	95
% identity	99
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	149582
Seq. ID	LIB3175-029-P1-K1-A3
Method	BLASTX
NCBI GI	g99688
BLAST score	666
E value	3.0e-70
Match length	130
% identity	99
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	149583
Seq. ID	LIB3175-029-P1-K1-A5
Method	BLASTX
NCBI GI	g2497753
BLAST score	263
E value	7.0e-23
Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	149584
Seq. ID	LIB3175-029-P1-K1-A6
Method	BLASTX
NCBI GI	g2688824
BLAST score	283
E value	4.0e-25
Match length	130
% identity	52
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	149585
Seq. ID	LIB3175-029-P1-K1-A7
Method	BLASTN
NCBI GI	g4519183
BLAST score	397

E value	0.0e+00
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	149586
Seq. ID	LIB3175-029-P1-K1-A8
Method	BLASTX
NCBI GI	g1086263
BLAST score	313
E value	8.0e-29
Match length	126
% identity	52
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	149587
Seq. ID	LIB3175-029-P1-K1-A9
Method	BLASTN
NCBI GI	g3766106
BLAST score	156
E value	3.0e-82
Match length	423
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149588
Seq. ID	LIB3175-029-P1-K1-B1
Method	BLASTN
NCBI GI	g3449331
BLAST score	63
E value	3.0e-27
Match length	143
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	149589
Seq. ID	LIB3175-029-P1-K1-B10
Method	BLASTX
NCBI GI	g115783
BLAST score	697
E value	9.0e-74
Match length	138
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149590
Seq. ID	LIB3175-029-P1-K1-B11
Method	BLASTX
NCBI GI	g2497753
BLAST score	276

E value	2.0e-24
Match length	110
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	149591
Seq. ID	LIB3175-029-P1-K1-B12
Method	BLASTN
NCBI GI	g3766106
BLAST score	170
E value	9.0e-91
Match length	292
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149592
Seq. ID	LIB3175-029-P1-K1-B2
Method	BLASTX
NCBI GI	g119143
BLAST score	714
E value	1.0e-75
Match length	138
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	149593
Seq. ID	LIB3175-029-P1-K1-B3
Method	BLASTX
NCBI GI	g1486472
BLAST score	578
E value	8.0e-60
Match length	128
% identity	88
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	149594
Seq. ID	LIB3175-029-P1-K1-B4
Method	BLASTN
NCBI GI	g4469002
BLAST score	339
E value	0.0e+00
Match length	413
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No.	149595
Seq. ID	LIB3175-029-P1-K1-B6
Method	BLASTX
NCBI GI	g3122622
BLAST score	215
E value	2.0e-31
Match length	111
% identity	63
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) >gi_2267237 (U70473) PEP carboxykinase [Candida albicans]

Seq. No.	149596
Seq. ID	LIB3175-029-P1-K1-B7
Method	BLASTX
NCBI GI	g267136
BLAST score	287
E value	5.0e-26
Match length	96
% identity	67
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN) (WSI-TIP) >gi_217869_dbj_BAA02520_ (D13254) transmembrane channel protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141_ (AC006260) putative plasma membrane intrinsic protein 2C [Arabidopsis thaliana] >gi_384324_prf__1905411A transmembrane channel [Arabidopsis thaliana]

Seq. No.	149597
Seq. ID	LIB3175-029-P1-K1-B8
Method	BLASTN
NCBI GI	g2584827
BLAST score	219
E value	1.0e-120
Match length	238
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149598
Seq. ID	LIB3175-029-P1-K1-B9
Method	BLASTX
NCBI GI	g3482924
BLAST score	326
E value	3.0e-30
Match length	119
% identity	55
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	149599
Seq. ID	LIB3175-029-P1-K1-C1
Method	BLASTN
NCBI GI	g4467094
BLAST score	159
E value	3.0e-84

Match length	268
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	149600
Seq. ID	LIB3175-029-P1-K1-C10
Method	BLASTN
NCBI GI	g2244991
BLAST score	445
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	149601
Seq. ID	LIB3175-029-P1-K1-C11
Method	BLASTX
NCBI GI	g120667
BLAST score	477
E value	5.0e-48
Match length	107
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	149602
Seq. ID	LIB3175-029-P1-K1-C12
Method	BLASTX
NCBI GI	g4507703
BLAST score	202
E value	1.0e-15
Match length	148
% identity	34
NCBI Description	tumor suppressing subtransferable candidate 1 >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]

Seq. No.	149603
Seq. ID	LIB3175-029-P1-K1-C2
Method	BLASTX
NCBI GI	g2961390
BLAST score	647
E value	9.0e-73
Match length	134
% identity	100
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	149604
Seq. ID	LIB3175-029-P1-K1-C3

Method	BLASTN
NCBI GI	g2264304
BLAST score	217
E value	1.0e-118
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	149605
Seq. ID	LIB3175-029-P1-K1-C6
Method	BLASTX
NCBI GI	g4455253
BLAST score	506
E value	2.0e-60
Match length	139
% identity	86
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	149606
Seq. ID	LIB3175-029-P1-K1-C7
Method	BLASTX
NCBI GI	g1402876
BLAST score	767
E value	6.0e-82
Match length	159
% identity	97
NCBI Description	(X98130) putative phosphate permease [Arabidopsis thaliana] >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis thaliana]

Seq. No.	149607
Seq. ID	LIB3175-029-P1-K1-C8
Method	BLASTX
NCBI GI	g1170601
BLAST score	313
E value	1.0e-28
Match length	151
% identity	41
NCBI Description	FRUIT PROTEIN PKIWI502 >gi_1085869_pir__S48036 hypothetical protein - kiwi fruit >gi_450237 (L27809) pKIWI502 [Actinidia deliciosa]

Seq. No.	149608
Seq. ID	LIB3175-029-P1-K1-C9
Method	BLASTN
NCBI GI	g3849811
BLAST score	431
E value	0.0e+00
Match length	439
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149609
Seq. ID	LIB3175-029-P1-K1-D1

Method	BLASTX
NCBI GI	g1345595
BLAST score	653
E value	1.0e-68
Match length	135
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	149610
Seq. ID	LIB3175-029-P1-K1-D10
Method	BLASTX
NCBI GI	g2924512
BLAST score	61
E value	1.0e-43
Match length	133
% identity	56
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	149611
Seq. ID	LIB3175-029-P1-K1-D11
Method	BLASTX
NCBI GI	g4567207
BLAST score	812
E value	3.0e-87
Match length	155
% identity	98
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	149612
Seq. ID	LIB3175-029-P1-K1-D12
Method	BLASTX
NCBI GI	g2342727
BLAST score	540
E value	2.0e-55
Match length	134
% identity	77
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149613
Seq. ID	LIB3175-029-P1-K1-D2
Method	BLASTX
NCBI GI	g4585882
BLAST score	740
E value	9.0e-79
Match length	141
% identity	99
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	149614
Seq. ID	LIB3175-029-P1-K1-D3
Method	BLASTX

NCBI GI	g132110
BLAST score	680
E value	9.0e-72
Match length	129
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	149615
Seq. ID	LIB3175-029-P1-K1-D4
Method	BLASTX
NCBI GI	g2218152
BLAST score	778
E value	3.0e-83
Match length	150
% identity	92
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	149616
Seq. ID	LIB3175-029-P1-K1-D5
Method	BLASTX
NCBI GI	g1203832
BLAST score	128
E value	8.0e-15
Match length	92
% identity	46
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No.	149617
Seq. ID	LIB3175-029-P1-K1-D7
Method	BLASTX
NCBI GI	g3169028
BLAST score	205
E value	5.0e-16
Match length	81
% identity	47
NCBI Description	(AL023702) putative cationic amino acid transporter [Streptomyces coelicolor]

Seq. No.	149618
Seq. ID	LIB3175-029-P1-K1-D8
Method	BLASTX
NCBI GI	g1171993
BLAST score	687
E value	1.0e-72
Match length	143
% identity	95
NCBI Description	PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__S52991 phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497421 (L33678) phenylalanine ammonia lyase

[Arabidopsis thaliana]

Seq. No.	149619
Seq. ID	LIB3175-029-P1-K1-D9
Method	BLASTX
NCBI GI	g4490329
BLAST score	441
E value	8.0e-44
Match length	106
% identity	80
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	149620
Seq. ID	LIB3175-029-P1-K1-E1
Method	BLASTX
NCBI GI	g2129727
BLAST score	167
E value	1.0e-11
Match length	72
% identity	56
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	149621
Seq. ID	LIB3175-029-P1-K1-E11
Method	BLASTX
NCBI GI	g1174847
BLAST score	823
E value	2.0e-88
Match length	158
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 1 (UBIQUITIN-PROTEIN LIGASE 4) (UBIQUITIN CARRIER PROTEIN 4) >gi_431266 (L19354) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	149622
Seq. ID	LIB3175-029-P1-K1-E12
Method	BLASTX
NCBI GI	g115783
BLAST score	470
E value	1.0e-74
Match length	149
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149623
Seq. ID	LIB3175-029-P1-K1-E2
Method	BLASTX
NCBI GI	g135467
BLAST score	142
E value	7.0e-81
Match length	154
% identity	95
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4

- Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	149624
Seq. ID	LIB3175-029-P1-K1-E3
Method	BLASTN
NCBI GI	g4159708
BLAST score	216
E value	1.0e-118
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	149625
Seq. ID	LIB3175-029-P1-K1-E4
Method	BLASTX
NCBI GI	g2129659
BLAST score	332
E value	5.0e-31
Match length	121
% identity	62
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	149626
Seq. ID	LIB3175-029-P1-K1-E5
Method	BLASTX
NCBI GI	g4566505
BLAST score	520
E value	6.0e-53
Match length	150
% identity	65
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	149627
Seq. ID	LIB3175-029-P1-K1-E6
Method	BLASTX
NCBI GI	g399013
BLAST score	556
E value	3.0e-57
Match length	111
% identity	99
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	149628
Seq. ID	LIB3175-029-P1-K1-E8
Method	BLASTX
NCBI GI	g625977
BLAST score	436

E value	2.0e-43
Match length	86
% identity	99
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	149629
Seq. ID	LIB3175-029-P1-K1-E9
Method	BLASTX
NCBI GI	g3785981
BLAST score	499
E value	1.0e-50
Match length	127
% identity	72
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	149630
Seq. ID	LIB3175-029-P1-K1-F1
Method	BLASTX
NCBI GI	g2062161
BLAST score	689
E value	8.0e-73
Match length	134
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	149631
Seq. ID	LIB3175-029-P1-K1-F10
Method	BLASTX
NCBI GI	g4585882
BLAST score	531
E value	3.0e-54
Match length	125
% identity	84
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	149632
Seq. ID	LIB3175-029-P1-K1-F11
Method	BLASTN
NCBI GI	g4582428
BLAST score	165
E value	1.0e-87
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	149633
Seq. ID	LIB3175-029-P1-K1-F12
Method	BLASTN
NCBI GI	g3212846
BLAST score	374
E value	0.0e+00

Match length	411
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149634
Seq. ID	LIB3175-029-P1-K1-F2
Method	BLASTN
NCBI GI	g4432847
BLAST score	41
E value	1.0e-14
Match length	73
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149635
Seq. ID	LIB3175-029-P1-K1-F3
Method	BLASTX
NCBI GI	g1706551
BLAST score	233
E value	2.0e-19
Match length	97
% identity	46
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	149636
Seq. ID	LIB3175-029-P1-K1-F4
Method	BLASTN
NCBI GI	g4582411
BLAST score	403
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	149637
Seq. ID	LIB3175-029-P1-K1-F5
Method	BLASTX
NCBI GI	g2982262
BLAST score	42
E value	4.0e-32
Match length	156
% identity	48
NCBI Description	(AF051214) probable glutathione S-transferase [Picea mariana]

Seq. No.	149638
Seq. ID	LIB3175-029-P1-K1-F7
Method	BLASTX
NCBI GI	g2244825
BLAST score	412
E value	2.0e-40

Match length	124
% identity	72
NCBI Description	(Z97336) light induced protein homolog [Arabidopsis thaliana]

Seq. No.	149639
Seq. ID	LIB3175-029-P1-K1-F8
Method	BLASTX
NCBI GI	g3212116
BLAST score	200
E value	2.0e-15
Match length	123
% identity	36
NCBI Description	(Y17393) prefoldin subunit 2 [Mus musculus]

Seq. No.	149640
Seq. ID	LIB3175-029-P1-K1-F9
Method	BLASTX
NCBI GI	g2129549
BLAST score	454
E value	3.0e-45
Match length	84
% identity	100
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 - Arabidopsis thaliana >gi_2129551_pir__S71778 calcium-dependent protein kinase 19 - Arabidopsis thaliana >gi_836942 (U20624) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836948 (U20627) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	149641
Seq. ID	LIB3175-029-P1-K1-G1
Method	BLASTX
NCBI GI	g3183568
BLAST score	245
E value	1.0e-20
Match length	130
% identity	42
NCBI Description	HYPOTHETICAL 45.1 KD PROTEIN IN CDD-MGLC INTERGENIC REGION

Seq. No.	149642
Seq. ID	LIB3175-029-P1-K1-G10
Method	BLASTX
NCBI GI	g4503363
BLAST score	534
E value	1.0e-54
Match length	159
% identity	59
NCBI Description	dolichyl-phosphate mannosyltransferase polypeptide 1 >gi_3062806_dbj_BAA25646_ (D86198) dolichol-phosphate-mannose synthase [Homo sapiens]

Seq. No.	149643
Seq. ID	LIB3175-029-P1-K1-G11
Method	BLASTX
NCBI GI	g2369714
BLAST score	660

E value	2.0e-69
Match length	156
% identity	81
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	149644
Seq. ID	LIB3175-029-P1-K1-G12
Method	BLASTX
NCBI GI	g266336
BLAST score	247
E value	5.0e-21
Match length	129
% identity	36
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-I (EIF-4A-I) >gi_109295_pir__S13269 initiation factor eIF-4A - rabbit

Seq. No.	149645
Seq. ID	LIB3175-029-P1-K1-G2
Method	BLASTX
NCBI GI	g3859659
BLAST score	380
E value	4.0e-37
Match length	131
% identity	72
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]

Seq. No.	149646
Seq. ID	LIB3175-029-P1-K1-G3
Method	BLASTX
NCBI GI	g529353
BLAST score	316
E value	3.0e-29
Match length	90
% identity	59
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	149647
Seq. ID	LIB3175-029-P1-K1-G6
Method	BLASTX
NCBI GI	g115385
BLAST score	727
E value	3.0e-77
Match length	139
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149648
Seq. ID	LIB3175-029-P1-K1-G7
Method	BLASTX
NCBI GI	g3861153
BLAST score	291
E value	4.0e-26
Match length	98
% identity	55

NCBI Description	(AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT) [Rickettsia prowazekii]
Seq. No.	149649
Seq. ID	LIB3175-029-P1-K1-G8
Method	BLASTN
NCBI GI	g4757415
BLAST score	426
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence
Seq. No.	149650
Seq. ID	LIB3175-029-P1-K1-G9
Method	BLASTX
NCBI GI	g1170606
BLAST score	356
E value	9.0e-34
Match length	88
% identity	78
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)
Seq. No.	149651
Seq. ID	LIB3175-029-P1-K1-H1
Method	BLASTN
NCBI GI	g3068702
BLAST score	67
E value	3.0e-29
Match length	95
% identity	93
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put
Seq. No.	149652
Seq. ID	LIB3175-029-P1-K1-H10
Method	BLASTX
NCBI GI	g4468802
BLAST score	766
E value	8.0e-82
Match length	153
% identity	99
NCBI Description	(AL035601) cytochrome p450-like protein [Arabidopsis thaliana]
Seq. No.	149653
Seq. ID	LIB3175-029-P1-K1-H12

Method	BLASTX
NCBI GI	g2119846
BLAST score	660
E value	2.0e-69
Match length	127
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149654
Seq. ID	LIB3175-029-P1-K1-H2
Method	BLASTX
NCBI GI	g3044218
BLAST score	418
E value	5.0e-41
Match length	110
% identity	75
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	149655
Seq. ID	LIB3175-029-P1-K1-H3
Method	BLASTX
NCBI GI	g4218123
BLAST score	176
E value	2.0e-29
Match length	129
% identity	60
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	149656
Seq. ID	LIB3175-029-P1-K1-H4
Method	BLASTN
NCBI GI	g3241925
BLAST score	199
E value	1.0e-108
Match length	478
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	149657
Seq. ID	LIB3175-029-P1-K1-H5
Method	BLASTX
NCBI GI	g1708313
BLAST score	548
E value	3.0e-56
Match length	113
% identity	99
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

thaliana]

Seq. No.	149658
Seq. ID	LIB3175-029-P1-K1-H6
Method	BLASTN
NCBI GI	g3869072
BLAST score	136
E value	1.0e-70
Match length	196
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	149659
Seq. ID	LIB3175-029-P1-K1-H7
Method	BLASTX
NCBI GI	g3024434
BLAST score	440
E value	1.0e-43
Match length	111
% identity	82
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	149660
Seq. ID	LIB3175-029-P1-K1-H8
Method	BLASTN
NCBI GI	g16363
BLAST score	36
E value	6.0e-11
Match length	56
% identity	91
NCBI Description	A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b binding protein

Seq. No.	149661
Seq. ID	LIB3175-029-P1-K1-H9
Method	BLASTX
NCBI GI	g1170689
BLAST score	318
E value	1.0e-32
Match length	82
% identity	85
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ATPK1/ATPK6 >gi_625979_pir__A54141 ribosomal protein S6 kinase (EC 2.7.1.-) Atpk1 - Arabidopsis thaliana >gi_2129542_pir__S68462 ATPK6 protein - Arabidopsis thaliana >gi_914080_bbs_160873 ATPK6=ribosomal-protein S6 kinase homolog [Arabidopsis thaliana, Peptide, 465 aa] >gi_508308 (L29030) protein-serine kinase [Arabidopsis thaliana] >gi_467997_dbj_BAA07656_ (D42056) risosomal-protein S6 kinase homolog [Arabidopsis thaliana]

Seq. No.	149662
Seq. ID	LIB3175-030-P1-K1-A11
Method	BLASTX

NCBI GI	g2119846
BLAST score	605
E value	5.0e-63
Match length	114
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149663
Seq. ID	LIB3175-030-P1-K1-A12
Method	BLASTX
NCBI GI	g2497753
BLAST score	253
E value	9.0e-22
Match length	94
% identity	48
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	149664
Seq. ID	LIB3175-030-P1-K1-A5
Method	BLASTX
NCBI GI	g4567304
BLAST score	248
E value	4.0e-21
Match length	124
% identity	44
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	149665
Seq. ID	LIB3175-030-P1-K1-A6
Method	BLASTN
NCBI GI	g2618602
BLAST score	213
E value	1.0e-116
Match length	323
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	149666
Seq. ID	LIB3175-030-P1-K1-A8
Method	BLASTX
NCBI GI	g3122572
BLAST score	408
E value	7.0e-40
Match length	128
% identity	65
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase

(ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	149667
Seq. ID	LIB3175-030-P1-K1-A9
Method	BLASTX
NCBI GI	g3335340
BLAST score	659
E value	3.0e-69
Match length	148
% identity	80
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	149668
Seq. ID	LIB3175-030-P1-K1-B1
Method	BLASTX
NCBI GI	g4544399
BLAST score	332
E value	6.0e-31
Match length	127
% identity	48
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	149669
Seq. ID	LIB3175-030-P1-K1-B11
Method	BLASTX
NCBI GI	g4580390
BLAST score	637
E value	9.0e-67
Match length	130
% identity	96
NCBI Description	(AC007171) putative disease resistance response protein [Arabidopsis thaliana]

Seq. No.	149670
Seq. ID	LIB3175-030-P1-K1-B12
Method	BLASTX
NCBI GI	g2506443
BLAST score	563
E value	5.0e-58
Match length	137
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	149671
Seq. ID	LIB3175-030-P1-K1-B2
Method	BLASTX
NCBI GI	g399298
BLAST score	217
E value	2.0e-17
Match length	66
% identity	70
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]

Seq. No.	149672
Seq. ID	LIB3175-030-P1-K1-B4
Method	BLASTX
NCBI GI	g3608261
BLAST score	314
E value	7.0e-29
Match length	84
% identity	64
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	149673
Seq. ID	LIB3175-030-P1-K1-B5
Method	BLASTN
NCBI GI	g4165340
BLAST score	90
E value	6.0e-43
Match length	346
% identity	82
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149674
Seq. ID	LIB3175-030-P1-K1-B6
Method	BLASTN
NCBI GI	g4585952
BLAST score	370
E value	0.0e+00
Match length	412
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	149675
Seq. ID	LIB3175-030-P1-K1-B7
Method	BLASTN
NCBI GI	g2880038
BLAST score	165
E value	1.0e-87
Match length	452
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149676
Seq. ID	LIB3175-030-P1-K1-B9
Method	BLASTX
NCBI GI	g2244866
BLAST score	782
E value	1.0e-83
Match length	152
% identity	97
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149677
Seq. ID	LIB3175-030-P1-K1-C10
Method	BLASTX
NCBI GI	g4567197
BLAST score	619
E value	1.0e-64
Match length	127
% identity	97
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	149678
Seq. ID	LIB3175-030-P1-K1-C12
Method	BLASTX
NCBI GI	g3075394
BLAST score	665
E value	5.0e-70
Match length	135
% identity	96
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	149679
Seq. ID	LIB3175-030-P1-K1-C2
Method	BLASTN
NCBI GI	g2262097
BLAST score	224
E value	1.0e-123
Match length	361
% identity	98
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	149680
Seq. ID	LIB3175-030-P1-K1-C3
Method	BLASTX
NCBI GI	g4263712
BLAST score	506
E value	2.0e-51
Match length	121
% identity	83
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No.	149681
Seq. ID	LIB3175-030-P1-K1-C4
Method	BLASTX

NCBI GI	g3157937
BLAST score	635
E value	2.0e-66
Match length	128
% identity	98
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	149682
Seq. ID	LIB3175-030-P1-K1-C7
Method	BLASTX
NCBI GI	g3377797
BLAST score	603
E value	1.0e-62
Match length	144
% identity	82
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	149683
Seq. ID	LIB3175-030-P1-K1-C8
Method	BLASTX
NCBI GI	g2129769
BLAST score	796
E value	2.0e-85
Match length	151
% identity	99
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	149684
Seq. ID	LIB3175-030-P1-K1-C9
Method	BLASTN
NCBI GI	g4662609
BLAST score	401
E value	0.0e+00
Match length	442
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	149685
Seq. ID	LIB3175-030-P1-K1-D1
Method	BLASTN
NCBI GI	g1086460
BLAST score	365
E value	0.0e+00
Match length	437
% identity	61
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein

(MT1c) gene, complete cds

Seq. No.	149686
Seq. ID	LIB3175-030-P1-K1-D10
Method	BLASTN
NCBI GI	g2618599
BLAST score	46
E value	1.0e-16
Match length	95
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	149687
Seq. ID	LIB3175-030-P1-K1-D11
Method	BLASTX
NCBI GI	g2062164
BLAST score	709
E value	4.0e-75
Match length	140
% identity	98
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	149688
Seq. ID	LIB3175-030-P1-K1-D12
Method	BLASTX
NCBI GI	g4164398
BLAST score	209
E value	2.0e-16
Match length	150
% identity	36
NCBI Description	(AL035248) serine threonine-protein kinase [Schizosaccharomyces pombe]

Seq. No.	149689
Seq. ID	LIB3175-030-P1-K1-D3
Method	BLASTX
NCBI GI	g2506443
BLAST score	640
E value	3.0e-67
Match length	130
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	149690
Seq. ID	LIB3175-030-P1-K1-D4
Method	BLASTX
NCBI GI	g2501188

BLAST score	640
E value	4.0e-67
Match length	145
% identity	89
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	149691
Seq. ID	LIB3175-030-P1-K1-D5
Method	BLASTX
NCBI GI	g2851508
BLAST score	724
E value	6.0e-77
Match length	139
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	149692
Seq. ID	LIB3175-030-P1-K1-D6
Method	BLASTX
NCBI GI	g2252841
BLAST score	63
E value	2.0e-62
Match length	152
% identity	71
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	149693
Seq. ID	LIB3175-030-P1-K1-D7
Method	BLASTX
NCBI GI	g4581146
BLAST score	601
E value	2.0e-62
Match length	131
% identity	92
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	149694
Seq. ID	LIB3175-030-P1-K1-D8
Method	BLASTN
NCBI GI	g3176695
BLAST score	208
E value	1.0e-113
Match length	451
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	149695
Seq. ID	LIB3175-030-P1-K1-D9

Method	BLASTX
NCBI GI	g112739
BLAST score	418
E value	4.0e-41
Match length	120
% identity	70
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	149696
Seq. ID	LIB3175-030-P1-K1-E1
Method	BLASTX
NCBI GI	g1076668
BLAST score	448
E value	1.0e-44
Match length	130
% identity	65
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	149697
Seq. ID	LIB3175-030-P1-K1-E12
Method	BLASTX
NCBI GI	g3201625
BLAST score	272
E value	6.0e-24
Match length	67
% identity	78
NCBI Description	(AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149698
Seq. ID	LIB3175-030-P1-K1-E2
Method	BLASTX
NCBI GI	g3451065
BLAST score	634
E value	2.0e-66
Match length	126
% identity	98
NCBI Description	(AL031326) water channel - like protein [Arabidopsis thaliana]

Seq. No.	149699
Seq. ID	LIB3175-030-P1-K1-E3
Method	BLASTN
NCBI GI	g4512646
BLAST score	224
E value	1.0e-123
Match length	286
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F23N11 genomic sequence, complete sequence

Seq. No.	149700
Seq. ID	LIB3175-030-P1-K1-E5
Method	BLASTX
NCBI GI	g4586265
BLAST score	533
E value	2.0e-54
Match length	123
% identity	80
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149701
Seq. ID	LIB3175-030-P1-K1-E7
Method	BLASTN
NCBI GI	g2924651
BLAST score	287
E value	1.0e-160
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	149702
Seq. ID	LIB3175-030-P1-K1-E8
Method	BLASTX
NCBI GI	g4741940
BLAST score	624
E value	3.0e-65
Match length	139
% identity	60
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	149703
Seq. ID	LIB3175-030-P1-K1-F10
Method	BLASTX
NCBI GI	g115767
BLAST score	54
E value	2.0e-78
Match length	150
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	149704
Seq. ID	LIB3175-030-P1-K1-F11
Method	BLASTN
NCBI GI	g2760164
BLAST score	397
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	149705
Seq. ID	LIB3175-030-P1-K1-F12
Method	BLASTX
NCBI GI	g119350
BLAST score	599
E value	2.0e-62
Match length	116
% identity	100
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	149706
Seq. ID	LIB3175-030-P1-K1-F2
Method	BLASTX
NCBI GI	g4263519
BLAST score	443
E value	3.0e-44
Match length	91
% identity	97
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	149707
Seq. ID	LIB3175-030-P1-K1-F4
Method	BLASTN
NCBI GI	g4589427
BLAST score	429
E value	0.0e+00
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	149708
Seq. ID	LIB3175-030-P1-K1-F5
Method	BLASTX
NCBI GI	g2498883
BLAST score	481
E value	2.0e-48
Match length	134
% identity	68
NCBI Description	SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) >gi_1173905 (U41371) spliceosome associated protein [Homo sapiens]

Seq. No.	149709
Seq. ID	LIB3175-030-P1-K1-F6
Method	BLASTN
NCBI GI	g710625

BLAST score 223
E value 1.0e-122
Match length 293
% identity 95
NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No. 149710
Seq. ID LIB3175-030-P1-K1-F7
Method BLASTX
NCBI GI g4558678
BLAST score 208
E value 1.0e-16
Match length 86
% identity 44
NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]

Seq. No. 149711
Seq. ID LIB3175-030-P1-K1-F8
Method BLASTX
NCBI GI g3608155
BLAST score 498
E value 2.0e-50
Match length 106
% identity 98
NCBI Description (AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 149712
Seq. ID LIB3175-030-P1-K1-F9
Method BLASTX
NCBI GI g544425
BLAST score 416
E value 6.0e-41
Match length 83
% identity 98
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No. 149713
Seq. ID LIB3175-030-P1-K1-G1
Method BLASTX
NCBI GI g730526
BLAST score 503
E value 4.0e-51
Match length 118
% identity 79
NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No. 149714
Seq. ID LIB3175-030-P1-K1-G10
Method BLASTX

NCBI GI	g529353
BLAST score	487
E value	4.0e-49
Match length	151
% identity	54
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	149715
Seq. ID	LIB3175-030-P1-K1-G11
Method	BLASTN
NCBI GI	g3702315
BLAST score	180
E value	1.0e-96
Match length	462
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149716
Seq. ID	LIB3175-030-P1-K1-G2
Method	BLASTN
NCBI GI	g2244991
BLAST score	205
E value	1.0e-111
Match length	352
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	149717
Seq. ID	LIB3175-030-P1-K1-G3
Method	BLASTN
NCBI GI	g4160401
BLAST score	38
E value	6.0e-12
Match length	62
% identity	90
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	149718
Seq. ID	LIB3175-030-P1-K1-G4
Method	BLASTN
NCBI GI	g4455168
BLAST score	329
E value	0.0e+00
Match length	465
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	149719
Seq. ID	LIB3175-030-P1-K1-G5
Method	BLASTX
NCBI GI	g3930517
BLAST score	160
E value	8.0e-11
Match length	106

% identity	40
NCBI Description	(AF059906) ubiquitin fusion degradation protein-2 [Schizosaccharomyces pombe]

Seq. No.	149720
Seq. ID	LIB3175-030-P1-K1-G6
Method	BLASTN
NCBI GI	g2947056
BLAST score	266
E value	1.0e-148
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149721
Seq. ID	LIB3175-030-P1-K1-G7
Method	BLASTX
NCBI GI	g132939
BLAST score	521
E value	3.0e-53
Match length	108
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	149722
Seq. ID	LIB3175-030-P1-K1-G9
Method	BLASTX
NCBI GI	g1841355
BLAST score	198
E value	3.0e-15
Match length	117
% identity	46
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	149723
Seq. ID	LIB3175-030-P1-K1-H1
Method	BLASTX
NCBI GI	g4539408
BLAST score	250
E value	2.0e-21
Match length	73
% identity	64
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	149724
Seq. ID	LIB3175-030-P1-K1-H11
Method	BLASTN
NCBI GI	g3212846
BLAST score	412
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149725
Seq. ID	LIB3175-030-P1-K1-H12
Method	BLASTN
NCBI GI	g4756963
BLAST score	326
E value	0.0e+00
Match length	384
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	149726
Seq. ID	LIB3175-030-P1-K1-H3
Method	BLASTX
NCBI GI	g549010
BLAST score	422
E value	1.0e-41
Match length	93
% identity	91
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	149727
Seq. ID	LIB3175-030-P1-K1-H4
Method	BLASTX
NCBI GI	g3169173
BLAST score	740
E value	8.0e-79
Match length	139
% identity	99
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	149728
Seq. ID	LIB3175-030-P1-K1-H5
Method	BLASTX
NCBI GI	g1076316
BLAST score	594
E value	9.0e-62
Match length	117
% identity	97
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No. 149729

Seq. ID	LIB3175-030-P1-K1-H6
Method	BLASTX
NCBI GI	g4544399
BLAST score	318
E value	2.0e-29
Match length	123
% identity	46
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	149730
Seq. ID	LIB3175-030-P1-K1-H9
Method	BLASTX
NCBI GI	g3080442
BLAST score	612
E value	8.0e-64
Match length	129
% identity	88
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	149731
Seq. ID	LIB3175-031-P1-K1-A1
Method	BLASTN
NCBI GI	g2252848
BLAST score	45
E value	4.0e-16
Match length	231
% identity	84
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	149732
Seq. ID	LIB3175-031-P1-K1-A11
Method	BLASTX
NCBI GI	g4336756
BLAST score	525
E value	1.0e-53
Match length	103
% identity	97
NCBI Description	(AF104453) catalase [Brassica juncea]

Seq. No.	149733
Seq. ID	LIB3175-031-P1-K1-A2
Method	BLASTX
NCBI GI	g4538963
BLAST score	518
E value	8.0e-53
Match length	130
% identity	78
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	149734
Seq. ID	LIB3175-031-P1-K1-A3
Method	BLASTX
NCBI GI	g4580389
BLAST score	636

E value	1.0e-66
Match length	134
% identity	58
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	149735
Seq. ID	LIB3175-031-P1-K1-A4
Method	BLASTX
NCBI GI	g2827710
BLAST score	771
E value	2.0e-82
Match length	147
% identity	97
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	149736
Seq. ID	LIB3175-031-P1-K1-A5
Method	BLASTX
NCBI GI	g1352681
BLAST score	92
E value	8.0e-56
Match length	111
% identity	100
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	149737
Seq. ID	LIB3175-031-P1-K1-A6
Method	BLASTN
NCBI GI	g4220638
BLAST score	47
E value	4.0e-18
Match length	71
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	149738
Seq. ID	LIB3175-031-P1-K1-A7
Method	BLASTX
NCBI GI	g1370186
BLAST score	586
E value	8.0e-61
Match length	114
% identity	98
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	149739
Seq. ID	LIB3175-031-P1-K1-A8
Method	BLASTX
NCBI GI	g1256509
BLAST score	266
E value	3.0e-23
Match length	90

% identity	58
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	149740
Seq. ID	LIB3175-031-P1-K1-A9
Method	BLASTX
NCBI GI	g3927825
BLAST score	545
E value	6.0e-56
Match length	115
% identity	86
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	149741
Seq. ID	LIB3175-031-P1-K1-B12
Method	BLASTN
NCBI GI	g4589430
BLAST score	132
E value	5.0e-68
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	149742
Seq. ID	LIB3175-031-P1-K1-B2
Method	BLASTN
NCBI GI	g3426033
BLAST score	182
E value	8.0e-98
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149743
Seq. ID	LIB3175-031-P1-K1-B3
Method	BLASTX
NCBI GI	g1175013
BLAST score	630
E value	6.0e-66
Match length	139
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	149744
Seq. ID	LIB3175-031-P1-K1-B5
Method	BLASTN
NCBI GI	g4589438
BLAST score	131
E value	2.0e-67
Match length	151
% identity	97

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence
Seq. No.	149745
Seq. ID	LIB3175-031-P1-K1-B7
Method	BLASTN
NCBI GI	g3776000
BLAST score	272
E value	1.0e-151
Match length	283
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12
Seq. No.	149746
Seq. ID	LIB3175-031-P1-K1-B8
Method	BLASTX
NCBI GI	g3169173
BLAST score	415
E value	5.0e-41
Match length	97
% identity	85
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]
Seq. No.	149747
Seq. ID	LIB3175-031-P1-K1-B9
Method	BLASTX
NCBI GI	g2435515
BLAST score	269
E value	1.0e-23
Match length	53
% identity	94
NCBI Description	(AF024504) No definition line found [Arabidopsis thaliana]
Seq. No.	149748
Seq. ID	LIB3175-031-P1-K1-C1
Method	BLASTX
NCBI GI	g1170040
BLAST score	444
E value	4.0e-44
Match length	86
% identity	100
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase [Arabidopsis thaliana]
Seq. No.	149749
Seq. ID	LIB3175-031-P1-K1-C11
Method	BLASTX
NCBI GI	g1209655
BLAST score	252
E value	1.0e-21
Match length	95

% identity	48
NCBI Description	(U37428) gl1 [Zea mays]

Seq. No.	149750
Seq. ID	LIB3175-031-P1-K1-C12
Method	BLASTX
NCBI GI	g2246621
BLAST score	573
E value	2.0e-59
Match length	119
% identity	96
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	149751
Seq. ID	LIB3175-031-P1-K1-C2
Method	BLASTX
NCBI GI	g122085
BLAST score	515
E value	2.0e-52
Match length	121
% identity	86
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	149752
Seq. ID	LIB3175-031-P1-K1-C3
Method	BLASTX
NCBI GI	g4337175
BLAST score	495
E value	4.0e-50
Match length	126
% identity	78
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,

gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	149753
Seq. ID	LIB3175-031-P1-K1-C4
Method	BLASTX
NCBI GI	g3785989
BLAST score	517
E value	6.0e-53
Match length	99
% identity	100
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	149754
Seq. ID	LIB3175-031-P1-K1-C5
Method	BLASTN
NCBI GI	g4049332
BLAST score	137
E value	3.0e-71
Match length	198
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	149755
Seq. ID	LIB3175-031-P1-K1-C6
Method	BLASTX
NCBI GI	g4263818
BLAST score	301
E value	2.0e-27
Match length	82
% identity	66
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]

Seq. No.	149756
Seq. ID	LIB3175-031-P1-K1-C7
Method	BLASTX
NCBI GI	g2252857
BLAST score	272
E value	5.0e-24
Match length	113
% identity	57
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	149757
Seq. ID	LIB3175-031-P1-K1-C8
Method	BLASTX
NCBI GI	g4006878
BLAST score	327
E value	9.0e-31
Match length	77
% identity	82
NCBI Description	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No.	149758
Seq. ID	LIB3175-031-P1-K1-D1

Method	BLASTX
NCBI GI	g4584255
BLAST score	215
E value	2.0e-17
Match length	49
% identity	76
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	149759
Seq. ID	LIB3175-031-P1-K1-D10
Method	BLASTN
NCBI GI	g2827513
BLAST score	193
E value	1.0e-104
Match length	255
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	149760
Seq. ID	LIB3175-031-P1-K1-D11
Method	BLASTN
NCBI GI	g405130
BLAST score	310
E value	1.0e-174
Match length	342
% identity	98
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	149761
Seq. ID	LIB3175-031-P1-K1-D12
Method	BLASTX
NCBI GI	g3122387
BLAST score	515
E value	2.0e-52
Match length	109
% identity	90
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394229 (AF016846) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	149762
Seq. ID	LIB3175-031-P1-K1-D2
Method	BLASTX
NCBI GI	g3435279
BLAST score	489
E value	2.0e-49
Match length	118
% identity	84
NCBI Description	(AF082391) protein kinase homolog [Arabidopsis thaliana]

Seq. No.	149763
Seq. ID	LIB3175-031-P1-K1-D4
Method	BLASTX
NCBI GI	g2781354
BLAST score	576
E value	8.0e-60

Match length	118
% identity	99
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	149764
Seq. ID	LIB3175-031-P1-K1-D5
Method	BLASTX
NCBI GI	g4502315
BLAST score	116
E value	1.0e-09
Match length	101
% identity	35
NCBI Description	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD >gi_401329_sp_P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) >gi_542836_pir__JN0907 H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - human >gi_37643_emb_CAA48903_ (X69151) vacuolar proton-ATPase [Homo sapiens]

Seq. No.	149765
Seq. ID	LIB3175-031-P1-K1-D6
Method	BLASTX
NCBI GI	g404670
BLAST score	539
E value	3.0e-55
Match length	121
% identity	88
NCBI Description	(L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No.	149766
Seq. ID	LIB3175-031-P1-K1-D8
Method	BLASTX
NCBI GI	g1669389
BLAST score	392
E value	4.0e-38
Match length	75
% identity	99
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	149767
Seq. ID	LIB3175-031-P1-K1-D9
Method	BLASTX
NCBI GI	g1669389
BLAST score	167
E value	9.0e-12
Match length	67
% identity	58
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	149768
Seq. ID	LIB3175-031-P1-K1-E1
Method	BLASTN
NCBI GI	g2160155
BLAST score	114
E value	2.0e-57
Match length	202

% identity	91
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	149769
Seq. ID	LIB3175-031-P1-K1-E10
Method	BLASTN
NCBI GI	g4582428
BLAST score	222
E value	1.0e-121
Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18C20 genomic sequence, complete sequence

Seq. No.	149770
Seq. ID	LIB3175-031-P1-K1-E11
Method	BLASTX
NCBI GI	g3063472
BLAST score	598
E value	3.0e-62
Match length	119
% identity	94
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	149771
Seq. ID	LIB3175-031-P1-K1-E12
Method	BLASTX
NCBI GI	g115385
BLAST score	442
E value	4.0e-44
Match length	89
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149772
Seq. ID	LIB3175-031-P1-K1-E2
Method	BLASTX
NCBI GI	g4490332
BLAST score	501
E value	5.0e-73
Match length	145
% identity	98
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	149773
Seq. ID	LIB3175-031-P1-K1-E3
Method	BLASTX
NCBI GI	g2341034
BLAST score	326
E value	1.0e-30
Match length	66
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	149774
Seq. ID	LIB3175-031-P1-K1-E5
Method	BLASTN
NCBI GI	g3985957
BLAST score	210
E value	1.0e-114
Match length	444
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	149775
Seq. ID	LIB3175-031-P1-K1-E6
Method	BLASTN
NCBI GI	g2435510
BLAST score	239
E value	1.0e-132
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	149776
Seq. ID	LIB3175-031-P1-K1-E7
Method	BLASTX
NCBI GI	g2244845
BLAST score	593
E value	1.0e-61
Match length	144
% identity	85
NCBI Description	(Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8) [Arabidopsis thaliana]

Seq. No.	149777
Seq. ID	LIB3175-031-P1-K1-E8
Method	BLASTX
NCBI GI	g1710114
BLAST score	397
E value	1.0e-38
Match length	123
% identity	74
NCBI Description	(U53865) PRH26 [Arabidopsis thaliana]

Seq. No.	149778
Seq. ID	LIB3175-031-P1-K1-F1
Method	BLASTX
NCBI GI	g2739389
BLAST score	162
E value	1.0e-11
Match length	57
% identity	54
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	149779
Seq. ID	LIB3175-031-P1-K1-F10
Method	BLASTX
NCBI GI	g2245093
BLAST score	94

E value	6.0e-45
Match length	122
% identity	84
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	149780
Seq. ID	LIB3175-031-P1-K1-F11
Method	BLASTN
NCBI GI	g2191126
BLAST score	354
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	149781
Seq. ID	LIB3175-031-P1-K1-F12
Method	BLASTX
NCBI GI	g3983125
BLAST score	161
E value	6.0e-11
Match length	51
% identity	69
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	149782
Seq. ID	LIB3175-031-P1-K1-F2
Method	BLASTN
NCBI GI	g4531433
BLAST score	411
E value	0.0e+00
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	149783
Seq. ID	LIB3175-031-P1-K1-F3
Method	BLASTX
NCBI GI	g1708313
BLAST score	552
E value	8.0e-57
Match length	117
% identity	97
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	149784
Seq. ID	LIB3175-031-P1-K1-F6
Method	BLASTX
NCBI GI	g3176666
BLAST score	260
E value	1.0e-22
Match length	119

% identity	52
NCBI Description	(AC004393) Contains similarity to hypothetical protein gb_Z97343 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	149785
Seq. ID	LIB3175-031-P1-K1-F7
Method	BLASTX
NCBI GI	g2244974
BLAST score	583
E value	2.0e-60
Match length	138
% identity	86
NCBI Description	(Z97340) similarity to pore protein Pisum sativum [Arabidopsis thaliana]

Seq. No.	149786
Seq. ID	LIB3175-031-P1-K1-F8
Method	BLASTX
NCBI GI	g115783
BLAST score	644
E value	1.0e-67
Match length	124
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149787
Seq. ID	LIB3175-031-P1-K1-G10
Method	BLASTN
NCBI GI	g1402874
BLAST score	166
E value	3.0e-88
Match length	347
% identity	98
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	149788
Seq. ID	LIB3175-031-P1-K1-G2
Method	BLASTX
NCBI GI	g4586265
BLAST score	498
E value	2.0e-50
Match length	124
% identity	76
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149789
Seq. ID	LIB3175-031-P1-K1-G3
Method	BLASTX
NCBI GI	g4586265
BLAST score	96
E value	2.0e-23
Match length	111
% identity	57
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149790
Seq. ID	LIB3175-031-P1-K1-G4
Method	BLASTX
NCBI GI	g1155261
BLAST score	600
E value	2.0e-62
Match length	120
% identity	98
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	149791
Seq. ID	LIB3175-031-P1-K1-G5
Method	BLASTX
NCBI GI	g4432856
BLAST score	618
E value	1.0e-64
Match length	118
% identity	100
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	149792
Seq. ID	LIB3175-031-P1-K1-G6
Method	BLASTN
NCBI GI	g4220643
BLAST score	115
E value	7.0e-58
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	149793
Seq. ID	LIB3175-031-P1-K1-G7
Method	BLASTX
NCBI GI	g112682
BLAST score	618
E value	1.0e-64
Match length	138
% identity	87
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	149794
Seq. ID	LIB3175-031-P1-K1-G8
Method	BLASTN
NCBI GI	g4580530
BLAST score	267
E value	1.0e-148
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA, partial cds

Seq. No.	149795
Seq. ID	LIB3175-031-P1-K1-H10
Method	BLASTX
NCBI GI	g4586265
BLAST score	409
E value	4.0e-40
Match length	115
% identity	71
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149796
Seq. ID	LIB3175-031-P1-K1-H3
Method	BLASTX
NCBI GI	g1402910
BLAST score	714
E value	9.0e-76
Match length	138
% identity	98
NCBI Description	(X98316) peroxidase [Arabidopsis thaliana] >gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis thaliana]

Seq. No.	149797
Seq. ID	LIB3175-031-P1-K1-H4
Method	BLASTN
NCBI GI	g3047100
BLAST score	81
E value	6.0e-38
Match length	93
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	149798
Seq. ID	LIB3175-031-P1-K1-H6
Method	BLASTX
NCBI GI	g2341034
BLAST score	633
E value	2.0e-66
Match length	126
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	149799
Seq. ID	LIB3175-031-P1-K1-H8
Method	BLASTN
NCBI GI	g4468976
BLAST score	265
E value	1.0e-147
Match length	377
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	149800
Seq. ID	LIB3175-031-P1-K1-H9
Method	BLASTN

NCBI GI	g4106339
BLAST score	344
E value	0.0e+00
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana protein phosphatase 2A regulatory subunit isoform B' delta mRNA, complete cds

Seq. No.	149801
Seq. ID	LIB3175-032-P1-K1-A10
Method	BLASTX
NCBI GI	g4581146
BLAST score	413
E value	4.0e-51
Match length	110
% identity	100
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	149802
Seq. ID	LIB3175-032-P1-K1-A12
Method	BLASTX
NCBI GI	g4586265
BLAST score	526
E value	9.0e-54
Match length	137
% identity	75
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149803
Seq. ID	LIB3175-032-P1-K1-A2
Method	BLASTX
NCBI GI	g120667
BLAST score	539
E value	3.0e-55
Match length	118
% identity	89
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	149804
Seq. ID	LIB3175-032-P1-K1-A3
Method	BLASTX
NCBI GI	g2811278
BLAST score	271
E value	7.0e-24
Match length	92
% identity	57
NCBI Description	(AF043284) expansin [Gossypium hirsutum]

Seq. No.	149805
Seq. ID	LIB3175-032-P1-K1-A4

Method	BLASTX
NCBI GI	g730544
BLAST score	325
E value	3.0e-30
Match length	122
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L24

Seq. No.	149806
Seq. ID	LIB3175-032-P1-K1-A5
Method	BLASTN
NCBI GI	g2182289
BLAST score	419
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149807
Seq. ID	LIB3175-032-P1-K1-A6
Method	BLASTX
NCBI GI	g3688799
BLAST score	618
E value	1.0e-64
Match length	124
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	149808
Seq. ID	LIB3175-032-P1-K1-A7
Method	BLASTX
NCBI GI	g4314378
BLAST score	405
E value	1.0e-39
Match length	113
% identity	69
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	149809
Seq. ID	LIB3175-032-P1-K1-A8
Method	BLASTX
NCBI GI	g417103
BLAST score	645
E value	1.0e-67
Match length	129
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	149810
Seq. ID	LIB3175-032-P1-K1-A9
Method	BLASTN
NCBI GI	g4510323
BLAST score	343
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	149811
Seq. ID	LIB3175-032-P1-K1-B10
Method	BLASTN
NCBI GI	g3046851
BLAST score	416
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	149812
Seq. ID	LIB3175-032-P1-K1-B11
Method	BLASTX
NCBI GI	g4314386
BLAST score	408
E value	6.0e-40
Match length	110
% identity	75
NCBI Description	(AC006232) putative rac GTPase activating protein [Arabidopsis thaliana]

Seq. No.	149813
Seq. ID	LIB3175-032-P1-K1-B12
Method	BLASTN
NCBI GI	g4755185
BLAST score	247
E value	1.0e-136
Match length	402
% identity	50
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	149814
Seq. ID	LIB3175-032-P1-K1-B3

Method	BLASTX
NCBI GI	g4185505
BLAST score	467
E value	8.0e-47
Match length	115
% identity	77
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	149815
Seq. ID	LIB3175-032-P1-K1-B6
Method	BLASTX
NCBI GI	g3006148
BLAST score	162
E value	4.0e-11
Match length	42
% identity	76
NCBI Description	(AL022299) rps9-b, 40s ribosomal protein s9 [Schizosaccharomyces pombe]

Seq. No.	149816
Seq. ID	LIB3175-032-P1-K1-B7
Method	BLASTN
NCBI GI	g2252848
BLAST score	45
E value	4.0e-16
Match length	231
% identity	84
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	149817
Seq. ID	LIB3175-032-P1-K1-B8
Method	BLASTX
NCBI GI	g2894574
BLAST score	640
E value	4.0e-67
Match length	122
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	149818
Seq. ID	LIB3175-032-P1-K1-B9
Method	BLASTN
NCBI GI	g4512656
BLAST score	273
E value	1.0e-152
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	149819
Seq. ID	LIB3175-032-P1-K1-C1
Method	BLASTN
NCBI GI	g3873174

BLAST score	387
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	149820
Seq. ID	LIB3175-032-P1-K1-C11
Method	BLASTN
NCBI GI	g2656029
BLAST score	411
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	149821
Seq. ID	LIB3175-032-P1-K1-C12
Method	BLASTX
NCBI GI	g2494119
BLAST score	719
E value	2.0e-76
Match length	138
% identity	100
NCBI Description	(AC002376) EST gb_T04104 comes from this gene. [Arabidopsis thaliana]

Seq. No.	149822
Seq. ID	LIB3175-032-P1-K1-C5
Method	BLASTX
NCBI GI	g4206197
BLAST score	714
E value	8.0e-76
Match length	139
% identity	17
NCBI Description	(AF071527) putative pre-mRNA splicing factor [Arabidopsis thaliana]

Seq. No.	149823
Seq. ID	LIB3175-032-P1-K1-C6
Method	BLASTX
NCBI GI	g2623962
BLAST score	598
E value	3.0e-62
Match length	138
% identity	80
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	149824
Seq. ID	LIB3175-032-P1-K1-C7
Method	BLASTX
NCBI GI	g2129636
BLAST score	635
E value	1.0e-66

Match length	122
% identity	100
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	149825
Seq. ID	LIB3175-032-P1-K1-C8
Method	BLASTN
NCBI GI	g3763915
BLAST score	52
E value	3.0e-20
Match length	355
% identity	31
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149826
Seq. ID	LIB3175-032-P1-K1-C9
Method	BLASTN
NCBI GI	g4519188
BLAST score	149
E value	3.0e-78
Match length	323
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	149827
Seq. ID	LIB3175-032-P1-K1-D1
Method	BLASTN
NCBI GI	g4689466
BLAST score	256
E value	1.0e-142
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence

Seq. No.	149828
Seq. ID	LIB3175-032-P1-K1-D10
Method	BLASTN
NCBI GI	g4510323
BLAST score	392
E value	0.0e+00
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	149829
Seq. ID	LIB3175-032-P1-K1-D11
Method	BLASTN
NCBI GI	g4589437
BLAST score	245
E value	1.0e-135
Match length	294
% identity	95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	149830
Seq. ID	LIB3175-032-P1-K1-D12
Method	BLASTX
NCBI GI	g4678328
BLAST score	410
E value	3.0e-40
Match length	85
% identity	95
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	149831
Seq. ID	LIB3175-032-P1-K1-D3
Method	BLASTN
NCBI GI	g3860243
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149832
Seq. ID	LIB3175-032-P1-K1-D4
Method	BLASTX
NCBI GI	g1710581
BLAST score	625
E value	2.0e-65
Match length	127
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	149833
Seq. ID	LIB3175-032-P1-K1-D5
Method	BLASTX
NCBI GI	g2119846
BLAST score	678
E value	1.0e-71
Match length	129
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149834
Seq. ID	LIB3175-032-P1-K1-D6
Method	BLASTN
NCBI GI	g2252848

BLAST score	45
E value	4.0e-16
Match length	231
% identity	84
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	149835
Seq. ID	LIB3175-032-P1-K1-D7
Method	BLASTN
NCBI GI	g1490552
BLAST score	262
E value	1.0e-145
Match length	358
% identity	94
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	149836
Seq. ID	LIB3175-032-P1-K1-D8
Method	BLASTN
NCBI GI	g3860243
BLAST score	356
E value	0.0e+00
Match length	417
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149837
Seq. ID	LIB3175-032-P1-K1-D9
Method	BLASTX
NCBI GI	g2129752
BLAST score	661
E value	1.0e-69
Match length	130
% identity	100
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ (Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No.	149838
Seq. ID	LIB3175-032-P1-K1-E1
Method	BLASTX
NCBI GI	g1169278
BLAST score	299
E value	4.0e-27
Match length	137
% identity	51
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	149839
Seq. ID	LIB3175-032-P1-K1-E10
Method	BLASTX
NCBI GI	g1352463
BLAST score	544
E value	7.0e-56
Match length	120

% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	149840
Seq. ID	LIB3175-032-P1-K1-E11
Method	BLASTX
NCBI GI	g3873710
BLAST score	351
E value	3.0e-33
Match length	101
% identity	61
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No.	149841
Seq. ID	LIB3175-032-P1-K1-E12
Method	BLASTX
NCBI GI	g1755162
BLAST score	704
E value	1.0e-74
Match length	138
% identity	99
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	149842
Seq. ID	LIB3175-032-P1-K1-E2
Method	BLASTN
NCBI GI	g2924651
BLAST score	326
E value	0.0e+00
Match length	347
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	149843
Seq. ID	LIB3175-032-P1-K1-E3
Method	BLASTX
NCBI GI	g119143
BLAST score	481
E value	3.0e-68
Match length	133
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana]

>gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	149844
Seq. ID	LIB3175-032-P1-K1-E4
Method	BLASTN
NCBI GI	g3600029
BLAST score	64
E value	1.0e-27
Match length	210
% identity	89
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	149845
Seq. ID	LIB3175-032-P1-K1-E5
Method	BLASTX
NCBI GI	g1175010
BLAST score	589
E value	4.0e-61
Match length	125
% identity	92
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	149846
Seq. ID	LIB3175-032-P1-K1-E6
Method	BLASTX
NCBI GI	g3785977
BLAST score	264
E value	8.0e-46
Match length	108
% identity	88
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	149847
Seq. ID	LIB3175-032-P1-K1-E7
Method	BLASTX
NCBI GI	g112681
BLAST score	571
E value	5.0e-59
Match length	132
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	149848
Seq. ID	LIB3175-032-P1-K1-E9
Method	BLASTN
NCBI GI	g4757409
BLAST score	135
E value	8.0e-70
Match length	413

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	149849
Seq. ID	LIB3175-032-P1-K1-F1
Method	BLASTX
NCBI GI	g2129622
BLAST score	722
E value	9.0e-77
Match length	138
% identity	100
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	149850
Seq. ID	LIB3175-032-P1-K1-F10
Method	BLASTX
NCBI GI	g4309758
BLAST score	307
E value	4.0e-28
Match length	64
% identity	100
NCBI Description	(AC006217) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149851
Seq. ID	LIB3175-032-P1-K1-F11
Method	BLASTX
NCBI GI	g832876
BLAST score	531
E value	2.0e-54
Match length	123
% identity	83
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	149852
Seq. ID	LIB3175-032-P1-K1-F12
Method	BLASTN
NCBI GI	g4757678
BLAST score	42
E value	3.0e-14
Match length	154
% identity	82
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	149853
Seq. ID	LIB3175-032-P1-K1-F2
Method	BLASTX
NCBI GI	g1336084
BLAST score	251
E value	4.0e-36
Match length	81
% identity	99
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2

(GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	149854
Seq. ID	LIB3175-032-P1-K1-F3
Method	BLASTX
NCBI GI	g2677828
BLAST score	383
E value	5.0e-37
Match length	100
% identity	72
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	149855
Seq. ID	LIB3175-032-P1-K1-F5
Method	BLASTX
NCBI GI	g2317902
BLAST score	749
E value	6.0e-80
Match length	139
% identity	100
NCBI Description	(U89959) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149856
Seq. ID	LIB3175-032-P1-K1-F6
Method	BLASTN
NCBI GI	g3941542
BLAST score	418
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana pelota (PEL1) mRNA, complete cds

Seq. No.	149857
Seq. ID	LIB3175-032-P1-K1-F7
Method	BLASTX
NCBI GI	g112681
BLAST score	726
E value	3.0e-77
Match length	138
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	149858
Seq. ID	LIB3175-032-P1-K1-F8
Method	BLASTX
NCBI GI	g3413714
BLAST score	405
E value	1.0e-39
Match length	122
% identity	22
NCBI Description	(AC004747) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	149859
Seq. ID	LIB3175-032-P1-K1-F9
Method	BLASTX
NCBI GI	g114339
BLAST score	581
E value	3.0e-60
Match length	138
% identity	86
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]

Seq. No.	149860
Seq. ID	LIB3175-032-P1-K1-G1
Method	BLASTX
NCBI GI	g4587685
BLAST score	424
E value	2.0e-54
Match length	118
% identity	93
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	149861
Seq. ID	LIB3175-032-P1-K1-G11
Method	BLASTX
NCBI GI	g2764941
BLAST score	600
E value	2.0e-62
Match length	105
% identity	100
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	149862
Seq. ID	LIB3175-032-P1-K1-G12
Method	BLASTN
NCBI GI	g3927822
BLAST score	324
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149863
Seq. ID	LIB3175-032-P1-K1-G2
Method	BLASTX
NCBI GI	g2586127
BLAST score	205
E value	6.0e-18
Match length	125
% identity	45
NCBI Description	(U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.	149864
Seq. ID	LIB3175-032-P1-K1-G3
Method	BLASTX
NCBI GI	g2832617
BLAST score	423
E value	1.0e-41
Match length	99
% identity	79
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	149865
Seq. ID	LIB3175-032-P1-K1-G4
Method	BLASTX
NCBI GI	g4567276
BLAST score	255
E value	5.0e-22
Match length	84
% identity	61
NCBI Description	(AC006841) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149866
Seq. ID	LIB3175-032-P1-K1-G5
Method	BLASTX
NCBI GI	g2505876
BLAST score	318
E value	2.0e-29
Match length	70
% identity	87
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	149867
Seq. ID	LIB3175-032-P1-K1-G6
Method	BLASTX
NCBI GI	g4586265
BLAST score	534
E value	1.0e-54
Match length	139
% identity	76
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149868
Seq. ID	LIB3175-032-P1-K1-G7
Method	BLASTN
NCBI GI	g2618605
BLAST score	143
E value	1.0e-74
Match length	423
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	149869
Seq. ID	LIB3175-032-P1-K1-G8
Method	BLASTX
NCBI GI	g3763925
BLAST score	549
E value	2.0e-56

Match length	105
% identity	100
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No.	149870
Seq. ID	LIB3175-032-P1-K1-G9
Method	BLASTN
NCBI GI	g4376087
BLAST score	237
E value	1.0e-131
Match length	312
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	149871
Seq. ID	LIB3175-032-P1-K1-H1
Method	BLASTX
NCBI GI	g2500082
BLAST score	369
E value	2.0e-35
Match length	93
% identity	86
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_984735_emb_CAA56907_ (X80932) photosystem II D1 protein [Vigna unguiculata]

Seq. No.	149872
Seq. ID	LIB3175-032-P1-K1-H10
Method	BLASTN
NCBI GI	g4539378
BLAST score	189
E value	1.0e-102
Match length	374
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	149873
Seq. ID	LIB3175-032-P1-K1-H11
Method	BLASTX
NCBI GI	g131150
BLAST score	703
E value	2.0e-74
Match length	138
% identity	97
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_81515_pir__S00445 photosystem I protein A2 - spinach chloroplast >gi_12271_emb_CAA27745_ (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] >gi_225422_prf__1303218B gene psaB [Spinacia oleracea]

Seq. No.	149874
Seq. ID	LIB3175-032-P1-K1-H12
Method	BLASTX
NCBI GI	g2851508

BLAST score	659
E value	2.0e-69
Match length	130
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	149875
Seq. ID	LIB3175-032-P1-K1-H2
Method	BLASTX
NCBI GI	g2317911
BLAST score	518
E value	8.0e-53
Match length	121
% identity	87
NCBI Description	(U89959) similar to GTP-binding protein [Arabidopsis thaliana]

Seq. No.	149876
Seq. ID	LIB3175-032-P1-K1-H4
Method	BLASTN
NCBI GI	g3510345
BLAST score	284
E value	1.0e-158
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	149877
Seq. ID	LIB3175-032-P1-K1-H5
Method	BLASTX
NCBI GI	g132074
BLAST score	682
E value	5.0e-72
Match length	124
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	149878
Seq. ID	LIB3175-032-P1-K1-H6
Method	BLASTX
NCBI GI	g2677828
BLAST score	438
E value	2.0e-43
Match length	117
% identity	68
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	149879
Seq. ID	LIB3175-032-P1-K1-H7

Method	BLASTX
NCBI GI	g1161926
BLAST score	548
E value	2.0e-56
Match length	138
% identity	76
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	149880
Seq. ID	LIB3175-032-P1-K1-H8
Method	BLASTX
NCBI GI	g4567261
BLAST score	425
E value	3.0e-46
Match length	125
% identity	80
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582439_gb_AAD24824.1_AC007142_2 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	149881
Seq. ID	LIB3175-032-P1-K1-H9
Method	BLASTX
NCBI GI	g1175012
BLAST score	691
E value	4.0e-73
Match length	133
% identity	100
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	149882
Seq. ID	LIB3175-033-P1-K1-A1
Method	BLASTX
NCBI GI	g2673904
BLAST score	250
E value	1.0e-21
Match length	109
% identity	61
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149883
Seq. ID	LIB3175-033-P1-K1-A10
Method	BLASTX
NCBI GI	g728868
BLAST score	200
E value	1.0e-15
Match length	66
% identity	56
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) >gi_99824_pir__S16748 proline-rich protein - rape (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich protein [Brassica napus]

Seq. No.	149884
Seq. ID	LIB3175-033-P1-K1-A11
Method	BLASTX
NCBI GI	g1706772
BLAST score	344
E value	2.0e-32
Match length	65
% identity	100
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	149885
Seq. ID	LIB3175-033-P1-K1-A2
Method	BLASTX
NCBI GI	g1053047
BLAST score	491
E value	1.0e-49
Match length	99
% identity	100
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	149886
Seq. ID	LIB3175-033-P1-K1-A3
Method	BLASTN
NCBI GI	g4678705
BLAST score	368
E value	0.0e+00
Match length	384
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	149887
Seq. ID	LIB3175-033-P1-K1-A4
Method	BLASTN
NCBI GI	g4220468
BLAST score	52
E value	1.0e-20
Match length	156
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 149888

Seq. ID LIB3175-033-P1-K1-A5
Method BLASTX
NCBI GI g3319350
BLAST score 680
E value 8.0e-72
Match length 135
% identity 99
NCBI Description (AF077407) No definition line found [Arabidopsis thaliana]

Seq. No. 149889
Seq. ID LIB3175-033-P1-K1-A6
Method BLASTX
NCBI GI g3043415
BLAST score 506
E value 2.0e-51
Match length 108
% identity 91
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 149890
Seq. ID LIB3175-033-P1-K1-A8
Method BLASTX
NCBI GI g3152606
BLAST score 665
E value 4.0e-70
Match length 133
% identity 89
NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No. 149891
Seq. ID LIB3175-033-P1-K1-A9
Method BLASTX
NCBI GI g1619300
BLAST score 390
E value 8.0e-38
Match length 81
% identity 88
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 149892
Seq. ID LIB3175-033-P1-K1-B1
Method BLASTX
NCBI GI g1170168
BLAST score 618
E value 1.0e-64
Match length 120
% identity 99
NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 149893
Seq. ID LIB3175-033-P1-K1-B10
Method BLASTX

NCBI GI	g2739376
BLAST score	350
E value	4.0e-33
Match length	85
% identity	80
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	149894
Seq. ID	LIB3175-033-P1-K1-B11
Method	BLASTX
NCBI GI	g2213595
BLAST score	518
E value	8.0e-53
Match length	127
% identity	80
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	149895
Seq. ID	LIB3175-033-P1-K1-B12
Method	BLASTX
NCBI GI	g3337356
BLAST score	203
E value	2.0e-29
Match length	79
% identity	90
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	149896
Seq. ID	LIB3175-033-P1-K1-B2
Method	BLASTX
NCBI GI	g1172872
BLAST score	259
E value	8.0e-23
Match length	54
% identity	93
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	149897
Seq. ID	LIB3175-033-P1-K1-B3
Method	BLASTX
NCBI GI	g132074
BLAST score	604
E value	6.0e-63
Match length	110
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	149898

Seq. ID	LIB3175-033-P1-K1-B5
Method	BLASTX
NCBI GI	g3688799
BLAST score	402
E value	2.0e-39
Match length	87
% identity	92
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	149899
Seq. ID	LIB3175-033-P1-K1-B6
Method	BLASTX
NCBI GI	g4586263
BLAST score	406
E value	1.0e-39
Match length	118
% identity	68
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	149900
Seq. ID	LIB3175-033-P1-K1-B7
Method	BLASTN
NCBI GI	g2924651
BLAST score	136
E value	2.0e-70
Match length	315
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	149901
Seq. ID	LIB3175-033-P1-K1-B8
Method	BLASTN
NCBI GI	g4314374
BLAST score	311
E value	1.0e-175
Match length	318
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149902
Seq. ID	LIB3175-033-P1-K1-B9
Method	BLASTX
NCBI GI	g2244814
BLAST score	69
E value	4.0e-32
Match length	94
% identity	79
NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	149903
Seq. ID	LIB3175-033-P1-K1-C10
Method	BLASTN
NCBI GI	g4469002
BLAST score	40

E value	3.0e-13
Match length	72
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	149904
Seq. ID	LIB3175-033-P1-K1-C12
Method	BLASTN
NCBI GI	g2252823
BLAST score	74
E value	2.0e-33
Match length	172
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	149905
Seq. ID	LIB3175-033-P1-K1-C3
Method	BLASTX
NCBI GI	g4163997
BLAST score	462
E value	3.0e-46
Match length	88
% identity	100
NCBI Description	(AF087483) alpha-xylosidase precursor [Arabidopsis thaliana]

Seq. No.	149906
Seq. ID	LIB3175-033-P1-K1-C4
Method	BLASTX
NCBI GI	g3163946
BLAST score	404
E value	1.0e-39
Match length	81
% identity	94
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No.	149907
Seq. ID	LIB3175-033-P1-K1-C5
Method	BLASTX
NCBI GI	g297381
BLAST score	377
E value	3.0e-36
Match length	115
% identity	72
NCBI Description	(X67421) extA [Arabidopsis thaliana]

Seq. No.	149908
Seq. ID	LIB3175-033-P1-K1-C8
Method	BLASTX
NCBI GI	g3158372
BLAST score	280
E value	6.0e-25
Match length	95
% identity	36
NCBI Description	(AF035383) polyubiquitin [Arabidopsis thaliana]

Seq. No.	149909
Seq. ID	LIB3175-033-P1-K1-C9
Method	BLASTN
NCBI GI	g4049332
BLAST score	76
E value	8.0e-35
Match length	131
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	149910
Seq. ID	LIB3175-033-P1-K1-D1
Method	BLASTX
NCBI GI	g687834
BLAST score	153
E value	5.0e-10
Match length	87
% identity	44
NCBI Description	(U21319) similar to alcohol dehydrogenase, highest similarity to B. japonicum FIXR protein (SP:FIXR_BRAJA, P05406) [Caenorhabditis elegans]

Seq. No.	149911
Seq. ID	LIB3175-033-P1-K1-D12
Method	BLASTX
NCBI GI	g132102
BLAST score	520
E value	4.0e-53
Match length	113
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	149912
Seq. ID	LIB3175-033-P1-K1-D3
Method	BLASTX
NCBI GI	g3914467
BLAST score	288
E value	7.0e-26
Match length	107
% identity	57
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	149913
Seq. ID	LIB3175-033-P1-K1-D4
Method	BLASTN
NCBI GI	g3510343
BLAST score	378
E value	0.0e+00
Match length	409

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	149914
Seq. ID	LIB3175-033-P1-K1-D5
Method	BLASTN
NCBI GI	g4220510
BLAST score	387
E value	0.0e+00
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	149915
Seq. ID	LIB3175-033-P1-K1-D6
Method	BLASTN
NCBI GI	g4220510
BLAST score	156
E value	3.0e-82
Match length	270
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	149916
Seq. ID	LIB3175-033-P1-K1-D7
Method	BLASTN
NCBI GI	g2853071
BLAST score	77
E value	1.0e-35
Match length	157
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	149917
Seq. ID	LIB3175-033-P1-K1-D8
Method	BLASTX
NCBI GI	g1864017
BLAST score	461
E value	3.0e-46
Match length	99
% identity	90
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	149918
Seq. ID	LIB3175-033-P1-K1-D9
Method	BLASTN
NCBI GI	g3080352
BLAST score	240
E value	1.0e-132
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	149919
Seq. ID	LIB3175-033-P1-K1-E1
Method	BLASTN
NCBI GI	g3687687
BLAST score	78
E value	4.0e-36
Match length	118
% identity	92
NCBI Description	Brassica napus response regulator protein mRNA, complete cds

Seq. No.	149920
Seq. ID	LIB3175-033-P1-K1-E10
Method	BLASTX
NCBI GI	g1750376
BLAST score	666
E value	3.0e-70
Match length	127
% identity	98
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	149921
Seq. ID	LIB3175-033-P1-K1-E11
Method	BLASTX
NCBI GI	g1245182
BLAST score	719
E value	2.0e-76
Match length	136
% identity	99
NCBI Description	(U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.	149922
Seq. ID	LIB3175-033-P1-K1-E12
Method	BLASTX
NCBI GI	g2119846
BLAST score	43
E value	5.0e-66
Match length	127
% identity	90
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149923
Seq. ID	LIB3175-033-P1-K1-E2
Method	BLASTX
NCBI GI	g1408460
BLAST score	292
E value	2.0e-26
Match length	86

% identity	70
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No.	149924
Seq. ID	LIB3175-033-P1-K1-E3
Method	BLASTN
NCBI GI	g4662609
BLAST score	312
E value	1.0e-175
Match length	415
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	149925
Seq. ID	LIB3175-033-P1-K1-E4
Method	BLASTX
NCBI GI	g1172872
BLAST score	86
E value	2.0e-45
Match length	118
% identity	86
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	149926
Seq. ID	LIB3175-033-P1-K1-E6
Method	BLASTN
NCBI GI	g2924651
BLAST score	69
E value	2.0e-30
Match length	175
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	149927
Seq. ID	LIB3175-033-P1-K1-E7
Method	BLASTX
NCBI GI	g3894172
BLAST score	510
E value	7.0e-52
Match length	97
% identity	100
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	149928
Seq. ID	LIB3175-033-P1-K1-E8
Method	BLASTX
NCBI GI	g4314386
BLAST score	196

E value	5.0e-25
Match length	126
% identity	59
NCBI Description	(AC006232) putative rac GTPase activating protein [Arabidopsis thaliana]

Seq. No.	149929
Seq. ID	LIB3175-033-P1-K1-F10
Method	BLASTX
NCBI GI	g135406
BLAST score	560
E value	9.0e-58
Match length	105
% identity	100
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	149930
Seq. ID	LIB3175-033-P1-K1-F11
Method	BLASTX
NCBI GI	g280386
BLAST score	615
E value	3.0e-64
Match length	128
% identity	95
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	149931
Seq. ID	LIB3175-033-P1-K1-F12
Method	BLASTX
NCBI GI	g2119846
BLAST score	578
E value	6.0e-60
Match length	117
% identity	93
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	149932
Seq. ID	LIB3175-033-P1-K1-F2
Method	BLASTN
NCBI GI	g2477521
BLAST score	271
E value	1.0e-151
Match length	407

% identity	25
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	149933
Seq. ID	LIB3175-033-P1-K1-F3
Method	BLASTN
NCBI GI	g4581161
BLAST score	156
E value	2.0e-82
Match length	334
% identity	73
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence
Seq. No.	149934
Seq. ID	LIB3175-033-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	149935
Seq. ID	LIB3175-033-P1-K1-F5
Method	BLASTN
NCBI GI	g2244901
BLAST score	198
E value	1.0e-107
Match length	258
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	149936
Seq. ID	LIB3175-033-P1-K1-F6
Method	BLASTX
NCBI GI	g2119846
BLAST score	647
E value	6.0e-68
Match length	126
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	149937
Seq. ID	LIB3175-033-P1-K1-F7
Method	BLASTX

NCBI GI	g4263525
BLAST score	535
E value	8.0e-55
Match length	126
% identity	83
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	149938
Seq. ID	LIB3175-033-P1-K1-F8
Method	BLASTN
NCBI GI	g4220510
BLAST score	58
E value	7.0e-24
Match length	228
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	149939
Seq. ID	LIB3175-033-P1-K1-F9
Method	BLASTN
NCBI GI	g1871173
BLAST score	91
E value	1.0e-43
Match length	170
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	149940
Seq. ID	LIB3175-033-P1-K1-G12
Method	BLASTN
NCBI GI	g4678291
BLAST score	101
E value	1.0e-49
Match length	213
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	149941
Seq. ID	LIB3175-033-P1-K1-G2
Method	BLASTN
NCBI GI	g3849811
BLAST score	150
E value	9.0e-79
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149942
Seq. ID	LIB3175-033-P1-K1-G3
Method	BLASTX
NCBI GI	g4589965
BLAST score	542

E value	1.0e-55
Match length	108
% identity	100
NCBI Description	(AC007169) putative glyoxalase II [Arabidopsis thaliana]

Seq. No.	149943
Seq. ID	LIB3175-033-P1-K1-G4
Method	BLASTX
NCBI GI	g1246019
BLAST score	635
E value	1.0e-66
Match length	122
% identity	99
NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No.	149944
Seq. ID	LIB3175-033-P1-K1-G6
Method	BLASTN
NCBI GI	g4757678
BLAST score	41
E value	1.0e-13
Match length	267
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	149945
Seq. ID	LIB3175-033-P1-K1-G8
Method	BLASTX
NCBI GI	g4741960
BLAST score	372
E value	8.0e-36
Match length	92
% identity	79
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	149946
Seq. ID	LIB3175-033-P1-K1-H1
Method	BLASTX
NCBI GI	g2369714
BLAST score	548
E value	2.0e-56
Match length	122
% identity	90
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	149947
Seq. ID	LIB3175-033-P1-K1-H10
Method	BLASTX
NCBI GI	g1076303
BLAST score	57
E value	3.0e-54
Match length	114
% identity	57
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis

thaliana]

Seq. No.	149948
Seq. ID	LIB3175-033-P1-K1-H11
Method	BLASTX
NCBI GI	g2911057
BLAST score	566
E value	2.0e-58
Match length	127
% identity	88
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	149949
Seq. ID	LIB3175-033-P1-K1-H12
Method	BLASTX
NCBI GI	g2911057
BLAST score	131
E value	5.0e-19
Match length	95
% identity	52
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	149950
Seq. ID	LIB3175-033-P1-K1-H2
Method	BLASTX
NCBI GI	g2369714
BLAST score	425
E value	6.0e-42
Match length	107
% identity	81
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	149951
Seq. ID	LIB3175-033-P1-K1-H4
Method	BLASTX
NCBI GI	g4263777
BLAST score	522
E value	3.0e-53
Match length	139
% identity	76
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	149952
Seq. ID	LIB3175-033-P1-K1-H5
Method	BLASTX
NCBI GI	g4538963
BLAST score	229
E value	4.0e-19
Match length	84
% identity	58
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	149953
Seq. ID	LIB3175-033-P1-K1-H8
Method	BLASTX
NCBI GI	g115783
BLAST score	595
E value	7.0e-62
Match length	116
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149954
Seq. ID	LIB3175-034-P1-K1-A10
Method	BLASTX
NCBI GI	g1172873
BLAST score	617
E value	2.0e-64
Match length	124
% identity	98
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	149955
Seq. ID	LIB3175-034-P1-K1-A12
Method	BLASTX
NCBI GI	g3128185
BLAST score	462
E value	6.0e-50
Match length	123
% identity	85
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	149956
Seq. ID	LIB3175-034-P1-K1-A2
Method	BLASTX
NCBI GI	g2208903
BLAST score	477
E value	4.0e-48
Match length	94
% identity	93
NCBI Description	(AB004798) ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	149957
Seq. ID	LIB3175-034-P1-K1-A3
Method	BLASTN
NCBI GI	g3250737
BLAST score	133
E value	1.0e-68
Match length	301
% identity	90
NCBI Description	Arabidopsis thaliana ASKbeta gene, complete CDS

Seq. No.	149958
Seq. ID	LIB3175-034-P1-K1-A5
Method	BLASTN
NCBI GI	g4757388
BLAST score	437
E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	149959
Seq. ID	LIB3175-034-P1-K1-A6
Method	BLASTX
NCBI GI	g4220474
BLAST score	196
E value	5.0e-15
Match length	60
% identity	72
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	149960
Seq. ID	LIB3175-034-P1-K1-A7
Method	BLASTX
NCBI GI	g119350
BLAST score	569
E value	6.0e-59
Match length	115
% identity	99
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	149961
Seq. ID	LIB3175-034-P1-K1-A8
Method	BLASTX
NCBI GI	g3183088
BLAST score	214
E value	4.0e-17
Match length	68
% identity	54
NCBI Description	PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer like protein [Vigna unguiculata]

Seq. No.	149962
Seq. ID	LIB3175-034-P1-K1-A9
Method	BLASTN
NCBI GI	g2656028
BLAST score	221

E value	1.0e-121
Match length	326
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	149963
Seq. ID	LIB3175-034-P1-K1-B10
Method	BLASTN
NCBI GI	g4220633
BLAST score	442
E value	0.0e+00
Match length	452
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	149964
Seq. ID	LIB3175-034-P1-K1-B11
Method	BLASTX
NCBI GI	g417103
BLAST score	612
E value	8.0e-64
Match length	122
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	149965
Seq. ID	LIB3175-034-P1-K1-B12
Method	BLASTN
NCBI GI	g3688169
BLAST score	33
E value	5.0e-09
Match length	97
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No. 149966

Seq. ID	LIB3175-034-P1-K1-B4
Method	BLASTN
NCBI GI	g2828186
BLAST score	163
E value	1.0e-86
Match length	336
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	149967
Seq. ID	LIB3175-034-P1-K1-B5
Method	BLASTX
NCBI GI	g2245020
BLAST score	449
E value	1.0e-44
Match length	90
% identity	100
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No.	149968
Seq. ID	LIB3175-034-P1-K1-B6
Method	BLASTX
NCBI GI	g1402904
BLAST score	642
E value	2.0e-67
Match length	125
% identity	99
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	149969
Seq. ID	LIB3175-034-P1-K1-B7
Method	BLASTX
NCBI GI	g115783
BLAST score	558
E value	1.0e-57
Match length	112
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	149970
Seq. ID	LIB3175-034-P1-K1-B8
Method	BLASTX
NCBI GI	g112682
BLAST score	639
E value	6.0e-67
Match length	147
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	149971
Seq. ID	LIB3175-034-P1-K1-B9
Method	BLASTX
NCBI GI	g480450
BLAST score	609
E value	1.0e-63
Match length	119
% identity	99
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	149972
Seq. ID	LIB3175-034-P1-K1-C1
Method	BLASTN
NCBI GI	g2351063
BLAST score	131
E value	8.0e-68
Match length	159
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	149973
Seq. ID	LIB3175-034-P1-K1-C10
Method	BLASTN
NCBI GI	g3128135
BLAST score	250
E value	1.0e-138
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	149974
Seq. ID	LIB3175-034-P1-K1-C11
Method	BLASTN
NCBI GI	g3212846
BLAST score	33
E value	7.0e-09
Match length	401
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	149975
Seq. ID	LIB3175-034-P1-K1-C12
Method	BLASTX
NCBI GI	g4262180
BLAST score	714
E value	9.0e-76
Match length	134
% identity	99
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	149976
Seq. ID	LIB3175-034-P1-K1-C2

Method	BLASTX
NCBI GI	g127041
BLAST score	513
E value	3.0e-52
Match length	98
% identity	100
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	149977
Seq. ID	LIB3175-034-P1-K1-C3
Method	BLASTX
NCBI GI	g3273751
BLAST score	633
E value	3.0e-66
Match length	144
% identity	88
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	149978
Seq. ID	LIB3175-034-P1-K1-C4
Method	BLASTN
NCBI GI	g3299824
BLAST score	182
E value	4.0e-98
Match length	212
% identity	95
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	149979
Seq. ID	LIB3175-034-P1-K1-C5
Method	BLASTX
NCBI GI	g4006893
BLAST score	569
E value	8.0e-59
Match length	111
% identity	97
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	149980
Seq. ID	LIB3175-034-P1-K1-C6
Method	BLASTX
NCBI GI	g4567236
BLAST score	226
E value	6.0e-19
Match length	44
% identity	100
NCBI Description	(AC007119) glycine-rich RNA binding protein Ccr2 [Arabidopsis thaliana]

Seq. No.	149981
Seq. ID	LIB3175-034-P1-K1-C7

Method	BLASTX
NCBI GI	g4689386
BLAST score	166
E value	1.0e-11
Match length	59
% identity	64
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	149982
Seq. ID	LIB3175-034-P1-K1-D10
Method	BLASTX
NCBI GI	g3236246
BLAST score	517
E value	7.0e-53
Match length	101
% identity	93
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	149983
Seq. ID	LIB3175-034-P1-K1-D11
Method	BLASTX
NCBI GI	g4455338
BLAST score	573
E value	2.0e-59
Match length	117
% identity	97
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	149984
Seq. ID	LIB3175-034-P1-K1-D2
Method	BLASTX
NCBI GI	g421836
BLAST score	459
E value	6.0e-46
Match length	93
% identity	100
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No.	149985
Seq. ID	LIB3175-034-P1-K1-D4
Method	BLASTX
NCBI GI	g3367521
BLAST score	194
E value	6.0e-15
Match length	117
% identity	20
NCBI Description	(AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana]

Seq. No.	149986
Seq. ID	LIB3175-034-P1-K1-D5
Method	BLASTX
NCBI GI	g2160133

BLAST score	416
E value	5.0e-41
Match length	96
% identity	89
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	149987
Seq. ID	LIB3175-034-P1-K1-D7
Method	BLASTN
NCBI GI	g2828183
BLAST score	188
E value	1.0e-101
Match length	381
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	149988
Seq. ID	LIB3175-034-P1-K1-D9
Method	BLASTX
NCBI GI	g2541876
BLAST score	300
E value	3.0e-27
Match length	120
% identity	42
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	149989
Seq. ID	LIB3175-034-P1-K1-E11
Method	BLASTX
NCBI GI	g2506443
BLAST score	624
E value	2.0e-65
Match length	127
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	149990
Seq. ID	LIB3175-034-P1-K1-E12
Method	BLASTX
NCBI GI	g1246019
BLAST score	551
E value	9.0e-57
Match length	105
% identity	100

NCBI Description	(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]

Seq. No.	149991
Seq. ID	LIB3175-034-P1-K1-E2
Method	BLASTX
NCBI GI	g1236190
BLAST score	272
E value	6.0e-30
Match length	73
% identity	95
NCBI Description	(U18365) cyclin dependent protein kinase homolog; similar to moth bean p34cdc2 protein, PIR Accession Number JQ2243 [Brassica napus]

Seq. No.	149992
Seq. ID	LIB3175-034-P1-K1-E5
Method	BLASTX
NCBI GI	g1363526
BLAST score	58
E value	4.0e-38
Match length	82
% identity	99
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - maize chloroplast >gi_902251_emb_CAA60315_ (X86563) cytochrome B6 [Zea mays]

Seq. No.	149993
Seq. ID	LIB3175-034-P1-K1-E6
Method	BLASTN
NCBI GI	g972924
BLAST score	197
E value	1.0e-107
Match length	277
% identity	93
NCBI Description	Arabidopsis thaliana IAA11 (IAA11) gene, complete cds

Seq. No.	149994
Seq. ID	LIB3175-034-P1-K1-E8
Method	BLASTX
NCBI GI	g3478700
BLAST score	529
E value	4.0e-54
Match length	118
% identity	87
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	149995
Seq. ID	LIB3175-034-P1-K1-E9
Method	BLASTX
NCBI GI	g3478700
BLAST score	532
E value	2.0e-54
Match length	119
% identity	87
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

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Seq. No.	149996
Seq. ID	LIB3175-034-P1-K1-F10
Method	BLASTX
NCBI GI	g4589398
BLAST score	333
E value	3.0e-31
Match length	74
% identity	80
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	149997
Seq. ID	LIB3175-034-P1-K1-F11
Method	BLASTX
NCBI GI	g3687238
BLAST score	470
E value	2.0e-47
Match length	109
% identity	78
NCBI Description	(AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.	149998
Seq. ID	LIB3175-034-P1-K1-F2
Method	BLASTX
NCBI GI	g3080402
BLAST score	628
E value	1.0e-65
Match length	124
% identity	100
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	149999
Seq. ID	LIB3175-034-P1-K1-F3
Method	BLASTX
NCBI GI	g2130521
BLAST score	513
E value	2.0e-52
Match length	99
% identity	95
NCBI Description	(U31565) reversibly glycosylatable polypeptide [Pisum sativum]

Seq. No.	150000
Seq. ID	LIB3175-034-P1-K1-F5
Method	BLASTX
NCBI GI	g3661595
BLAST score	640
E value	4.0e-67
Match length	126
% identity	98
NCBI Description	(AF091844) aminoalcoholphosphotransferase [Arabidopsis thaliana]

Seq. No.	150001
Seq. ID	LIB3175-034-P1-K1-F6

Method	BLASTX
NCBI GI	g2642432
BLAST score	519
E value	6.0e-53
Match length	138
% identity	80
NCBI Description	(AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]

Seq. No.	150002
Seq. ID	LIB3175-034-P1-K1-F7
Method	BLASTX
NCBI GI	g2351374
BLAST score	557
E value	2.0e-57
Match length	111
% identity	97
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No.	150003
Seq. ID	LIB3175-034-P1-K1-F8
Method	BLASTX
NCBI GI	g3941543
BLAST score	342
E value	4.0e-32
Match length	83
% identity	83
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	150004
Seq. ID	LIB3175-034-P1-K1-G1
Method	BLASTX
NCBI GI	g1619300
BLAST score	390
E value	8.0e-38
Match length	81
% identity	88
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	150005
Seq. ID	LIB3175-034-P1-K1-G10
Method	BLASTN
NCBI GI	g3798730
BLAST score	42
E value	2.0e-14
Match length	42
% identity	100
NCBI Description	Arabidopsis thaliana transgenic line C DNA

Seq. No.	150006
Seq. ID	LIB3175-034-P1-K1-G11
Method	BLASTN
NCBI GI	g2351069
BLAST score	201

E value	1.0e-109
Match length	334
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	150007
Seq. ID	LIB3175-034-P1-K1-G2
Method	BLASTX
NCBI GI	g3121825
BLAST score	549
E value	1.0e-56
Match length	111
% identity	95
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	150008
Seq. ID	LIB3175-034-P1-K1-G3
Method	BLASTX
NCBI GI	g481827
BLAST score	541
E value	2.0e-55
Match length	125
% identity	79
NCBI Description	thioglucosidase (EC 3.2.3.1) - rape >gi_414103_emb_CAA79990_ (Z21978) myrosinase, thioglucoside glucohydrolase [Brassica napus]

Seq. No.	150009
Seq. ID	LIB3175-034-P1-K1-G4
Method	BLASTX
NCBI GI	g3915085
BLAST score	546
E value	3.0e-56
Match length	107
% identity	99
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase [Arabidopsis thaliana]

Seq. No.	150010
Seq. ID	LIB3175-034-P1-K1-G5
Method	BLASTX
NCBI GI	g4582443
BLAST score	430
E value	1.0e-42
Match length	88
% identity	91
NCBI Description	(AC007142) putative auxin-induced protein [Arabidopsis thaliana]

Seq. No.	150011
Seq. ID	LIB3175-034-P1-K1-G6

Method	BLASTX
NCBI GI	g1769905
BLAST score	370
E value	1.0e-35
Match length	102
% identity	71
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	150012
Seq. ID	LIB3175-034-P1-K1-G7
Method	BLASTX
NCBI GI	g2129774
BLAST score	528
E value	6.0e-54
Match length	115
% identity	91
NCBI Description	xyloglucan endotransglycosylase-related protein XTR4 - Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	150013
Seq. ID	LIB3175-034-P1-K1-G8
Method	BLASTX
NCBI GI	g4218127
BLAST score	606
E value	3.0e-63
Match length	127
% identity	94
NCBI Description	(AL035353) myosin heavy chain-like protein (fragment) [Arabidopsis thaliana]

Seq. No.	150014
Seq. ID	LIB3175-034-P1-K1-G9
Method	BLASTX
NCBI GI	g4539335
BLAST score	270
E value	8.0e-24
Match length	75
% identity	59
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	150015
Seq. ID	LIB3175-034-P1-K1-H1
Method	BLASTX
NCBI GI	g126985
BLAST score	619
E value	1.0e-64
Match length	120
% identity	99
NCBI Description	MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis thaliana]

Seq. No.	150016
Seq. ID	LIB3175-034-P1-K1-H10
Method	BLASTX

NCBI GI	g2642450
BLAST score	439
E value	1.0e-43
Match length	81
% identity	99
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	150017
Seq. ID	LIB3175-034-P1-K1-H2
Method	BLASTX
NCBI GI	g3600058
BLAST score	579
E value	5.0e-60
Match length	119
% identity	100
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	150018
Seq. ID	LIB3175-034-P1-K1-H3
Method	BLASTX
NCBI GI	g4567260
BLAST score	574
E value	2.0e-59
Match length	131
% identity	85
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	150019
Seq. ID	LIB3175-034-P1-K1-H4
Method	BLASTX
NCBI GI	g2388574
BLAST score	595
E value	6.0e-62
Match length	118
% identity	98
NCBI Description	(AC000098) Strong similarity to Phalaenopsis homeobox protein (gb_U34743). [Arabidopsis thaliana]

Seq. No.	150020
Seq. ID	LIB3175-034-P1-K1-H5
Method	BLASTX
NCBI GI	g3080400
BLAST score	183
E value	7.0e-33
Match length	81
% identity	91
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana] >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.	150021
Seq. ID	LIB3175-034-P1-K1-H6
Method	BLASTN
NCBI GI	g2914688
BLAST score	90
E value	5.0e-43
Match length	352
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150022
Seq. ID	LIB3175-034-P1-K1-H7
Method	BLASTX
NCBI GI	g3367568
BLAST score	190
E value	2.0e-14
Match length	62
% identity	58
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	150023
Seq. ID	LIB3175-035-P1-K1-A1
Method	BLASTX
NCBI GI	g4490332
BLAST score	634
E value	2.0e-66
Match length	126
% identity	98
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	150024
Seq. ID	LIB3175-035-P1-K1-A10
Method	BLASTX
NCBI GI	g3367568
BLAST score	533
E value	2.0e-54
Match length	117
% identity	87
NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	150025
Seq. ID	LIB3175-035-P1-K1-A12
Method	BLASTN
NCBI GI	g2160132
BLAST score	41
E value	1.0e-13
Match length	103
% identity	48
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	150026
Seq. ID	LIB3175-035-P1-K1-A2
Method	BLASTN

NCBI GI	g3298532
BLAST score	73
E value	6.0e-33
Match length	77
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150027
Seq. ID	LIB3175-035-P1-K1-A3
Method	BLASTX
NCBI GI	g2507092
BLAST score	213
E value	3.0e-17
Match length	47
% identity	94
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_968977 (U29785) NADPH:protochlorophyllide oxidoreductase B [Arabidopsis thaliana] >gi_1583456_prf__2120441B protochlorophyllide oxidoreductase [Arabidopsis thaliana]

Seq. No.	150028
Seq. ID	LIB3175-035-P1-K1-A4
Method	BLASTN
NCBI GI	g2696018
BLAST score	151
E value	3.0e-79
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	150029
Seq. ID	LIB3175-035-P1-K1-A5
Method	BLASTX
NCBI GI	g3522929
BLAST score	111
E value	8.0e-76
Match length	148
% identity	98
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	150030
Seq. ID	LIB3175-035-P1-K1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	596
E value	6.0e-62
Match length	152
% identity	79
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	150031
Seq. ID	LIB3175-035-P1-K1-A7
Method	BLASTN
NCBI GI	g3298532
BLAST score	248
E value	1.0e-137
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150032
Seq. ID	LIB3175-035-P1-K1-A8
Method	BLASTX
NCBI GI	g3355483
BLAST score	314
E value	6.0e-29
Match length	89
% identity	64
NCBI Description	(AC004218) gibberellin-regulated protein (GASA5)-like [Arabidopsis thaliana]

Seq. No.	150033
Seq. ID	LIB3175-035-P1-K1-A9
Method	BLASTX
NCBI GI	g2507092
BLAST score	271
E value	6.0e-24
Match length	58
% identity	97
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_968977 (U29785) NADPH:protochlorophyllide oxidoreductase B [Arabidopsis thaliana] >gi_1583456_prf__2120441B protochlorophyllide oxidoreductase [Arabidopsis thaliana]

Seq. No.	150034
Seq. ID	LIB3175-035-P1-K1-B1
Method	BLASTX
NCBI GI	g119143
BLAST score	205
E value	1.0e-16
Match length	50
% identity	84
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	150035
Seq. ID	LIB3175-035-P1-K1-B10

Method	BLASTN
NCBI GI	g3985954
BLAST score	243
E value	1.0e-134
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No.	150036
Seq. ID	LIB3175-035-P1-K1-B11
Method	BLASTN
NCBI GI	g3128135
BLAST score	443
E value	0.0e+00
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	150037
Seq. ID	LIB3175-035-P1-K1-B12
Method	BLASTN
NCBI GI	g1419473
BLAST score	355
E value	0.0e+00
Match length	454
% identity	93
NCBI Description	A.thaliana chloroplast ndhA gene

Seq. No.	150038
Seq. ID	LIB3175-035-P1-K1-B2
Method	BLASTX
NCBI GI	g3062791
BLAST score	168
E value	1.0e-11
Match length	64
% identity	45
NCBI Description	(AB010433) Lipid transfer protein [Brassica rapa]

Seq. No.	150039
Seq. ID	LIB3175-035-P1-K1-B3
Method	BLASTX
NCBI GI	g4586264
BLAST score	101
E value	7.0e-04
Match length	125
% identity	77
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	150040
Seq. ID	LIB3175-035-P1-K1-B5
Method	BLASTN
NCBI GI	g431257
BLAST score	381
E value	0.0e+00

Match length	449
% identity	97
NCBI Description	Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds

Seq. No.	150041
Seq. ID	LIB3175-035-P1-K1-B6
Method	BLASTX
NCBI GI	g3367592
BLAST score	376
E value	4.0e-36
Match length	121
% identity	70
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	150042
Seq. ID	LIB3175-035-P1-K1-B8
Method	BLASTN
NCBI GI	g4757405
BLAST score	183
E value	2.0e-98
Match length	344
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	150043
Seq. ID	LIB3175-035-P1-K1-B9
Method	BLASTX
NCBI GI	g3123188
BLAST score	676
E value	3.0e-71
Match length	138
% identity	95
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	150044
Seq. ID	LIB3175-035-P1-K1-C10
Method	BLASTX
NCBI GI	g1619602
BLAST score	211
E value	9.0e-17
Match length	116
% identity	38
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	150045
Seq. ID	LIB3175-035-P1-K1-C11
Method	BLASTN
NCBI GI	g4056476
BLAST score	52
E value	3.0e-20
Match length	96
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150046
Seq. ID	LIB3175-035-P1-K1-C12
Method	BLASTN
NCBI GI	g2281081
BLAST score	224
E value	1.0e-123
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150047
Seq. ID	LIB3175-035-P1-K1-C3
Method	BLASTX
NCBI GI	g115385
BLAST score	313
E value	6.0e-29
Match length	84
% identity	76
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150048
Seq. ID	LIB3175-035-P1-K1-C4
Method	BLASTN
NCBI GI	g3659908
BLAST score	227
E value	1.0e-125
Match length	239
% identity	99
NCBI Description	Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds

Seq. No.	150049
Seq. ID	LIB3175-035-P1-K1-C5
Method	BLASTN
NCBI GI	g4325340
BLAST score	247
E value	1.0e-136
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	150050
Seq. ID	LIB3175-035-P1-K1-C7
Method	BLASTN
NCBI GI	g4467094
BLAST score	401
E value	0.0e+00
Match length	454
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	150051

Seq. ID	LIB3175-035-P1-K1-D1
Method	BLASTN
NCBI GI	g3776000
BLAST score	312
E value	1.0e-175
Match length	374
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12

Seq. No.	150052
Seq. ID	LIB3175-035-P1-K1-D10
Method	BLASTX
NCBI GI	g1175395
BLAST score	153
E value	5.0e-10
Match length	105
% identity	31
NCBI Description	HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I >gi_2130413_pir__S58099 hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe) >gi_914880_emb_CAA90460_ (Z50113) unknown [Schizosaccharomyces pombe]

Seq. No.	150053
Seq. ID	LIB3175-035-P1-K1-D11
Method	BLASTX
NCBI GI	g2911057
BLAST score	631
E value	5.0e-66
Match length	123
% identity	100
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	150054
Seq. ID	LIB3175-035-P1-K1-D2
Method	BLASTX
NCBI GI	g4371293
BLAST score	67
E value	6.5e+00
Match length	139
% identity	18
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150055
Seq. ID	LIB3175-035-P1-K1-D3
Method	BLASTN
NCBI GI	g2564049
BLAST score	141
E value	2.0e-73
Match length	253
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	150056
Seq. ID	LIB3175-035-P1-K1-D4

Method	BLASTX
NCBI GI	g4210449
BLAST score	693
E value	3.0e-73
Match length	151
% identity	91
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	150057
Seq. ID	LIB3175-035-P1-K1-D5
Method	BLASTN
NCBI GI	g4733952
BLAST score	433
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	150058
Seq. ID	LIB3175-035-P1-K1-D7
Method	BLASTX
NCBI GI	g4049335
BLAST score	389
E value	9.0e-38
Match length	88
% identity	89
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	150059
Seq. ID	LIB3175-035-P1-K1-D8
Method	BLASTN
NCBI GI	g4337026
BLAST score	48
E value	7.0e-18
Match length	132
% identity	84
NCBI Description	Arabidopsis thaliana MFP2 mRNA, complete cds

Seq. No.	150060
Seq. ID	LIB3175-035-P1-K1-D9
Method	BLASTN
NCBI GI	g3367500
BLAST score	397
E value	0.0e+00
Match length	442
% identity	55
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	150061
Seq. ID	LIB3175-035-P1-K1-E10
Method	BLASTX
NCBI GI	g4587615
BLAST score	479
E value	3.0e-48
Match length	150

% identity	63
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	150062
Seq. ID	LIB3175-035-P1-K1-E11
Method	BLASTX
NCBI GI	g3600055
BLAST score	714
E value	9.0e-76
Match length	134
% identity	100
NCBI Description	(AF080120) contains similarity to Pisum sativum disease resistance response protein 206-d (GB:U11716) [Arabidopsis thaliana]

Seq. No.	150063
Seq. ID	LIB3175-035-P1-K1-E12
Method	BLASTX
NCBI GI	g2864614
BLAST score	238
E value	6.0e-20
Match length	137
% identity	42
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	150064
Seq. ID	LIB3175-035-P1-K1-E2
Method	BLASTX
NCBI GI	g4585981
BLAST score	52
E value	4.0e-29
Match length	134
% identity	75
NCBI Description	(AC005287) similar to Na+/H+-exchanging proteins [Arabidopsis thaliana]

Seq. No.	150065
Seq. ID	LIB3175-035-P1-K1-E3
Method	BLASTX
NCBI GI	g3894172
BLAST score	569
E value	9.0e-59
Match length	109
% identity	100
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	150066
Seq. ID	LIB3175-035-P1-K1-E5
Method	BLASTX
NCBI GI	g4455199
BLAST score	334
E value	3.0e-31
Match length	78
% identity	85

NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	150067
Seq. ID	LIB3175-035-P1-K1-E6
Method	BLASTX
NCBI GI	g1076402
BLAST score	629
E value	7.0e-66
Match length	125
% identity	90
NCBI Description	S-like ribonuclease RNS2 - Arabidopsis thaliana
Seq. No.	150068
Seq. ID	LIB3175-035-P1-K1-E7
Method	BLASTN
NCBI GI	g3869069
BLAST score	77
E value	3.0e-35
Match length	263
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.	150069
Seq. ID	LIB3175-035-P1-K1-E8
Method	BLASTX
NCBI GI	g4531444
BLAST score	773
E value	1.0e-82
Match length	149
% identity	99
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.	150070
Seq. ID	LIB3175-035-P1-K1-E9
Method	BLASTX
NCBI GI	g1418990
BLAST score	391
E value	7.0e-38
Match length	108
% identity	69
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]
Seq. No.	150071
Seq. ID	LIB3175-035-P1-K1-F10
Method	BLASTN
NCBI GI	g4699904
BLAST score	259
E value	1.0e-144
Match length	294
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence
Seq. No.	150072
Seq. ID	LIB3175-035-P1-K1-F11
Method	BLASTN

NCBI GI	g4589411
BLAST score	35
E value	3.0e-10
Match length	83
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	150073
Seq. ID	LIB3175-035-P1-K1-F12
Method	BLASTX
NCBI GI	g4469003
BLAST score	625
E value	3.0e-65
Match length	118
% identity	99
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	150074
Seq. ID	LIB3175-035-P1-K1-F2
Method	BLASTX
NCBI GI	g2244977
BLAST score	580
E value	4.0e-60
Match length	129
% identity	88
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	150075
Seq. ID	LIB3175-035-P1-K1-F3
Method	BLASTX
NCBI GI	g3493611
BLAST score	374
E value	7.0e-36
Match length	118
% identity	62
NCBI Description	(AF068318) regulatory subunit of protein kinase CK2; CK2 beta-subunit [Arabidopsis thaliana]

Seq. No.	150076
Seq. ID	LIB3175-035-P1-K1-F4
Method	BLASTX
NCBI GI	g1708924
BLAST score	310
E value	2.0e-28
Match length	81
% identity	68
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate dehydrogenase (NADP+) [Vitis vinifera]

Seq. No.	150077
Seq. ID	LIB3175-035-P1-K1-F6
Method	BLASTN
NCBI GI	g3063690
BLAST score	418
E value	0.0e+00

Match length	454
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	150078
Seq. ID	LIB3175-035-P1-K1-F7
Method	BLASTN
NCBI GI	g2351064
BLAST score	374
E value	0.0e+00
Match length	386
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	150079
Seq. ID	LIB3175-035-P1-K1-F8
Method	BLASTX
NCBI GI	g3687301
BLAST score	152
E value	6.0e-10
Match length	92
% identity	38
NCBI Description	(AJ006376) subtilisin-like protease [Lycopersicon esculentum] >gi_3687309_emb_CAA07001_ (AJ006380) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	150080
Seq. ID	LIB3175-035-P1-K1-F9
Method	BLASTX
NCBI GI	g1169476
BLAST score	613
E value	6.0e-64
Match length	120
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	150081
Seq. ID	LIB3175-035-P1-K1-G1
Method	BLASTN
NCBI GI	g4589969
BLAST score	170
E value	1.0e-90
Match length	291
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	150082
Seq. ID	LIB3175-035-P1-K1-G10
Method	BLASTX
NCBI GI	g2252844
BLAST score	716
E value	5.0e-76

Match length	128
% identity	100
NCBI Description	(AF013293) belongs to the cytochrome p450 family [Arabidopsis thaliana]

Seq. No.	150083
Seq. ID	LIB3175-035-P1-K1-G11
Method	BLASTN
NCBI GI	g3241922
BLAST score	276
E value	1.0e-154
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	150084
Seq. ID	LIB3175-035-P1-K1-G12
Method	BLASTX
NCBI GI	g1076393
BLAST score	607
E value	3.0e-63
Match length	125
% identity	98
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	150085
Seq. ID	LIB3175-035-P1-K1-G2
Method	BLASTN
NCBI GI	g4159703
BLAST score	162
E value	7.0e-86
Match length	427
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	150086
Seq. ID	LIB3175-035-P1-K1-G3
Method	BLASTX
NCBI GI	g4539389
BLAST score	373
E value	9.0e-36
Match length	76
% identity	100
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No.	150087
Seq. ID	LIB3175-035-P1-K1-G5
Method	BLASTX
NCBI GI	g4455354
BLAST score	264
E value	5.0e-23
Match length	117
% identity	53

NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	150088
Seq. ID	LIB3175-035-P1-K1-G8
Method	BLASTX
NCBI GI	g4376815
BLAST score	166
E value	2.0e-11
Match length	118
% identity	32
NCBI Description	(AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia pneumoniae]

Seq. No.	150089
Seq. ID	LIB3175-035-P1-K1-G9
Method	BLASTX
NCBI GI	g120667
BLAST score	453
E value	3.0e-45
Match length	89
% identity	98
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	150090
Seq. ID	LIB3175-035-P1-K1-H1
Method	BLASTX
NCBI GI	g939726
BLAST score	507
E value	1.0e-51
Match length	113
% identity	87
NCBI Description	(U31370) cyclophilin [Arabidopsis thaliana]

Seq. No.	150091
Seq. ID	LIB3175-035-P1-K1-H10
Method	BLASTX
NCBI GI	g1170606
BLAST score	427
E value	4.0e-42
Match length	148
% identity	54
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	150092

Seq. ID	LIB3175-035-P1-K1-H11
Method	BLASTN
NCBI GI	g3449333
BLAST score	236
E value	1.0e-130
Match length	414
% identity	46
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]

Seq. No.	150093
Seq. ID	LIB3175-035-P1-K1-H12
Method	BLASTX
NCBI GI	g4581114
BLAST score	268
E value	2.0e-23
Match length	98
% identity	58
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	150094
Seq. ID	LIB3175-035-P1-K1-H2
Method	BLASTX
NCBI GI	g3286693
BLAST score	597
E value	4.0e-62
Match length	124
% identity	96
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	150095
Seq. ID	LIB3175-035-P1-K1-H4
Method	BLASTX
NCBI GI	g2160133
BLAST score	409
E value	6.0e-40
Match length	141
% identity	62
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	150096
Seq. ID	LIB3175-035-P1-K1-H5
Method	BLASTN
NCBI GI	g3449325
BLAST score	370
E value	0.0e+00
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	150097
Seq. ID	LIB3175-035-P1-K1-H6
Method	BLASTX
NCBI GI	g4417280
BLAST score	746
E value	2.0e-79
Match length	152
% identity	99
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	150098
Seq. ID	LIB3175-035-P1-K1-H7
Method	BLASTN
NCBI GI	g2656025
BLAST score	409
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	150099
Seq. ID	LIB3175-035-P1-K1-H9
Method	BLASTX
NCBI GI	g120675
BLAST score	547
E value	4.0e-56
Match length	129
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	150100
Seq. ID	LIB3175-036-P1-K1-A1
Method	BLASTX
NCBI GI	g3318611
BLAST score	210
E value	1.0e-16
Match length	52
% identity	79
NCBI Description	(AB016063) mitochondrial phosphate transporter [Glycine max]

Seq. No.	150101
Seq. ID	LIB3175-036-P1-K1-A11
Method	BLASTX
NCBI GI	g2864617
BLAST score	290
E value	2.0e-45
Match length	127
% identity	81
NCBI Description	(AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No.	150102
Seq. ID	LIB3175-036-P1-K1-A2
Method	BLASTX
NCBI GI	g2829870
BLAST score	684
E value	3.0e-72
Match length	156
% identity	86
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	150103
Seq. ID	LIB3175-036-P1-K1-A4
Method	BLASTX
NCBI GI	g1169201
BLAST score	522
E value	3.0e-53
Match length	135
% identity	80
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	150104
Seq. ID	LIB3175-036-P1-K1-A5
Method	BLASTX
NCBI GI	g1169201
BLAST score	270
E value	7.0e-24
Match length	86
% identity	66
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	150105
Seq. ID	LIB3175-036-P1-K1-B10
Method	BLASTX
NCBI GI	g3107903
BLAST score	257
E value	3.0e-22
Match length	84
% identity	55
NCBI Description	(D83719) polycomb-like protein [Daucus carota]

Seq. No.	150106
Seq. ID	LIB3175-036-P1-K1-B11
Method	BLASTX
NCBI GI	g1170767
BLAST score	264
E value	4.0e-23
Match length	112
% identity	53
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN) >gi_626074_pir__S45176 transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) >gi_406051 (U02280) Let1 [Schizosaccharomyces pombe] >gi_4106689_emb_CAA22628_ (AL035065) 26s protease

regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No.	150107
Seq. ID	LIB3175-036-P1-K1-B12
Method	BLASTX
NCBI GI	g3157931
BLAST score	550
E value	1.0e-56
Match length	125
% identity	90
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	150108
Seq. ID	LIB3175-036-P1-K1-B2
Method	BLASTX
NCBI GI	g130708
BLAST score	274
E value	5.0e-24
Match length	55
% identity	89
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_81693_pir__S12985 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - rape (fragment) >gi_17846_emb_CAA40686_ (X57438) phosphatase 1 catalytic subunit [Brassica napus]

Seq. No.	150109
Seq. ID	LIB3175-036-P1-K1-B3
Method	BLASTX
NCBI GI	g3164140
BLAST score	385
E value	7.0e-42
Match length	152
% identity	59
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	150110
Seq. ID	LIB3175-036-P1-K1-B4
Method	BLASTN
NCBI GI	g4220640
BLAST score	282
E value	1.0e-157
Match length	418
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	150111
Seq. ID	LIB3175-036-P1-K1-B6
Method	BLASTX
NCBI GI	g1402908
BLAST score	536
E value	6.0e-55

Match length	127
% identity	83
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	150112
Seq. ID	LIB3175-036-P1-K1-B7
Method	BLASTX
NCBI GI	g2246621
BLAST score	246
E value	2.0e-60
Match length	130
% identity	96
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	150113
Seq. ID	LIB3175-036-P1-K1-C1
Method	BLASTX
NCBI GI	g2842490
BLAST score	448
E value	1.0e-44
Match length	87
% identity	97
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	150114
Seq. ID	LIB3175-036-P1-K1-C10
Method	BLASTN
NCBI GI	g3860243
BLAST score	37
E value	3.0e-11
Match length	117
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150115
Seq. ID	LIB3175-036-P1-K1-C11
Method	BLASTX
NCBI GI	g4455329
BLAST score	693
E value	2.0e-73
Match length	142
% identity	99
NCBI Description	(AL035525) lysine-ketoglutarate reductase/saccharopine [Arabidopsis thaliana]

Seq. No.	150116
Seq. ID	LIB3175-036-P1-K1-C12
Method	BLASTN
NCBI GI	g4455262
BLAST score	229
E value	1.0e-126
Match length	395

% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	150117
Seq. ID	LIB3175-036-P1-K1-C3
Method	BLASTX
NCBI GI	g1353352
BLAST score	342
E value	4.0e-32
Match length	100
% identity	71
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	150118
Seq. ID	LIB3175-036-P1-K1-C5
Method	BLASTX
NCBI GI	g1169201
BLAST score	385
E value	3.0e-37
Match length	112
% identity	73
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	150119
Seq. ID	LIB3175-036-P1-K1-C6
Method	BLASTX
NCBI GI	g3461848
BLAST score	163
E value	3.0e-11
Match length	62
% identity	65
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	150120
Seq. ID	LIB3175-036-P1-K1-C7
Method	BLASTX
NCBI GI	g4586047
BLAST score	334
E value	4.0e-31
Match length	146
% identity	53
NCBI Description	(AC007020) putative ferritin protein [Arabidopsis thaliana] >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279) hypothetical ferritin subunit [Arabidopsis thaliana]

Seq. No.	150121
Seq. ID	LIB3175-036-P1-K1-C8
Method	BLASTN
NCBI GI	g3337347
BLAST score	146
E value	2.0e-76
Match length	434
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150122
Seq. ID	LIB3175-036-P1-K1-D1
Method	BLASTX
NCBI GI	g1084335
BLAST score	318
E value	2.0e-48
Match length	102
% identity	96
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	150123
Seq. ID	LIB3175-036-P1-K1-D11
Method	BLASTX
NCBI GI	g2829891
BLAST score	550
E value	1.0e-56
Match length	118
% identity	91
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	150124
Seq. ID	LIB3175-036-P1-K1-D12
Method	BLASTN
NCBI GI	g3860243
BLAST score	184
E value	5.0e-99
Match length	394
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150125
Seq. ID	LIB3175-036-P1-K1-D5
Method	BLASTN
NCBI GI	g166695
BLAST score	92
E value	2.0e-44
Match length	252
% identity	84
NCBI Description	Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT112) mRNA, complete cds

Seq. No.	150126
Seq. ID	LIB3175-036-P1-K1-D8
Method	BLASTX
NCBI GI	g3461848
BLAST score	200
E value	2.0e-15
Match length	89
% identity	56
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	150127
Seq. ID	LIB3175-036-P1-K1-E1
Method	BLASTX
NCBI GI	g1402877
BLAST score	502
E value	3.0e-56
Match length	154
% identity	79
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis thaliana]

Seq. No.	150128
Seq. ID	LIB3175-036-P1-K1-E10
Method	BLASTX
NCBI GI	g132074
BLAST score	497
E value	2.0e-50
Match length	97
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	150129
Seq. ID	LIB3175-036-P1-K1-E11
Method	BLASTN
NCBI GI	g2645198
BLAST score	103
E value	9.0e-51
Match length	367
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150130
Seq. ID	LIB3175-036-P1-K1-E12
Method	BLASTN
NCBI GI	g2335089
BLAST score	107
E value	4.0e-53
Match length	379
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150131
Seq. ID	LIB3175-036-P1-K1-E2
Method	BLASTX
NCBI GI	g4006890
BLAST score	368
E value	2.0e-40
Match length	91
% identity	97
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	150132
Seq. ID	LIB3175-036-P1-K1-E3
Method	BLASTX
NCBI GI	g417103
BLAST score	417
E value	2.0e-58
Match length	131
% identity	96
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	150133
Seq. ID	LIB3175-036-P1-K1-E4
Method	BLASTX
NCBI GI	g2911057
BLAST score	469
E value	5.0e-47
Match length	115
% identity	85
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	150134
Seq. ID	LIB3175-036-P1-K1-E5
Method	BLASTX
NCBI GI	g2911057
BLAST score	51
E value	4.0e-13
Match length	75
% identity	59
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	150135
Seq. ID	LIB3175-036-P1-K1-E6
Method	BLASTX
NCBI GI	g1755162
BLAST score	683
E value	3.0e-80

Match length	156
% identity	94
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	150136
Seq. ID	LIB3175-036-P1-K1-E7
Method	BLASTX
NCBI GI	g1363488
BLAST score	369
E value	3.0e-43
Match length	102
% identity	94
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	150137
Seq. ID	LIB3175-036-P1-K1-E9
Method	BLASTX
NCBI GI	g114335
BLAST score	729
E value	2.0e-77
Match length	148
% identity	97
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	150138
Seq. ID	LIB3175-036-P1-K1-F1
Method	BLASTX
NCBI GI	g112681
BLAST score	587
E value	9.0e-65
Match length	135
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	150139
Seq. ID	LIB3175-036-P1-K1-F10
Method	BLASTN
NCBI GI	g3927822
BLAST score	46
E value	9.0e-17
Match length	70
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150140
Seq. ID	LIB3175-036-P1-K1-F12

Method	BLASTN
NCBI GI	g4455262
BLAST score	82
E value	3.0e-38
Match length	214
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	150141
Seq. ID	LIB3175-036-P1-K1-F2
Method	BLASTX
NCBI GI	g1362007
BLAST score	743
E value	3.0e-79
Match length	140
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	150142
Seq. ID	LIB3175-036-P1-K1-F4
Method	BLASTX
NCBI GI	g4741948
BLAST score	614
E value	4.0e-64
Match length	116
% identity	99
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	150143
Seq. ID	LIB3175-036-P1-K1-F7
Method	BLASTX
NCBI GI	g3158376
BLAST score	75
E value	2.0e-61
Match length	127
% identity	94
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	150144
Seq. ID	LIB3175-036-P1-K1-G1
Method	BLASTN
NCBI GI	g4191771
BLAST score	184
E value	5.0e-99
Match length	463
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150145
Seq. ID	LIB3175-036-P1-K1-G10
Method	BLASTX
NCBI GI	g2829892
BLAST score	829

E value	3.0e-89
Match length	157
% identity	99
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	150146
Seq. ID	LIB3175-036-P1-K1-G12
Method	BLASTX
NCBI GI	g1429209
BLAST score	617
E value	2.0e-64
Match length	121
% identity	99
NCBI Description	(X99111) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	150147
Seq. ID	LIB3175-036-P1-K1-G2
Method	BLASTX
NCBI GI	g131770
BLAST score	355
E value	6.0e-37
Match length	119
% identity	58
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	150148
Seq. ID	LIB3175-036-P1-K1-G3
Method	BLASTX
NCBI GI	g4262156
BLAST score	360
E value	1.0e-48
Match length	126
% identity	88
NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]

Seq. No.	150149
Seq. ID	LIB3175-036-P1-K1-G8
Method	BLASTN
NCBI GI	g3341671
BLAST score	215
E value	1.0e-117
Match length	271
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150150
Seq. ID	LIB3175-036-P1-K1-H10
Method	BLASTX
NCBI GI	g2464913
BLAST score	591
E value	3.0e-61

Match length	120
% identity	99
NCBI Description	(Z99708) sugar transporter like protein [Arabidopsis thaliana]

Seq. No.	150151
Seq. ID	LIB3175-036-P1-K1-H12
Method	BLASTN
NCBI GI	g4455262
BLAST score	46
E value	8.0e-17
Match length	288
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	150152
Seq. ID	LIB3175-036-P1-K1-H2
Method	BLASTX
NCBI GI	g4406767
BLAST score	224
E value	3.0e-60
Match length	121
% identity	98
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	150153
Seq. ID	LIB3175-036-P1-K1-H3
Method	BLASTX
NCBI GI	g1707013
BLAST score	216
E value	2.0e-17
Match length	100
% identity	44
NCBI Description	(U78721) Brassica napus hypothetical protein 2 isolog [Arabidopsis thaliana]

Seq. No.	150154
Seq. ID	LIB3175-036-P1-K1-H5
Method	BLASTX
NCBI GI	g4567283
BLAST score	452
E value	4.0e-45
Match length	112
% identity	82
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	150155
Seq. ID	LIB3175-036-P1-K1-H6
Method	BLASTX
NCBI GI	g3157937
BLAST score	333
E value	2.0e-31
Match length	75
% identity	87
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036

from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	150156
Seq. ID	LIB3175-036-P1-K1-H7
Method	BLASTN
NCBI GI	g2618602
BLAST score	152
E value	6.0e-80
Match length	391
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	150157
Seq. ID	LIB3175-036-P1-K1-H9
Method	BLASTX
NCBI GI	g4337175
BLAST score	672
E value	4.0e-72
Match length	140
% identity	98
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	150158
Seq. ID	LIB3175-037-P1-K1-A10
Method	BLASTX
NCBI GI	g4510345
BLAST score	436
E value	5.0e-43
Match length	90
% identity	97
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	150159
Seq. ID	LIB3175-037-P1-K1-A11
Method	BLASTN
NCBI GI	g2924257
BLAST score	329
E value	0.0e+00
Match length	398
% identity	48
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	150160
Seq. ID	LIB3175-037-P1-K1-A12
Method	BLASTX
NCBI GI	g4249382
BLAST score	268
E value	1.0e-23
Match length	73
% identity	67

NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	150161
Seq. ID	LIB3175-037-P1-K1-A4
Method	BLASTX
NCBI GI	g3004557
BLAST score	113
E value	3.0e-15
Match length	64
% identity	86
NCBI Description	(AC003673) plasma membrane proton pump H+ ATPase, PMA1 [Arabidopsis thaliana]

Seq. No.	150162
Seq. ID	LIB3175-037-P1-K1-A5
Method	BLASTX
NCBI GI	g2338712
BLAST score	262
E value	8.0e-23
Match length	69
% identity	74
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	150163
Seq. ID	LIB3175-037-P1-K1-A9
Method	BLASTN
NCBI GI	g2618602
BLAST score	235
E value	1.0e-129
Match length	383
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	150164
Seq. ID	LIB3175-037-P1-K1-B1
Method	BLASTN
NCBI GI	g1657616
BLAST score	99
E value	2.0e-48
Match length	245
% identity	85
NCBI Description	Arabidopsis thaliana putative nuclear DNA-binding protein G2p (AtG2) mRNA, complete cds

Seq. No.	150165
Seq. ID	LIB3175-037-P1-K1-B11
Method	BLASTN
NCBI GI	g4512690
BLAST score	198
E value	1.0e-107
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic

sequence, complete sequence

Seq. No.	150166
Seq. ID	LIB3175-037-P1-K1-B12
Method	BLASTX
NCBI GI	g3236238
BLAST score	632
E value	3.0e-66
Match length	122
% identity	98
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	150167
Seq. ID	LIB3175-037-P1-K1-C1
Method	BLASTX
NCBI GI	g4559332
BLAST score	322
E value	7.0e-30
Match length	66
% identity	98
NCBI Description	(AC007087) putative phosphoenolpyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	150168
Seq. ID	LIB3175-037-P1-K1-C11
Method	BLASTN
NCBI GI	g405130
BLAST score	234
E value	1.0e-129
Match length	314
% identity	94
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	150169
Seq. ID	LIB3175-037-P1-K1-C12
Method	BLASTX
NCBI GI	g1755162
BLAST score	565
E value	2.0e-58
Match length	112
% identity	96
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	150170
Seq. ID	LIB3175-037-P1-K1-C3
Method	BLASTX
NCBI GI	g3482931
BLAST score	539
E value	2.0e-55
Match length	115
% identity	93
NCBI Description	(AC003970) germin-like protein [Arabidopsis thaliana]

Seq. No.	150171

Seq. ID	LIB3175-037-P1-K1-C6
Method	BLASTX
NCBI GI	g1170939
BLAST score	353
E value	1.0e-33
Match length	70
% identity	96
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	150172
Seq. ID	LIB3175-037-P1-K1-C7
Method	BLASTX
NCBI GI	g548653
BLAST score	425
E value	5.0e-42
Match length	104
% identity	85
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	150173
Seq. ID	LIB3175-037-P1-K1-C8
Method	BLASTX
NCBI GI	g1705998
BLAST score	345
E value	2.0e-32
Match length	120
% identity	60
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_1082254_pir__A55136 beta-coat protein - human (fragment) >gi_620110_emb_CAA57622_ (X82103) beta-Coat protein [Homo sapiens]

Seq. No.	150174
Seq. ID	LIB3175-037-P1-K1-C9
Method	BLASTX
NCBI GI	g3851636
BLAST score	397
E value	1.0e-38
Match length	103
% identity	71
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	150175
Seq. ID	LIB3175-037-P1-K1-D1
Method	BLASTX
NCBI GI	g1086252
BLAST score	173
E value	2.0e-12

Match length	63
% identity	54
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	150176
Seq. ID	LIB3175-037-P1-K1-D10
Method	BLASTX
NCBI GI	g4006881
BLAST score	43
E value	6.0e-51
Match length	116
% identity	67
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	150177
Seq. ID	LIB3175-037-P1-K1-D11
Method	BLASTN
NCBI GI	g3650026
BLAST score	277
E value	1.0e-154
Match length	380
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150178
Seq. ID	LIB3175-037-P1-K1-D12
Method	BLASTX
NCBI GI	g2909783
BLAST score	584
E value	1.0e-60
Match length	125
% identity	93
NCBI Description	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	150179
Seq. ID	LIB3175-037-P1-K1-D2
Method	BLASTN
NCBI GI	g4581138
BLAST score	322
E value	0.0e+00
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	150180
Seq. ID	LIB3175-037-P1-K1-D3
Method	BLASTN
NCBI GI	g3985950
BLAST score	261
E value	1.0e-145
Match length	362

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]

Seq. No.	150181
Seq. ID	LIB3175-037-P1-K1-D4
Method	BLASTX
NCBI GI	g1170089
BLAST score	609
E value	5.0e-64
Match length	132
% identity	96
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	150182
Seq. ID	LIB3175-037-P1-K1-D5
Method	BLASTX
NCBI GI	g3914917
BLAST score	333
E value	3.0e-31
Match length	64
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S3A

Seq. No.	150183
Seq. ID	LIB3175-037-P1-K1-D6
Method	BLASTN
NCBI GI	g3242970
BLAST score	198
E value	1.0e-107
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	150184
Seq. ID	LIB3175-037-P1-K1-D7
Method	BLASTN
NCBI GI	g2244788
BLAST score	75
E value	5.0e-34
Match length	236
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150185
Seq. ID	LIB3175-037-P1-K1-E1
Method	BLASTN
NCBI GI	g4589419
BLAST score	174
E value	5.0e-93

Match length	433
% identity	53
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	150186
Seq. ID	LIB3175-037-P1-K1-E10
Method	BLASTX
NCBI GI	g3169172
BLAST score	452
E value	4.0e-45
Match length	122
% identity	70
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445214 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	150187
Seq. ID	LIB3175-037-P1-K1-E12
Method	BLASTX
NCBI GI	g3885343
BLAST score	249
E value	3.0e-21
Match length	119
% identity	39
NCBI Description	(AC005623) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150188
Seq. ID	LIB3175-037-P1-K1-E2
Method	BLASTX
NCBI GI	g2664210
BLAST score	121
E value	3.0e-70
Match length	138
% identity	93
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	150189
Seq. ID	LIB3175-037-P1-K1-E5
Method	BLASTX
NCBI GI	g115783
BLAST score	527
E value	5.0e-54
Match length	104
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150190
Seq. ID	LIB3175-037-P1-K1-E6
Method	BLASTX
NCBI GI	g4580460
BLAST score	392
E value	3.0e-38

Match length	100
% identity	81
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	150191
Seq. ID	LIB3175-037-P1-K1-E8
Method	BLASTX
NCBI GI	g462579
BLAST score	337
E value	2.0e-31
Match length	93
% identity	74
NCBI Description	MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR (NADP-MDH) >gi_481222_pir__S38346 malate dehydrogenase (NADP+) (EC 1.1.1.82) - garden pea >gi_397475_emb_CAA52614_ (X74507) malate dehydrogenase (NADP+) [Pisum sativum]

Seq. No.	150192
Seq. ID	LIB3175-037-P1-K1-E9
Method	BLASTX
NCBI GI	g4544399
BLAST score	318
E value	3.0e-29
Match length	123
% identity	46
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	150193
Seq. ID	LIB3175-037-P1-K1-F1
Method	BLASTN
NCBI GI	g3420042
BLAST score	139
E value	4.0e-72
Match length	458
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150194
Seq. ID	LIB3175-037-P1-K1-F10
Method	BLASTX
NCBI GI	g2829899
BLAST score	399
E value	7.0e-39
Match length	115
% identity	65
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	150195
Seq. ID	LIB3175-037-P1-K1-F11
Method	BLASTN
NCBI GI	g2351069
BLAST score	309

E value	1.0e-173
Match length	361
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	150196
Seq. ID	LIB3175-037-P1-K1-F12
Method	BLASTX
NCBI GI	g2961356
BLAST score	637
E value	1.0e-66
Match length	135
% identity	90
NCBI Description	(AL022140) alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	150197
Seq. ID	LIB3175-037-P1-K1-F2
Method	BLASTN
NCBI GI	g2062153
BLAST score	272
E value	1.0e-151
Match length	371
% identity	97
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150198
Seq. ID	LIB3175-037-P1-K1-F3
Method	BLASTX
NCBI GI	g3859536
BLAST score	371
E value	4.0e-36
Match length	74
% identity	93
NCBI Description	(AF095453) asparagine synthetase [Arabidopsis thaliana]

Seq. No.	150199
Seq. ID	LIB3175-037-P1-K1-F4
Method	BLASTX
NCBI GI	g4741940
BLAST score	242
E value	1.0e-20
Match length	72
% identity	69
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	150200
Seq. ID	LIB3175-037-P1-K1-F5
Method	BLASTX
NCBI GI	g4204277
BLAST score	233
E value	1.0e-19
Match length	79
% identity	61
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	150201
Seq. ID	LIB3175-037-P1-K1-F6
Method	BLASTX
NCBI GI	g4490292
BLAST score	622
E value	5.0e-65
Match length	123
% identity	99
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	150202
Seq. ID	LIB3175-037-P1-K1-F8
Method	BLASTN
NCBI GI	g4063737
BLAST score	290
E value	1.0e-162
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150203
Seq. ID	LIB3175-037-P1-K1-F9
Method	BLASTN
NCBI GI	g2832611
BLAST score	295
E value	1.0e-165
Match length	327
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	150204
Seq. ID	LIB3175-037-P1-K1-G10
Method	BLASTX
NCBI GI	g2244828
BLAST score	472
E value	3.0e-50
Match length	114
% identity	100
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150205
Seq. ID	LIB3175-037-P1-K1-G11
Method	BLASTN
NCBI GI	g2244991
BLAST score	331
E value	0.0e+00
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150206
Seq. ID	LIB3175-037-P1-K1-G12
Method	BLASTX

NCBI GI	g3548801
BLAST score	210
E value	9.0e-17
Match length	119
% identity	35
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	150207
Seq. ID	LIB3175-037-P1-K1-G2
Method	BLASTX
NCBI GI	g2506031
BLAST score	636
E value	1.0e-66
Match length	131
% identity	95
NCBI Description	(D43962) homeodomein containing protein 1 [Arabidopsis thaliana] >gi_3858938_emb_CAA16585.1_ (AL021636) homeodomain containing protein 1 [Arabidopsis thaliana]

Seq. No.	150208
Seq. ID	LIB3175-037-P1-K1-G4
Method	BLASTX
NCBI GI	g625977
BLAST score	607
E value	3.0e-63
Match length	118
% identity	99
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	150209
Seq. ID	LIB3175-037-P1-K1-G5
Method	BLASTX
NCBI GI	g4678261
BLAST score	61
E value	9.0e-54
Match length	124
% identity	94
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	150210
Seq. ID	LIB3175-037-P1-K1-G6
Method	BLASTN
NCBI GI	g3641835
BLAST score	184
E value	3.0e-99
Match length	235
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	150211
Seq. ID	LIB3175-037-P1-K1-G7

Method	BLASTN
NCBI GI	g3510343
BLAST score	376
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	150212
Seq. ID	LIB3175-037-P1-K1-H1
Method	BLASTX
NCBI GI	g2760606
BLAST score	514
E value	3.0e-52
Match length	99
% identity	99
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	150213
Seq. ID	LIB3175-037-P1-K1-H10
Method	BLASTX
NCBI GI	g3298542
BLAST score	133
E value	6.0e-15
Match length	84
% identity	55
NCBI Description	(AC004681) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	150214
Seq. ID	LIB3175-037-P1-K1-H11
Method	BLASTN
NCBI GI	g4585891
BLAST score	211
E value	1.0e-115
Match length	258
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	150215
Seq. ID	LIB3175-037-P1-K1-H12
Method	BLASTN
NCBI GI	g4063756
BLAST score	112
E value	1.0e-56
Match length	150
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150216
Seq. ID	LIB3175-037-P1-K1-H3
Method	BLASTX
NCBI GI	g4586576
BLAST score	235
E value	3.0e-20
Match length	63
% identity	68
NCBI Description	(AB024992) multidrug resistance protein [Cicer arietinum]

Seq. No.	150217
Seq. ID	LIB3175-037-P1-K1-H4
Method	BLASTN
NCBI GI	g3550981
BLAST score	77
E value	3.0e-35
Match length	268
% identity	100
NCBI Description	Arabidopsis thaliana mutM homologue gene, complete cds

Seq. No.	150218
Seq. ID	LIB3175-037-P1-K1-H5
Method	BLASTN
NCBI GI	g2760172
BLAST score	297
E value	1.0e-166
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	150219
Seq. ID	LIB3175-037-P1-K1-H6
Method	BLASTX
NCBI GI	g2565036
BLAST score	227
E value	6.0e-19
Match length	75
% identity	53
NCBI Description	(U75921) APC binding protein EB1 [Rattus norvegicus]

Seq. No.	150220
Seq. ID	LIB3175-037-P1-K1-H9
Method	BLASTX
NCBI GI	g2645971
BLAST score	533
E value	1.0e-54
Match length	116
% identity	83
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	150221
Seq. ID	LIB3175-038-P1-K1-A1
Method	BLASTX
NCBI GI	g4539316
BLAST score	457

E value	8.0e-46
Match length	96
% identity	98
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	150222
Seq. ID	LIB3175-038-P1-K1-A10
Method	BLASTN
NCBI GI	g4558656
BLAST score	248
E value	1.0e-137
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T10F5 genomic sequence, complete sequence

Seq. No.	150223
Seq. ID	LIB3175-038-P1-K1-A11
Method	BLASTN
NCBI GI	g16726
BLAST score	38
E value	1.0e-11
Match length	98
% identity	91
NCBI Description	ATTS0156 Gif-SeedA+B Arabidopsis thaliana cDNA clone YAP007T, mRNA sequence [Arabidopsis thaliana] >gi_1107498_emb_X91953_ATORF007 A.thaliana mRNA for unknown protein (clone YAP007)

Seq. No.	150224
Seq. ID	LIB3175-038-P1-K1-A12
Method	BLASTN
NCBI GI	g4220641
BLAST score	48
E value	3.0e-18
Match length	157
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	150225
Seq. ID	LIB3175-038-P1-K1-A2
Method	BLASTX
NCBI GI	g2454184
BLAST score	305
E value	4.0e-28
Match length	76
% identity	86
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	150226
Seq. ID	LIB3175-038-P1-K1-A5
Method	BLASTX
NCBI GI	g3170525
BLAST score	378

E value	2.0e-36
Match length	125
% identity	55
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	150227
Seq. ID	LIB3175-038-P1-K1-A6
Method	BLASTX
NCBI GI	g2688824
BLAST score	322
E value	9.0e-30
Match length	134
% identity	57
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	150228
Seq. ID	LIB3175-038-P1-K1-A7
Method	BLASTN
NCBI GI	g3510343
BLAST score	258
E value	1.0e-143
Match length	486
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	150229
Seq. ID	LIB3175-038-P1-K1-A8
Method	BLASTN
NCBI GI	g4406805
BLAST score	297
E value	1.0e-166
Match length	466
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150230
Seq. ID	LIB3175-038-P1-K1-A9
Method	BLASTX
NCBI GI	g1345655
BLAST score	369
E value	7.0e-44
Match length	126
% identity	75
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	150231
Seq. ID	LIB3175-038-P1-K1-B1
Method	BLASTN
NCBI GI	g2827513
BLAST score	270
E value	1.0e-150
Match length	286

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	150232
Seq. ID	LIB3175-038-P1-K1-B10
Method	BLASTX
NCBI GI	g2062161
BLAST score	642
E value	2.0e-67
Match length	133
% identity	46
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	150233
Seq. ID	LIB3175-038-P1-K1-B12
Method	BLASTN
NCBI GI	g402551
BLAST score	179
E value	5.0e-96
Match length	191
% identity	99
NCBI Description	A.thaliana gene for acetohydroxy acid isomeroreductase

Seq. No.	150234
Seq. ID	LIB3175-038-P1-K1-B4
Method	BLASTN
NCBI GI	g1931636
BLAST score	244
E value	1.0e-135
Match length	340
% identity	99
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	150235
Seq. ID	LIB3175-038-P1-K1-B5
Method	BLASTX
NCBI GI	g544425
BLAST score	292
E value	1.0e-26
Match length	59
% identity	98
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	150236
Seq. ID	LIB3175-038-P1-K1-B7
Method	BLASTN
NCBI GI	g4585952
BLAST score	433
E value	0.0e+00
Match length	433

% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	150237
Seq. ID	LIB3175-038-P1-K1-B8
Method	BLASTX
NCBI GI	g3335357
BLAST score	748
E value	1.0e-79
Match length	140
% identity	97
NCBI Description	(AC003028) putative diphenol oxidase [Arabidopsis thaliana]

Seq. No.	150238
Seq. ID	LIB3175-038-P1-K1-B9
Method	BLASTX
NCBI GI	g3927831
BLAST score	602
E value	3.0e-80
Match length	154
% identity	46
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	150239
Seq. ID	LIB3175-038-P1-K1-C1
Method	BLASTN
NCBI GI	g3510347
BLAST score	155
E value	1.0e-81
Match length	480
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	150240
Seq. ID	LIB3175-038-P1-K1-C10
Method	BLASTN
NCBI GI	g3702731
BLAST score	178
E value	2.0e-95
Match length	480
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	150241
Seq. ID	LIB3175-038-P1-K1-C11
Method	BLASTX
NCBI GI	g4507433
BLAST score	220
E value	8.0e-18
Match length	124
% identity	40
NCBI Description	testis enhanced gene transcript >gi_1729891_sp_P55061_TEGT_HUMAN TEGT PROTEIN (TESTIS

ENHANCED GENE TRANSCRIPT) >gi_2136254_pir__I38334 TEGT (testis enhanced gene transcript) - human >gi_458545_emb_CAA53472_ (X75861) TEGT [Homo sapiens]

Seq. No.	150242
Seq. ID	LIB3175-038-P1-K1-C12
Method	BLASTX
NCBI GI	g3929364
BLAST score	280
E value	6.0e-25
Match length	64
% identity	86
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	150243
Seq. ID	LIB3175-038-P1-K1-C2
Method	BLASTN
NCBI GI	g3510347
BLAST score	115
E value	8.0e-58
Match length	338
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	150244
Seq. ID	LIB3175-038-P1-K1-C4
Method	BLASTN
NCBI GI	g2564214
BLAST score	393
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for glycyl-tRNA synthetase

Seq. No.	150245
Seq. ID	LIB3175-038-P1-K1-C5
Method	BLASTX
NCBI GI	g4586265
BLAST score	572
E value	4.0e-59
Match length	153
% identity	74
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150246
Seq. ID	LIB3175-038-P1-K1-C6
Method	BLASTN
NCBI GI	g3293583
BLAST score	154

E value	5.0e-81
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana BAC T27D20

Seq. No.	150247
Seq. ID	LIB3175-038-P1-K1-C8
Method	BLASTX
NCBI GI	g3860277
BLAST score	540
E value	3.0e-55
Match length	134
% identity	80
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	150248
Seq. ID	LIB3175-038-P1-K1-C9
Method	BLASTX
NCBI GI	g135467
BLAST score	527
E value	1.0e-65
Match length	125
% identity	99
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	150249
Seq. ID	LIB3175-038-P1-K1-D11
Method	BLASTN
NCBI GI	g4678705
BLAST score	185
E value	1.0e-99
Match length	389
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	150250
Seq. ID	LIB3175-038-P1-K1-D12
Method	BLASTX
NCBI GI	g3461820
BLAST score	564
E value	3.0e-58
Match length	118
% identity	87
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	150251
Seq. ID	LIB3175-038-P1-K1-D3
Method	BLASTN
NCBI GI	g2760165
BLAST score	442
E value	0.0e+00
Match length	483

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	150252
Seq. ID	LIB3175-038-P1-K1-D5
Method	BLASTX
NCBI GI	g2829894
BLAST score	191
E value	1.0e-14
Match length	70
% identity	66
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	150253
Seq. ID	LIB3175-038-P1-K1-D6
Method	BLASTX
NCBI GI	g2688820
BLAST score	232
E value	3.0e-19
Match length	105
% identity	45
NCBI Description	(U93271) enoyl-CoA hydratase [Prunus armeniaca]

Seq. No.	150254
Seq. ID	LIB3175-038-P1-K1-D7
Method	BLASTX
NCBI GI	g119350
BLAST score	622
E value	5.0e-65
Match length	132
% identity	95
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	150255
Seq. ID	LIB3175-038-P1-K1-D8
Method	BLASTX
NCBI GI	g1708462
BLAST score	669
E value	2.0e-70
Match length	131
% identity	98
NCBI Description	IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi_902791 (U23796) ILL2 [Arabidopsis thaliana]

Seq. No.	150256
Seq. ID	LIB3175-038-P1-K1-E1
Method	BLASTX
NCBI GI	g113782
BLAST score	408

E value	5.0e-40
Match length	90
% identity	87
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	150257
Seq. ID	LIB3175-038-P1-K1-E10
Method	BLASTX
NCBI GI	g3914425
BLAST score	265
E value	3.0e-23
Match length	85
% identity	65
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No.	150258
Seq. ID	LIB3175-038-P1-K1-E11
Method	BLASTN
NCBI GI	g2494106
BLAST score	419
E value	0.0e+00
Match length	450
% identity	70
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150259
Seq. ID	LIB3175-038-P1-K1-E12
Method	BLASTN
NCBI GI	g4432829
BLAST score	265
E value	1.0e-147
Match length	469
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150260
Seq. ID	LIB3175-038-P1-K1-E2
Method	BLASTN
NCBI GI	g2959729
BLAST score	283
E value	1.0e-158
Match length	311
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	150261

Seq. ID	LIB3175-038-P1-K1-E3
Method	BLASTX
NCBI GI	g3892050
BLAST score	289
E value	4.0e-26
Match length	96
% identity	61
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150262
Seq. ID	LIB3175-038-P1-K1-E5
Method	BLASTX
NCBI GI	g543841
BLAST score	439
E value	1.0e-43
Match length	85
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	150263
Seq. ID	LIB3175-038-P1-K1-E6
Method	BLASTX
NCBI GI	g115783
BLAST score	378
E value	4.0e-57
Match length	115
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150264
Seq. ID	LIB3175-038-P1-K1-E7
Method	BLASTN
NCBI GI	g2959729
BLAST score	324
E value	0.0e+00
Match length	340
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	150265
Seq. ID	LIB3175-038-P1-K1-E8
Method	BLASTX
NCBI GI	g3769472
BLAST score	231
E value	4.0e-26
Match length	76
% identity	74
NCBI Description	(AF064732) putative phospholipase A2 [Dianthus caryophyllus]

Seq. No.	150266
Seq. ID	LIB3175-038-P1-K1-E9
Method	BLASTX
NCBI GI	g3914425
BLAST score	665
E value	5.0e-70
Match length	146
% identity	89
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No.	150267
Seq. ID	LIB3175-038-P1-K1-F10
Method	BLASTX
NCBI GI	g115783
BLAST score	383
E value	7.0e-37
Match length	102
% identity	77
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150268
Seq. ID	LIB3175-038-P1-K1-F2
Method	BLASTN
NCBI GI	g3869067
BLAST score	264
E value	1.0e-147
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	150269
Seq. ID	LIB3175-038-P1-K1-F3
Method	BLASTX
NCBI GI	g2160168
BLAST score	605
E value	2.0e-65
Match length	131
% identity	95
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	150270
Seq. ID	LIB3175-038-P1-K1-F4
Method	BLASTX
NCBI GI	g4539292

BLAST score	480
E value	2.0e-48
Match length	111
% identity	85
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	150271
Seq. ID	LIB3175-038-P1-K1-F5
Method	BLASTN
NCBI GI	g4468976
BLAST score	111
E value	2.0e-55
Match length	322
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	150272
Seq. ID	LIB3175-038-P1-K1-F7
Method	BLASTN
NCBI GI	g4159704
BLAST score	440
E value	0.0e+00
Match length	476
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	150273
Seq. ID	LIB3175-038-P1-K1-F8
Method	BLASTX
NCBI GI	g3142300
BLAST score	446
E value	3.0e-44
Match length	136
% identity	60
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	150274
Seq. ID	LIB3175-038-P1-K1-F9
Method	BLASTN
NCBI GI	g2749918
BLAST score	402
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150275
Seq. ID	LIB3175-038-P1-K1-G12
Method	BLASTX
NCBI GI	g2498732

BLAST score	645
E value	1.0e-67
Match length	123
% identity	99
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi_1362014_pir__S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	150276
Seq. ID	LIB3175-038-P1-K1-G2
Method	BLASTX
NCBI GI	g404670
BLAST score	316
E value	2.0e-29
Match length	72
% identity	88
NCBI Description	(L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No.	150277
Seq. ID	LIB3175-038-P1-K1-G3
Method	BLASTN
NCBI GI	g4263762
BLAST score	144
E value	4.0e-75
Match length	307
% identity	77
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150278
Seq. ID	LIB3175-038-P1-K1-G4
Method	BLASTN
NCBI GI	g2244950
BLAST score	180
E value	1.0e-96
Match length	378
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150279
Seq. ID	LIB3175-038-P1-K1-G7
Method	BLASTX
NCBI GI	g115783
BLAST score	618
E value	2.0e-64
Match length	116
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150280
Seq. ID	LIB3175-038-P1-K1-G8

Method	BLASTN
NCBI GI	g3063438
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	150281
Seq. ID	LIB3175-038-P1-K1-G9
Method	BLASTX
NCBI GI	g2160133
BLAST score	373
E value	8.0e-36
Match length	94
% identity	84
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	150282
Seq. ID	LIB3175-038-P1-K1-H1
Method	BLASTN
NCBI GI	g4335744
BLAST score	71
E value	1.0e-31
Match length	167
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150283
Seq. ID	LIB3175-038-P1-K1-H12
Method	BLASTX
NCBI GI	g115783
BLAST score	582
E value	2.0e-60
Match length	111
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150284
Seq. ID	LIB3175-038-P1-K1-H2
Method	BLASTX
NCBI GI	g2677828
BLAST score	210
E value	9.0e-21
Match length	79
% identity	70
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	150285

Seq. ID	LIB3175-038-P1-K1-H3
Method	BLASTX
NCBI GI	g132110
BLAST score	466
E value	6.0e-63
Match length	126
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	150286
Seq. ID	LIB3175-038-P1-K1-H4
Method	BLASTX
NCBI GI	g1652082
BLAST score	146
E value	3.0e-09
Match length	102
% identity	39
NCBI Description	(D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase [Synechocystis sp.]

Seq. No.	150287
Seq. ID	LIB3175-038-P1-K1-H6
Method	BLASTN
NCBI GI	g16375
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	150288
Seq. ID	LIB3175-038-P1-K1-H7
Method	BLASTX
NCBI GI	g267069
BLAST score	292
E value	2.0e-59
Match length	114
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	150289
Seq. ID	LIB3175-038-P1-K1-H8
Method	BLASTX
NCBI GI	g399013
BLAST score	102
E value	6.0e-23
Match length	92
% identity	72

NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	150290
Seq. ID	LIB3175-038-P1-K1-H9
Method	BLASTN
NCBI GI	g2564046
BLAST score	424
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	150291
Seq. ID	LIB3175-039-P1-K1-A10
Method	BLASTX
NCBI GI	g2245006
BLAST score	230
E value	5.0e-19
Match length	87
% identity	51
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150292
Seq. ID	LIB3175-039-P1-K1-A11
Method	BLASTX
NCBI GI	g3158376
BLAST score	659
E value	3.0e-69
Match length	130
% identity	96
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	150293
Seq. ID	LIB3175-039-P1-K1-A3
Method	BLASTX
NCBI GI	g4539324
BLAST score	556
E value	3.0e-57
Match length	137
% identity	86
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	150294
Seq. ID	LIB3175-039-P1-K1-A6
Method	BLASTX
NCBI GI	g1169278
BLAST score	305
E value	8.0e-28
Match length	75
% identity	84

NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	150295
Seq. ID	LIB3175-039-P1-K1-A8
Method	BLASTX
NCBI GI	g82734
BLAST score	560
E value	9.0e-58
Match length	114
% identity	29
NCBI Description	ubiquitin precursor - maize (fragment) >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No.	150296
Seq. ID	LIB3175-039-P1-K1-A9
Method	BLASTN
NCBI GI	g2618600
BLAST score	221
E value	1.0e-121
Match length	375
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	150297
Seq. ID	LIB3175-039-P1-K1-B1
Method	BLASTX
NCBI GI	g167012
BLAST score	444
E value	3.0e-44
Match length	124
% identity	64
NCBI Description	(J03897) carboxypeptidase I precursor [Hordeum vulgare]

Seq. No.	150298
Seq. ID	LIB3175-039-P1-K1-B10
Method	BLASTN
NCBI GI	g3241927
BLAST score	246
E value	1.0e-136
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	150299
Seq. ID	LIB3175-039-P1-K1-B11
Method	BLASTX
NCBI GI	g3123188
BLAST score	717
E value	4.0e-76
Match length	140
% identity	99
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	150300
Seq. ID	LIB3175-039-P1-K1-B12
Method	BLASTX
NCBI GI	g2887500
BLAST score	338
E value	1.0e-31
Match length	70
% identity	84
NCBI Description	(AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No.	150301
Seq. ID	LIB3175-039-P1-K1-B2
Method	BLASTN
NCBI GI	g2673901
BLAST score	93
E value	3.0e-45
Match length	158
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150302
Seq. ID	LIB3175-039-P1-K1-B3
Method	BLASTX
NCBI GI	g4584110
BLAST score	289
E value	5.0e-26
Match length	106
% identity	54
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	150303
Seq. ID	LIB3175-039-P1-K1-B7
Method	BLASTX
NCBI GI	g4154281
BLAST score	312
E value	8.0e-29
Match length	70
% identity	80
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	150304
Seq. ID	LIB3175-039-P1-K1-B8
Method	BLASTX
NCBI GI	g4204274
BLAST score	442
E value	8.0e-44
Match length	78
% identity	100
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	150305
Seq. ID	LIB3175-039-P1-K1-C1
Method	BLASTN

NCBI GI	g3510347
BLAST score	434
E value	0.0e+00
Match length	442
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	150306
Seq. ID	LIB3175-039-P1-K1-C10
Method	BLASTX
NCBI GI	g2980798
BLAST score	559
E value	1.0e-57
Match length	147
% identity	73
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	150307
Seq. ID	LIB3175-039-P1-K1-C11
Method	BLASTX
NCBI GI	g4741940
BLAST score	544
E value	7.0e-56
Match length	99
% identity	65
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	150308
Seq. ID	LIB3175-039-P1-K1-C12
Method	BLASTX
NCBI GI	g4580460
BLAST score	517
E value	1.0e-52
Match length	118
% identity	87
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	150309
Seq. ID	LIB3175-039-P1-K1-C2
Method	BLASTX
NCBI GI	g2829893
BLAST score	385
E value	1.0e-37
Match length	87
% identity	86
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	150310
Seq. ID	LIB3175-039-P1-K1-C3
Method	BLASTN
NCBI GI	g4159709
BLAST score	91
E value	1.0e-43
Match length	195
% identity	94

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	150311
Seq. ID	LIB3175-039-P1-K1-C6
Method	BLASTX
NCBI GI	g4678226
BLAST score	512
E value	3.0e-52
Match length	103
% identity	98
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	150312
Seq. ID	LIB3175-039-P1-K1-C7
Method	BLASTN
NCBI GI	g3510341
BLAST score	405
E value	0.0e+00
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	150313
Seq. ID	LIB3175-039-P1-K1-C8
Method	BLASTX
NCBI GI	g2160147
BLAST score	485
E value	7.0e-49
Match length	134
% identity	75
NCBI Description	(AC000375) EST gb_ATTS3706 comes from this gene. [Arabidopsis thaliana]

Seq. No.	150314
Seq. ID	LIB3175-039-P1-K1-C9
Method	BLASTX
NCBI GI	g2702268
BLAST score	473
E value	2.0e-47
Match length	95
% identity	96
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	150315
Seq. ID	LIB3175-039-P1-K1-D1
Method	BLASTX
NCBI GI	g4503515
BLAST score	202
E value	9.0e-16
Match length	138
% identity	33
NCBI Description	UNKNOWN >gi_2351380 (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens]

Seq. No.	150316
Seq. ID	LIB3175-039-P1-K1-D10
Method	BLASTN
NCBI GI	g2351065
BLAST score	359
E value	0.0e+00
Match length	393
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	150317
Seq. ID	LIB3175-039-P1-K1-D11
Method	BLASTX
NCBI GI	g3668069
BLAST score	201
E value	1.0e-15
Match length	74
% identity	49
NCBI Description	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No.	150318
Seq. ID	LIB3175-039-P1-K1-D2
Method	BLASTX
NCBI GI	g231683
BLAST score	381
E value	5.0e-37
Match length	72
% identity	99
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	150319
Seq. ID	LIB3175-039-P1-K1-D3
Method	BLASTX
NCBI GI	g3608261
BLAST score	285
E value	2.0e-25
Match length	69
% identity	68
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	150320
Seq. ID	LIB3175-039-P1-K1-D6
Method	BLASTX
NCBI GI	g4240116
BLAST score	307
E value	3.0e-28
Match length	83
% identity	76
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	150321

Seq. ID	LIB3175-039-P1-K1-D7
Method	BLASTX
NCBI GI	g2119927
BLAST score	211
E value	8.0e-17
Match length	101
% identity	50
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	150322
Seq. ID	LIB3175-039-P1-K1-D8
Method	BLASTX
NCBI GI	g282848
BLAST score	409
E value	6.0e-40
Match length	94
% identity	79
NCBI Description	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) (clone 064) - western balsam poplar x cottonwood

Seq. No.	150323
Seq. ID	LIB3175-039-P1-K1-D9
Method	BLASTX
NCBI GI	g4206210
BLAST score	761
E value	3.0e-81
Match length	149
% identity	64
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	150324
Seq. ID	LIB3175-039-P1-K1-E10
Method	BLASTX
NCBI GI	g1486472
BLAST score	385
E value	3.0e-37
Match length	92
% identity	82
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	150325
Seq. ID	LIB3175-039-P1-K1-E11
Method	BLASTX
NCBI GI	g2129597
BLAST score	656
E value	6.0e-69
Match length	130
% identity	98
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	150326
Seq. ID	LIB3175-039-P1-K1-E12
Method	BLASTX
NCBI GI	g2829925
BLAST score	331
E value	5.0e-31
Match length	69
% identity	97
NCBI Description	(AC002291) Similar to dnaj-like protein, gp_Y11969_2230757 [Arabidopsis thaliana]

Seq. No.	150327
Seq. ID	LIB3175-039-P1-K1-E2
Method	BLASTX
NCBI GI	g4567262
BLAST score	450
E value	5.0e-45
Match length	88
% identity	95
NCBI Description	(AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No.	150328
Seq. ID	LIB3175-039-P1-K1-E6
Method	BLASTX
NCBI GI	g4193382
BLAST score	423
E value	1.0e-41
Match length	86
% identity	91
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	150329
Seq. ID	LIB3175-039-P1-K1-E7
Method	BLASTN
NCBI GI	g4589440
BLAST score	388
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	150330
Seq. ID	LIB3175-039-P1-K1-E8
Method	BLASTX
NCBI GI	g462273
BLAST score	380
E value	1.0e-36
Match length	127
% identity	63
NCBI Description	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi_437213 (U02689) imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana]

Seq. No.	150331

Seq. ID	LIB3175-039-P1-K1-E9
Method	BLASTX
NCBI GI	g2558962
BLAST score	437
E value	3.0e-43
Match length	92
% identity	97
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	150332
Seq. ID	LIB3175-039-P1-K1-F1
Method	BLASTX
NCBI GI	g2506277
BLAST score	51
E value	3.0e-10
Match length	99
% identity	54
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	150333
Seq. ID	LIB3175-039-P1-K1-F10
Method	BLASTX
NCBI GI	g4586263
BLAST score	337
E value	8.0e-32
Match length	97
% identity	69
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150334
Seq. ID	LIB3175-039-P1-K1-F11
Method	BLASTX
NCBI GI	g543565
BLAST score	205
E value	4.0e-16
Match length	66
% identity	52
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	150335
Seq. ID	LIB3175-039-P1-K1-F12
Method	BLASTN
NCBI GI	g4432847
BLAST score	348
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150336
Seq. ID	LIB3175-039-P1-K1-F3

Method	BLASTN
NCBI GI	g4417299
BLAST score	110
E value	3.0e-55
Match length	172
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F15O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150337
Seq. ID	LIB3175-039-P1-K1-F7
Method	BLASTX
NCBI GI	g4741198
BLAST score	529
E value	4.0e-54
Match length	96
% identity	100
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	150338
Seq. ID	LIB3175-039-P1-K1-F8
Method	BLASTX
NCBI GI	g2507477
BLAST score	182
E value	1.0e-13
Match length	122
% identity	35
NCBI Description	TRANSALDOLASE A >gi_1788807 (AE000333) transaldolase A [Escherichia coli] >gi_1799888_dbj_BAA16339_ (D90875) similar to [PIR Accession Number S40535] [Escherichia coli] >gi_2337774_dbj_BAA21821_ (D13159) transaldolase [Escherichia coli]

Seq. No.	150339
Seq. ID	LIB3175-039-P1-K1-G1
Method	BLASTX
NCBI GI	g2055374
BLAST score	209
E value	1.0e-16
Match length	50
% identity	82
NCBI Description	(U29095) serine-threonine protein kinase [Triticum aestivum]

Seq. No.	150340
Seq. ID	LIB3175-039-P1-K1-G10
Method	BLASTX
NCBI GI	g1172872
BLAST score	470
E value	2.0e-47
Match length	111
% identity	84
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible

cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	150341
Seq. ID	LIB3175-039-P1-K1-G11
Method	BLASTX
NCBI GI	g4432856
BLAST score	523
E value	2.0e-53
Match length	109
% identity	95
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	150342
Seq. ID	LIB3175-039-P1-K1-G12
Method	BLASTX
NCBI GI	g1175010
BLAST score	541
E value	2.0e-55
Match length	119
% identity	89
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	150343
Seq. ID	LIB3175-039-P1-K1-G3
Method	BLASTN
NCBI GI	g166745
BLAST score	136
E value	9.0e-71
Match length	148
% identity	98
NCBI Description	A.thaliana plasma membrane proton ATPase (PMA) mRNA, complete cds

Seq. No.	150344
Seq. ID	LIB3175-039-P1-K1-G5
Method	BLASTX
NCBI GI	g4583544
BLAST score	468
E value	5.0e-47
Match length	97
% identity	90
NCBI Description	(Z95637) acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	150345
Seq. ID	LIB3175-039-P1-K1-G7
Method	BLASTX
NCBI GI	g3193292
BLAST score	577
E value	8.0e-60
Match length	129
% identity	88
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

Seq. No.	150346
Seq. ID	LIB3175-039-P1-K1-G8
Method	BLASTX
NCBI GI	g132110
BLAST score	539
E value	2.0e-55
Match length	104
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	150347
Seq. ID	LIB3175-039-P1-K1-G9
Method	BLASTN
NCBI GI	g4519185
BLAST score	280
E value	1.0e-156
Match length	331
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15O15, complete sequence

Seq. No.	150348
Seq. ID	LIB3175-039-P1-K1-H1
Method	BLASTX
NCBI GI	g2894574
BLAST score	607
E value	3.0e-63
Match length	115
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	150349
Seq. ID	LIB3175-039-P1-K1-H11
Method	BLASTX
NCBI GI	g2352921
BLAST score	515
E value	1.0e-52
Match length	105
% identity	90
NCBI Description	(AF012862) cytosolic glucose-6-phosphate dehydrogenase 1 [Petroselinum crispum]

Seq. No.	150350
Seq. ID	LIB3175-039-P1-K1-H12
Method	BLASTN
NCBI GI	g4733953
BLAST score	123
E value	7.0e-63

Match length	163
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	150351
Seq. ID	LIB3175-039-P1-K1-H3
Method	BLASTX
NCBI GI	g2791900
BLAST score	231
E value	1.0e-19
Match length	80
% identity	59
NCBI Description	(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No.	150352
Seq. ID	LIB3175-039-P1-K1-H7
Method	BLASTX
NCBI GI	g266693
BLAST score	263
E value	6.0e-23
Match length	119
% identity	50
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	150353
Seq. ID	LIB3175-039-P1-K1-H8
Method	BLASTN
NCBI GI	g3449320
BLAST score	191
E value	1.0e-103
Match length	449
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	150354
Seq. ID	LIB3175-039-P1-K1-H9
Method	BLASTX
NCBI GI	g3421094
BLAST score	698
E value	7.0e-74
Match length	141
% identity	97
NCBI Description	(AF043527) 20S proteasome subunit PAF2 [Arabidopsis thaliana]

Seq. No.	150355
Seq. ID	LIB3175-040-P1-K1-A10
Method	BLASTX
NCBI GI	g602764
BLAST score	756
E value	1.0e-80
Match length	146

% identity	96
NCBI Description	(D43783) beta-amylase [Arabidopsis thaliana] >gi_998369_bbs_163908 (S77076) beta-amylase {EC 3.2.1.2} [Arabidopsis thaliana=thale cress, Heynh., Peptide, 498 aa] [Arabidopsis thaliana]

Seq. No.	150356
Seq. ID	LIB3175-040-P1-K1-A12
Method	BLASTX
NCBI GI	g3292814
BLAST score	292
E value	2.0e-26
Match length	85
% identity	75
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	150357
Seq. ID	LIB3175-040-P1-K1-A2
Method	BLASTX
NCBI GI	g4220480
BLAST score	267
E value	2.0e-23
Match length	99
% identity	53
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	150358
Seq. ID	LIB3175-040-P1-K1-A3
Method	BLASTX
NCBI GI	g1175012
BLAST score	115
E value	1.0e-05
Match length	137
% identity	79
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	150359
Seq. ID	LIB3175-040-P1-K1-A5
Method	BLASTN
NCBI GI	g1402874
BLAST score	320
E value	1.0e-180
Match length	386
% identity	100
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	150360
Seq. ID	LIB3175-040-P1-K1-A6
Method	BLASTX
NCBI GI	g2829876
BLAST score	655
E value	7.0e-69
Match length	132
% identity	98
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	150361
Seq. ID	LIB3175-040-P1-K1-A8
Method	BLASTN
NCBI GI	g2088638
BLAST score	300
E value	1.0e-168
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150362
Seq. ID	LIB3175-040-P1-K1-A9
Method	BLASTX
NCBI GI	g21913
BLAST score	201
E value	1.0e-15
Match length	83
% identity	45
NCBI Description	(X62626) vicilin [Theobroma cacao]

Seq. No.	150363
Seq. ID	LIB3175-040-P1-K1-B10
Method	BLASTN
NCBI GI	g3650026
BLAST score	223
E value	1.0e-122
Match length	297
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150364
Seq. ID	LIB3175-040-P1-K1-B11
Method	BLASTX
NCBI GI	g3184285
BLAST score	155
E value	3.0e-10
Match length	59
% identity	46
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150365
Seq. ID	LIB3175-040-P1-K1-B12
Method	BLASTN
NCBI GI	g902200
BLAST score	45
E value	1.0e-16
Match length	93
% identity	87
NCBI Description	Z.mays complete chloroplast genome

Seq. No.	150366
Seq. ID	LIB3175-040-P1-K1-B3
Method	BLASTX
NCBI GI	g282865

BLAST score 283
E value 3.0e-25
Match length 95
% identity 61
NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 150367
Seq. ID LIB3175-040-P1-K1-B4
Method BLASTN
NCBI GI g4263694
BLAST score 136
E value 2.0e-70
Match length 403
% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 150368
Seq. ID LIB3175-040-P1-K1-B5
Method BLASTX
NCBI GI g4741960
BLAST score 517
E value 1.0e-52
Match length 118
% identity 85
NCBI Description (AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No. 150369
Seq. ID LIB3175-040-P1-K1-B6
Method BLASTX
NCBI GI g112682
BLAST score 667
E value 3.0e-70
Match length 142
% identity 89
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 150370
Seq. ID LIB3175-040-P1-K1-B7
Method BLASTX
NCBI GI g3478700
BLAST score 647
E value 6.0e-68
Match length 140
% identity 90
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 150371

Seq. ID	LIB3175-040-P1-K1-B8
Method	BLASTX
NCBI GI	g1076316
BLAST score	741
E value	6.0e-79
Match length	144
% identity	99
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	150372
Seq. ID	LIB3175-040-P1-K1-C10
Method	BLASTN
NCBI GI	g4519193
BLAST score	353
E value	0.0e+00
Match length	406
% identity	34
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	150373
Seq. ID	LIB3175-040-P1-K1-C11
Method	BLASTX
NCBI GI	g3132475
BLAST score	602
E value	1.0e-62
Match length	141
% identity	82
NCBI Description	(AC003096) similar to proline-rich protein [Arabidopsis thaliana]

Seq. No.	150374
Seq. ID	LIB3175-040-P1-K1-C12
Method	BLASTN
NCBI GI	g4056476
BLAST score	224
E value	1.0e-123
Match length	353
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150375
Seq. ID	LIB3175-040-P1-K1-C3
Method	BLASTN
NCBI GI	g4220636
BLAST score	44
E value	4.0e-16
Match length	88
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	150376
Seq. ID	LIB3175-040-P1-K1-C4

Method	BLASTX
NCBI GI	g4557495
BLAST score	177
E value	8.0e-13
Match length	101
% identity	34
NCBI Description	cleavage stimulation factor subunit 3 >gi_1082704_pir__S50852 cleavage stimulation factor 77K chain - human >gi_632498 (U15782) cleavage stimulation factor 77kDa subunit [Homo sapiens] >gi_1092656_prf__2024339A cleavage stimulation factor [Homo sapiens]

Seq. No.	150377
Seq. ID	LIB3175-040-P1-K1-C5
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	150378
Seq. ID	LIB3175-040-P1-K1-C6
Method	BLASTX
NCBI GI	g1174718
BLAST score	484
E value	7.0e-49
Match length	128
% identity	71
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	150379
Seq. ID	LIB3175-040-P1-K1-C7
Method	BLASTN
NCBI GI	g4589439
BLAST score	210
E value	1.0e-114
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	150380
Seq. ID	LIB3175-040-P1-K1-C8
Method	BLASTN
NCBI GI	g3883123
BLAST score	332
E value	0.0e+00
Match length	380
% identity	97
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,

complete cds

Seq. No.	150381
Seq. ID	LIB3175-040-P1-K1-C9
Method	BLASTX
NCBI GI	g3355468
BLAST score	429
E value	2.0e-42
Match length	123
% identity	76
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	150382
Seq. ID	LIB3175-040-P1-K1-D10
Method	BLASTX
NCBI GI	g2226202
BLAST score	174
E value	2.0e-12
Match length	83
% identity	51
NCBI Description	(Y14082) hypothetical protein [Bacillus subtilis] >gi_2633281_emb_CAB12785_ (Z99109) similar to amino acid transporter [Bacillus subtilis]

Seq. No.	150383
Seq. ID	LIB3175-040-P1-K1-D3
Method	BLASTN
NCBI GI	g4220638
BLAST score	109
E value	9.0e-55
Match length	125
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	150384
Seq. ID	LIB3175-040-P1-K1-D4
Method	BLASTX
NCBI GI	g4160280
BLAST score	360
E value	3.0e-34
Match length	108
% identity	60
NCBI Description	(AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No.	150385
Seq. ID	LIB3175-040-P1-K1-D5
Method	BLASTX
NCBI GI	g3608263
BLAST score	301
E value	2.0e-27
Match length	60
% identity	85
NCBI Description	(AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No. 150386

Seq. ID	LIB3175-040-P1-K1-D7
Method	BLASTX
NCBI GI	g2244750
BLAST score	512
E value	5.0e-58
Match length	127
% identity	88
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	150387
Seq. ID	LIB3175-040-P1-K1-D8
Method	BLASTX
NCBI GI	g2668744
BLAST score	591
E value	2.0e-61
Match length	120
% identity	89
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No.	150388
Seq. ID	LIB3175-040-P1-K1-D9
Method	BLASTX
NCBI GI	g3914740
BLAST score	514
E value	2.0e-52
Match length	131
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	150389
Seq. ID	LIB3175-040-P1-K1-E11
Method	BLASTN
NCBI GI	g2564048
BLAST score	129
E value	3.0e-66
Match length	335
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	150390
Seq. ID	LIB3175-040-P1-K1-E4
Method	BLASTN
NCBI GI	g2828188
BLAST score	193
E value	1.0e-104
Match length	429
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	150391
Seq. ID	LIB3175-040-P1-K1-F10
Method	BLASTX

NCBI GI	g1864017
BLAST score	508
E value	1.0e-51
Match length	104
% identity	92
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	150392
Seq. ID	LIB3175-040-P1-K1-F11
Method	BLASTX
NCBI GI	g417383
BLAST score	376
E value	3.0e-36
Match length	77
% identity	97
NCBI Description	NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958) nitrilase [Arabidopsis thaliana]

Seq. No.	150393
Seq. ID	LIB3175-040-P1-K1-F12
Method	BLASTX
NCBI GI	g544424
BLAST score	442
E value	6.0e-44
Match length	89
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	150394
Seq. ID	LIB3175-040-P1-K1-F3
Method	BLASTN
NCBI GI	g16249
BLAST score	160
E value	5.0e-85
Match length	176
% identity	98
NCBI Description	A.thaliana mRNA for Cu,Zn superoxide dismutase

Seq. No.	150395
Seq. ID	LIB3175-040-P1-K1-F4
Method	BLASTN
NCBI GI	g2618601
BLAST score	167
E value	3.0e-89
Match length	191
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	150396
Seq. ID	LIB3175-040-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	621
E value	7.0e-65
Match length	141
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	150397
Seq. ID	LIB3175-040-P1-K1-F7
Method	BLASTX
NCBI GI	g4580394
BLAST score	264
E value	4.0e-23
Match length	116
% identity	44
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	150398
Seq. ID	LIB3175-040-P1-K1-F8
Method	BLASTX
NCBI GI	g4469022
BLAST score	726
E value	3.0e-77
Match length	142
% identity	99
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	150399
Seq. ID	LIB3175-040-P1-K1-G11
Method	BLASTN
NCBI GI	g4519195
BLAST score	159
E value	3.0e-84
Match length	307
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	150400
Seq. ID	LIB3175-040-P1-K1-G5
Method	BLASTN
NCBI GI	g2477521
BLAST score	309
E value	1.0e-173
Match length	433
% identity	19
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150401
Seq. ID	LIB3175-040-P1-K1-G6
Method	BLASTN
NCBI GI	g12279
BLAST score	81
E value	1.0e-37
Match length	105
% identity	94
NCBI Description	Spinach chloroplast genes for the D2 and 44 kd reaction centre, chlorophyll a-binding protein and for tRNA-Ser (UGA)

Seq. No.	150402
Seq. ID	LIB3175-040-P1-K1-G7
Method	BLASTN
NCBI GI	g3319365
BLAST score	53
E value	7.0e-21
Match length	192
% identity	87
NCBI Description	Arabidopsis thaliana BAC T24M8

Seq. No.	150403
Seq. ID	LIB3175-040-P1-K1-G8
Method	BLASTX
NCBI GI	g400650
BLAST score	203
E value	7.0e-16
Match length	96
% identity	43
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir__S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 - bovine >gi_238_emb_CAA44903_ (X63218) NADH dehydrogenase [Bos taurus]

Seq. No.	150404
Seq. ID	LIB3175-040-P1-K1-H10
Method	BLASTN
NCBI GI	g4468103
BLAST score	181
E value	3.0e-97
Match length	321
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	150405
Seq. ID	LIB3175-040-P1-K1-H11
Method	BLASTX
NCBI GI	g4324967
BLAST score	289
E value	6.0e-26
Match length	55
% identity	98
NCBI Description	(AF114796) ADP-ribosylation factor [Glycine max]

Seq. No.	150406
Seq. ID	LIB3175-040-P1-K1-H12
Method	BLASTX
NCBI GI	g3859998
BLAST score	306
E value	5.0e-28
Match length	107
% identity	52
NCBI Description	(AF091080) unknown [Homo sapiens]

Seq. No.	150407
Seq. ID	LIB3175-040-P1-K1-H5
Method	BLASTX
NCBI GI	g600178
BLAST score	578
E value	7.0e-60
Match length	131
% identity	87
NCBI Description	(L27074) acetyl-CoA carboxylase [Arabidopsis thaliana] >gi_1090217_prf__2018327A Ac-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	150408
Seq. ID	LIB3175-040-P1-K1-H6
Method	BLASTX
NCBI GI	g3128205
BLAST score	717
E value	4.0e-76
Match length	144
% identity	97
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]

Seq. No.	150409
Seq. ID	LIB3175-040-P1-K1-H7
Method	BLASTX
NCBI GI	g1172872
BLAST score	464
E value	1.0e-46
Match length	91
% identity	99
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	150410
Seq. ID	LIB3175-041-P1-K1-A1
Method	BLASTN
NCBI GI	g3927822
BLAST score	318
E value	1.0e-179
Match length	394
% identity	98

NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150411
Seq. ID	LIB3175-041-P1-K1-A10
Method	BLASTX
NCBI GI	g2832625
BLAST score	640
E value	4.0e-67
Match length	123
% identity	100
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	150412
Seq. ID	LIB3175-041-P1-K1-A11
Method	BLASTX
NCBI GI	g2832625
BLAST score	412
E value	2.0e-40
Match length	140
% identity	66
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	150413
Seq. ID	LIB3175-041-P1-K1-A12
Method	BLASTX
NCBI GI	g2924779
BLAST score	623
E value	4.0e-65
Match length	124
% identity	99
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	150414
Seq. ID	LIB3175-041-P1-K1-A2
Method	BLASTX
NCBI GI	g3415117
BLAST score	82
E value	2.0e-38
Match length	88
% identity	51
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	150415
Seq. ID	LIB3175-041-P1-K1-A3
Method	BLASTX
NCBI GI	g119350
BLAST score	654
E value	9.0e-69
Match length	127
% identity	100
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187

phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	150416
Seq. ID	LIB3175-041-P1-K1-A5
Method	BLASTN
NCBI GI	g2618599
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	150417
Seq. ID	LIB3175-041-P1-K1-A6
Method	BLASTX
NCBI GI	g2739389
BLAST score	389
E value	8.0e-38
Match length	106
% identity	68
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	150418
Seq. ID	LIB3175-041-P1-K1-A7
Method	BLASTN
NCBI GI	g3449330
BLAST score	85
E value	2.0e-40
Match length	105
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	150419
Seq. ID	LIB3175-041-P1-K1-A8
Method	BLASTN
NCBI GI	g4589435
BLAST score	405
E value	0.0e+00
Match length	425
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	150420
Seq. ID	LIB3175-041-P1-K1-A9
Method	BLASTN
NCBI GI	g1931636
BLAST score	221
E value	1.0e-121
Match length	441

% identity	99
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	150421
Seq. ID	LIB3175-041-P1-K1-B1
Method	BLASTX
NCBI GI	g4689386
BLAST score	346
E value	1.0e-32
Match length	91
% identity	73
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	150422
Seq. ID	LIB3175-041-P1-K1-B10
Method	BLASTX
NCBI GI	g3421123
BLAST score	646
E value	8.0e-68
Match length	125
% identity	99
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	150423
Seq. ID	LIB3175-041-P1-K1-B12
Method	BLASTX
NCBI GI	g2342687
BLAST score	584
E value	1.0e-60
Match length	112
% identity	100
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	150424
Seq. ID	LIB3175-041-P1-K1-B2
Method	BLASTX
NCBI GI	g4455192
BLAST score	241
E value	3.0e-20
Match length	127
% identity	24
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	150425
Seq. ID	LIB3175-041-P1-K1-B3
Method	BLASTN
NCBI GI	g4678705
BLAST score	422
E value	0.0e+00
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	150426
Seq. ID	LIB3175-041-P1-K1-B5
Method	BLASTN
NCBI GI	g3264774
BLAST score	123
E value	1.0e-62
Match length	207
% identity	100
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	150427
Seq. ID	LIB3175-041-P1-K1-B7
Method	BLASTX
NCBI GI	g629669
BLAST score	165
E value	2.0e-11
Match length	139
% identity	31
NCBI Description	hypothetical protein - tomato

Seq. No.	150428
Seq. ID	LIB3175-041-P1-K1-B9
Method	BLASTX
NCBI GI	g3068713
BLAST score	482
E value	1.0e-48
Match length	140
% identity	72
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	150429
Seq. ID	LIB3175-041-P1-K1-C1
Method	BLASTX
NCBI GI	g112743
BLAST score	698
E value	7.0e-74
Match length	146
% identity	90
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	150430
Seq. ID	LIB3175-041-P1-K1-C11
Method	BLASTN
NCBI GI	g2244950
BLAST score	176
E value	2.0e-94
Match length	308
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No.	150431
Seq. ID	LIB3175-041-P1-K1-C12
Method	BLASTX
NCBI GI	g2827143
BLAST score	600
E value	2.0e-62
Match length	122
% identity	94
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	150432
Seq. ID	LIB3175-041-P1-K1-C2
Method	BLASTX
NCBI GI	g585350
BLAST score	647
E value	7.0e-68
Match length	142
% identity	86
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 2 (CK II) >gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA2) - Arabidopsis thaliana >gi_391605_dbj_BAA01091_ (D10247) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	150433
Seq. ID	LIB3175-041-P1-K1-C3
Method	BLASTX
NCBI GI	g3894172
BLAST score	399
E value	7.0e-39
Match length	130
% identity	57
NCBI Description	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	150434
Seq. ID	LIB3175-041-P1-K1-C4
Method	BLASTX
NCBI GI	g3152587
BLAST score	227
E value	8.0e-19
Match length	97
% identity	46
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	150435
Seq. ID	LIB3175-041-P1-K1-C5
Method	BLASTX
NCBI GI	g3860274
BLAST score	277
E value	1.0e-24

Match length	58
% identity	91
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	150436
Seq. ID	LIB3175-041-P1-K1-C6
Method	BLASTX
NCBI GI	g4406777
BLAST score	148
E value	2.0e-09
Match length	128
% identity	31
NCBI Description	(AC006532) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	150437
Seq. ID	LIB3175-041-P1-K1-C8
Method	BLASTX
NCBI GI	g134025
BLAST score	511
E value	6.0e-52
Match length	130
% identity	80
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	150438
Seq. ID	LIB3175-041-P1-K1-C9
Method	BLASTX
NCBI GI	g134025
BLAST score	338
E value	8.0e-32
Match length	107
% identity	68
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8 ribosomal protein S8 - common tobacco chloroplast >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8 [Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal protein S8 [Nicotiana tabacum]

Seq. No.	150439
Seq. ID	LIB3175-041-P1-K1-D12
Method	BLASTN
NCBI GI	g4589410
BLAST score	144
E value	3.0e-75
Match length	305
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	150440

Seq. ID	LIB3175-041-P1-K1-D2
Method	BLASTX
NCBI GI	g1170373
BLAST score	251
E value	1.0e-21
Match length	69
% identity	74
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	150441
Seq. ID	LIB3175-041-P1-K1-D3
Method	BLASTX
NCBI GI	g1353352
BLAST score	326
E value	3.0e-30
Match length	86
% identity	72
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	150442
Seq. ID	LIB3175-041-P1-K1-D5
Method	BLASTX
NCBI GI	g2507281
BLAST score	646
E value	7.0e-68
Match length	122
% identity	95
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	150443
Seq. ID	LIB3175-041-P1-K1-D6
Method	BLASTX
NCBI GI	g3121853
BLAST score	154
E value	4.0e-10
Match length	141
% identity	30
NCBI Description	CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) >gi_2584785_emb_CAA73228_ (Y12696) p64 bovine chloride channel-like protein [Homo sapiens]

Seq. No.	150444
Seq. ID	LIB3175-041-P1-K1-D7
Method	BLASTX
NCBI GI	g2119846
BLAST score	572
E value	3.0e-59
Match length	124
% identity	90
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein

[Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150445
Seq. ID	LIB3175-041-P1-K1-D8
Method	BLASTX
NCBI GI	g4741954
BLAST score	671
E value	1.0e-70
Match length	130
% identity	99
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	150446
Seq. ID	LIB3175-041-P1-K1-D9
Method	BLASTX
NCBI GI	g3676294
BLAST score	338
E value	1.0e-31
Match length	112
% identity	68
NCBI Description	(U96496) mitochondrial ATPase beta subunit [Nicotiana sylvestris]

Seq. No.	150447
Seq. ID	LIB3175-041-P1-K1-E1
Method	BLASTN
NCBI GI	g2494110
BLAST score	403
E value	0.0e+00
Match length	403
% identity	90
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	150448
Seq. ID	LIB3175-041-P1-K1-E11
Method	BLASTX
NCBI GI	g4185515
BLAST score	545
E value	6.0e-56
Match length	105
% identity	99
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	150449
Seq. ID	LIB3175-041-P1-K1-E12
Method	BLASTX
NCBI GI	g4185515
BLAST score	190
E value	7.0e-19
Match length	80
% identity	70
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis

thaliana]

Seq. No.	150450
Seq. ID	LIB3175-041-P1-K1-E2
Method	BLASTN
NCBI GI	g3851669
BLAST score	210
E value	1.0e-114
Match length	218
% identity	99
NCBI Description	Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	150451
Seq. ID	LIB3175-041-P1-K1-E3
Method	BLASTX
NCBI GI	g3337361
BLAST score	486
E value	5.0e-49
Match length	110
% identity	79
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	150452
Seq. ID	LIB3175-041-P1-K1-E4
Method	BLASTX
NCBI GI	g3851636
BLAST score	452
E value	5.0e-45
Match length	117
% identity	73
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	150453
Seq. ID	LIB3175-041-P1-K1-E5
Method	BLASTX
NCBI GI	g3851636
BLAST score	480
E value	2.0e-48
Match length	119
% identity	76
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	150454
Seq. ID	LIB3175-041-P1-K1-E6
Method	BLASTX
NCBI GI	g3851636
BLAST score	388
E value	1.0e-37
Match length	113
% identity	67
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	150455

Seq. ID	LIB3175-041-P1-K1-E7
Method	BLASTX
NCBI GI	g3033375
BLAST score	191
E value	2.0e-14
Match length	135
% identity	39
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	150456
Seq. ID	LIB3175-041-P1-K1-E9
Method	BLASTX
NCBI GI	g4586265
BLAST score	488
E value	3.0e-49
Match length	115
% identity	79
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150457
Seq. ID	LIB3175-041-P1-K1-F1
Method	BLASTX
NCBI GI	g2129672
BLAST score	294
E value	1.0e-26
Match length	117
% identity	55
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	150458
Seq. ID	LIB3175-041-P1-K1-F10
Method	BLASTX
NCBI GI	g1864017
BLAST score	547
E value	2.0e-56
Match length	105
% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	150459
Seq. ID	LIB3175-041-P1-K1-F11
Method	BLASTX
NCBI GI	g1175013
BLAST score	597
E value	5.0e-62
Match length	131
% identity	90
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	150460

Seq. ID	LIB3175-041-P1-K1-F12
Method	BLASTX
NCBI GI	g267069
BLAST score	617
E value	2.0e-64
Match length	114
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	150461
Seq. ID	LIB3175-041-P1-K1-F2
Method	BLASTX
NCBI GI	g1946362
BLAST score	385
E value	3.0e-37
Match length	120
% identity	66
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	150462
Seq. ID	LIB3175-041-P1-K1-F3
Method	BLASTX
NCBI GI	g1790922
BLAST score	679
E value	1.0e-71
Match length	135
% identity	100
NCBI Description	(U76670) AtDMC1 [Arabidopsis thaliana]

Seq. No.	150463
Seq. ID	LIB3175-041-P1-K1-F4
Method	BLASTN
NCBI GI	g4220510
BLAST score	46
E value	1.0e-16
Match length	135
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	150464
Seq. ID	LIB3175-041-P1-K1-F5
Method	BLASTX
NCBI GI	g2062164
BLAST score	503
E value	4.0e-51
Match length	115
% identity	85
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	150465
Seq. ID	LIB3175-041-P1-K1-F6

Method	BLASTX
NCBI GI	g3355471
BLAST score	496
E value	3.0e-50
Match length	115
% identity	77
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	150466
Seq. ID	LIB3175-041-P1-K1-F7
Method	BLASTX
NCBI GI	g1170939
BLAST score	469
E value	5.0e-47
Match length	97
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	150467
Seq. ID	LIB3175-041-P1-K1-F8
Method	BLASTX
NCBI GI	g4755189
BLAST score	342
E value	2.0e-37
Match length	124
% identity	67
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	150468
Seq. ID	LIB3175-041-P1-K1-G1
Method	BLASTN
NCBI GI	g2244901
BLAST score	176
E value	3.0e-94
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150469
Seq. ID	LIB3175-041-P1-K1-G10
Method	BLASTX
NCBI GI	g345829
BLAST score	261
E value	1.0e-22
Match length	87
% identity	60
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	150470
Seq. ID	LIB3175-041-P1-K1-G12

Method	BLASTX
NCBI GI	g2738248
BLAST score	631
E value	5.0e-66
Match length	126
% identity	93
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	150471
Seq. ID	LIB3175-041-P1-K1-G3
Method	BLASTX
NCBI GI	g4741940
BLAST score	627
E value	1.0e-65
Match length	128
% identity	65
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	150472
Seq. ID	LIB3175-041-P1-K1-G5
Method	BLASTX
NCBI GI	g4098272
BLAST score	353
E value	1.0e-33
Match length	65
% identity	97
NCBI Description	(U76558) alpha-tubulin [Triticum aestivum]

Seq. No.	150473
Seq. ID	LIB3175-041-P1-K1-G6
Method	BLASTN
NCBI GI	g3047100
BLAST score	269
E value	1.0e-149
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	150474
Seq. ID	LIB3175-041-P1-K1-H10
Method	BLASTX
NCBI GI	g4589398
BLAST score	48
E value	1.0e-29
Match length	98
% identity	68
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	150475
Seq. ID	LIB3175-041-P1-K1-H11
Method	BLASTN
NCBI GI	g4760411
BLAST score	364
E value	0.0e+00
Match length	388
% identity	99

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	150476
Seq. ID	LIB3175-041-P1-K1-H2
Method	BLASTX
NCBI GI	g1169598
BLAST score	248
E value	3.0e-21
Match length	58
% identity	84
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	150477
Seq. ID	LIB3175-041-P1-K1-H5
Method	BLASTX
NCBI GI	g1561730
BLAST score	157
E value	1.0e-10
Match length	61
% identity	46
NCBI Description	(U65491) Dreg-3 protein [Drosophila melanogaster]

Seq. No.	150478
Seq. ID	LIB3175-041-P1-K1-H6
Method	BLASTX
NCBI GI	g4263523
BLAST score	454
E value	2.0e-45
Match length	91
% identity	67
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150479
Seq. ID	LIB3175-041-P1-K1-H7
Method	BLASTX
NCBI GI	g4689386
BLAST score	386
E value	3.0e-37
Match length	99
% identity	74
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	150480
Seq. ID	LIB3175-041-P1-K1-H8
Method	BLASTX
NCBI GI	g4056467
BLAST score	656
E value	5.0e-69
Match length	127
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256

come from this gene. [Arabidopsis thaliana]

Seq. No.	150481
Seq. ID	LIB3175-041-P1-K1-H9
Method	BLASTX
NCBI GI	g3395938
BLAST score	474
E value	1.0e-47
Match length	96
% identity	96
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	150482
Seq. ID	LIB3175-042-P1-K1-A1
Method	BLASTX
NCBI GI	g1621268
BLAST score	564
E value	3.0e-58
Match length	131
% identity	78
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	150483
Seq. ID	LIB3175-042-P1-K1-A10
Method	BLASTX
NCBI GI	g417381
BLAST score	665
E value	4.0e-70
Match length	132
% identity	98
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	150484
Seq. ID	LIB3175-042-P1-K1-A4
Method	BLASTX
NCBI GI	g4758946
BLAST score	186
E value	6.0e-14
Match length	71
% identity	55
NCBI Description	POP2 (yeast homolog) >gi_4106061_gb_AAD02685_ (AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	150485
Seq. ID	LIB3175-042-P1-K1-A5
Method	BLASTX
NCBI GI	g4587564
BLAST score	498
E value	2.0e-50
Match length	96
% identity	98
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,

gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	150486
Seq. ID	LIB3175-042-P1-K1-A6
Method	BLASTX
NCBI GI	g2642158
BLAST score	159
E value	2.0e-11
Match length	61
% identity	56
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150487
Seq. ID	LIB3175-042-P1-K1-A7
Method	BLASTX
NCBI GI	g114649
BLAST score	205
E value	4.0e-16
Match length	43
% identity	100
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67899_pir__LWLVA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - liverwort (Marchantia polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465) atpH [Marchantia polymorpha]

Seq. No.	150488
Seq. ID	LIB3175-042-P1-K1-A8
Method	BLASTN
NCBI GI	g2244747
BLAST score	289
E value	1.0e-161
Match length	415
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150489
Seq. ID	LIB3175-042-P1-K1-A9
Method	BLASTN
NCBI GI	g3985934
BLAST score	163
E value	2.0e-86
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	150490
Seq. ID	LIB3175-042-P1-K1-B1
Method	BLASTX
NCBI GI	g2827529
BLAST score	680
E value	8.0e-72
Match length	136
% identity	96
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	150491
Seq. ID	LIB3175-042-P1-K1-B11
Method	BLASTN
NCBI GI	g4589420
BLAST score	52
E value	2.0e-20
Match length	149
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3G17, complete sequence

Seq. No.	150492
Seq. ID	LIB3175-042-P1-K1-B12
Method	BLASTX
NCBI GI	g132110
BLAST score	610
E value	1.0e-63
Match length	112
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	150493
Seq. ID	LIB3175-042-P1-K1-B2
Method	BLASTX
NCBI GI	g134976
BLAST score	501
E value	7.0e-51
Match length	96
% identity	100
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	150494
Seq. ID	LIB3175-042-P1-K1-B3
Method	BLASTX
NCBI GI	g4432865
BLAST score	676
E value	2.0e-71
Match length	134
% identity	92
NCBI Description	(AC006300) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	150495
Seq. ID	LIB3175-042-P1-K1-B4
Method	BLASTX
NCBI GI	g2245087
BLAST score	443
E value	5.0e-44

Match length	103
% identity	81
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150496
Seq. ID	LIB3175-042-P1-K1-B5
Method	BLASTN
NCBI GI	g871991
BLAST score	63
E value	3.0e-27
Match length	139
% identity	86
NCBI Description	A.thaliana TGG2 gene for myrosinase

Seq. No.	150497
Seq. ID	LIB3175-042-P1-K1-B6
Method	BLASTN
NCBI GI	g4586241
BLAST score	69
E value	2.0e-30
Match length	286
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	150498
Seq. ID	LIB3175-042-P1-K1-B8
Method	BLASTX
NCBI GI	g282865
BLAST score	203
E value	6.0e-16
Match length	101
% identity	48
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	150499
Seq. ID	LIB3175-042-P1-K1-B9
Method	BLASTN
NCBI GI	g4586241
BLAST score	62
E value	3.0e-26
Match length	218
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	150500
Seq. ID	LIB3175-042-P1-K1-C1
Method	BLASTX
NCBI GI	g119350
BLAST score	594
E value	9.0e-62

Match length	114
% identity	100
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	150501
Seq. ID	LIB3175-042-P1-K1-C10
Method	BLASTX
NCBI GI	g4090884
BLAST score	518
E value	7.0e-53
Match length	102
% identity	98
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	150502
Seq. ID	LIB3175-042-P1-K1-C11
Method	BLASTX
NCBI GI	g4586263
BLAST score	635
E value	1.0e-66
Match length	122
% identity	98
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150503
Seq. ID	LIB3175-042-P1-K1-C12
Method	BLASTX
NCBI GI	g1903357
BLAST score	610
E value	1.0e-63
Match length	132
% identity	89
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	150504
Seq. ID	LIB3175-042-P1-K1-C2
Method	BLASTN
NCBI GI	g1865678
BLAST score	266
E value	1.0e-148
Match length	364
% identity	99
NCBI Description	A.thaliana ATB2 gene

Seq. No.	150505
Seq. ID	LIB3175-042-P1-K1-C3
Method	BLASTX
NCBI GI	g4185505

BLAST score	343
E value	2.0e-32
Match length	89
% identity	75
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	150506
Seq. ID	LIB3175-042-P1-K1-C4
Method	BLASTX
NCBI GI	g267079
BLAST score	661
E value	1.0e-69
Match length	122
% identity	99
NCBI Description	TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6 chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6 tubulin [Arabidopsis thaliana]

Seq. No.	150507
Seq. ID	LIB3175-042-P1-K1-C6
Method	BLASTX
NCBI GI	g1709446
BLAST score	486
E value	4.0e-49
Match length	115
% identity	83
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi_710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	150508
Seq. ID	LIB3175-042-P1-K1-C7
Method	BLASTX
NCBI GI	g4586263
BLAST score	404
E value	2.0e-39
Match length	112
% identity	71
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150509
Seq. ID	LIB3175-042-P1-K1-C8
Method	BLASTX
NCBI GI	g1755162
BLAST score	225
E value	2.0e-18
Match length	126
% identity	48
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	150510
Seq. ID	LIB3175-042-P1-K1-D10
Method	BLASTN

NCBI GI	g2062153
BLAST score	41
E value	9.0e-14
Match length	188
% identity	87
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150511
Seq. ID	LIB3175-042-P1-K1-D11
Method	BLASTN
NCBI GI	g4220645
BLAST score	283
E value	1.0e-158
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	150512
Seq. ID	LIB3175-042-P1-K1-D2
Method	BLASTX
NCBI GI	g1174623
BLAST score	246
E value	6.0e-21
Match length	87
% identity	59
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) >gi_529705 (U13070) C. elegans cct-6 (similar to T complex proteins, Tcp-1-related, Cctz) [Caenorhabditis elegans]

Seq. No.	150513
Seq. ID	LIB3175-042-P1-K1-D4
Method	BLASTN
NCBI GI	g1209241
BLAST score	372
E value	0.0e+00
Match length	387
% identity	99
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	150514
Seq. ID	LIB3175-042-P1-K1-D5
Method	BLASTN
NCBI GI	g4063737
BLAST score	247
E value	1.0e-137
Match length	287
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150515
Seq. ID	LIB3175-042-P1-K1-D6
Method	BLASTN
NCBI GI	g3420042
BLAST score	72

E value	2.0e-32
Match length	176
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150516
Seq. ID	LIB3175-042-P1-K1-D7
Method	BLASTX
NCBI GI	g2317913
BLAST score	533
E value	1.0e-54
Match length	106
% identity	99
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	150517
Seq. ID	LIB3175-042-P1-K1-D8
Method	BLASTN
NCBI GI	g3420042
BLAST score	278
E value	1.0e-155
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150518
Seq. ID	LIB3175-042-P1-K1-D9
Method	BLASTN
NCBI GI	g4206764
BLAST score	377
E value	0.0e+00
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	150519
Seq. ID	LIB3175-042-P1-K1-E1
Method	BLASTX
NCBI GI	g2500430
BLAST score	364
E value	8.0e-35
Match length	73
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	150520
Seq. ID	LIB3175-042-P1-K1-E10
Method	BLASTN
NCBI GI	g4220645
BLAST score	34
E value	2.0e-09
Match length	94
% identity	85

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	150521
Seq. ID	LIB3175-042-P1-K1-E11
Method	BLASTX
NCBI GI	g4454036
BLAST score	277
E value	1.0e-24
Match length	76
% identity	64
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	150522
Seq. ID	LIB3175-042-P1-K1-E12
Method	BLASTN
NCBI GI	g4586241
BLAST score	45
E value	4.0e-16
Match length	61
% identity	66
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	150523
Seq. ID	LIB3175-042-P1-K1-E2
Method	BLASTX
NCBI GI	g1213536
BLAST score	151
E value	8.0e-10
Match length	91
% identity	41
NCBI Description	(U50193) the above GenBank entry begins at aa 120 [Caenorhabditis elegans]

Seq. No.	150524
Seq. ID	LIB3175-042-P1-K1-E7
Method	BLASTX
NCBI GI	g3080372
BLAST score	651
E value	2.0e-68
Match length	124
% identity	99
NCBI Description	(AL022580) putative pectinacetylesterase [Arabidopsis thaliana]

Seq. No.	150525
Seq. ID	LIB3175-042-P1-K1-E8
Method	BLASTX
NCBI GI	g4432856
BLAST score	695
E value	1.0e-73
Match length	132
% identity	100
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	150526
Seq. ID	LIB3175-042-P1-K1-E9
Method	BLASTX
NCBI GI	g2129672
BLAST score	207
E value	1.0e-16
Match length	67
% identity	66
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	150527
Seq. ID	LIB3175-042-P1-K1-F1
Method	BLASTN
NCBI GI	g4159707
BLAST score	98
E value	1.0e-47
Match length	346
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	150528
Seq. ID	LIB3175-042-P1-K1-F10
Method	BLASTX
NCBI GI	g4204299
BLAST score	709
E value	3.0e-75
Match length	134
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	150529
Seq. ID	LIB3175-042-P1-K1-F11
Method	BLASTN
NCBI GI	g2062153
BLAST score	45
E value	3.0e-16
Match length	189
% identity	85
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150530
Seq. ID	LIB3175-042-P1-K1-F3
Method	BLASTX
NCBI GI	g3024526
BLAST score	470
E value	2.0e-47
Match length	105
% identity	91
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	150531
Seq. ID	LIB3175-042-P1-K1-F4
Method	BLASTX
NCBI GI	g1170639
BLAST score	166
E value	1.0e-11
Match length	130
% identity	33
NCBI Description	3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE (KDO TRANSFERASE) >gi_1073787_pir__F64084 3-deoxy-d-manno-octulosonic-acid transferase (kdtA) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1573651 (U32748) 3-deoxy-d-manno-octulosonic-acid transferase (kdtA) [Haemophilus influenzae Rd]

Seq. No.	150532
Seq. ID	LIB3175-042-P1-K1-F5
Method	BLASTN
NCBI GI	g2264319
BLAST score	59
E value	5.0e-25
Match length	109
% identity	68
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	150533
Seq. ID	LIB3175-042-P1-K1-F6
Method	BLASTX
NCBI GI	g529353
BLAST score	202
E value	2.0e-23
Match length	92
% identity	60
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	150534
Seq. ID	LIB3175-042-P1-K1-F7
Method	BLASTX
NCBI GI	g4185505
BLAST score	460
E value	5.0e-46
Match length	112
% identity	78
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	150535
Seq. ID	LIB3175-042-P1-K1-F8
Method	BLASTX
NCBI GI	g115783
BLAST score	561
E value	7.0e-58
Match length	105
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150536
Seq. ID	LIB3175-042-P1-K1-F9
Method	BLASTX
NCBI GI	g2829885
BLAST score	369
E value	2.0e-35
Match length	102
% identity	70
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	150537
Seq. ID	LIB3175-042-P1-K1-G10
Method	BLASTX
NCBI GI	g4567279
BLAST score	498
E value	2.0e-50
Match length	134
% identity	71
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	150538
Seq. ID	LIB3175-042-P1-K1-G11
Method	BLASTX
NCBI GI	g127041
BLAST score	506
E value	2.0e-51
Match length	99
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	150539
Seq. ID	LIB3175-042-P1-K1-G12
Method	BLASTX
NCBI GI	g130720
BLAST score	277
E value	1.0e-24
Match length	103
% identity	50
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	150540
Seq. ID	LIB3175-042-P1-K1-G2
Method	BLASTX

NCBI GI	g2119846
BLAST score	424
E value	7.0e-42
Match length	110
% identity	78
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150541
Seq. ID	LIB3175-042-P1-K1-G3
Method	BLASTX
NCBI GI	g3540185
BLAST score	362
E value	2.0e-34
Match length	133
% identity	48
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	150542
Seq. ID	LIB3175-042-P1-K1-G4
Method	BLASTX
NCBI GI	g1174162
BLAST score	476
E value	4.0e-48
Match length	85
% identity	98
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	150543
Seq. ID	LIB3175-042-P1-K1-G5
Method	BLASTN
NCBI GI	g2564049
BLAST score	52
E value	1.0e-20
Match length	76
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	150544
Seq. ID	LIB3175-042-P1-K1-G7
Method	BLASTN
NCBI GI	g4760411
BLAST score	42
E value	3.0e-14
Match length	143
% identity	71
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	150545
Seq. ID	LIB3175-042-P1-K1-G8
Method	BLASTX
NCBI GI	g2583108
BLAST score	605
E value	5.0e-63
Match length	133
% identity	92
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	150546
Seq. ID	LIB3175-042-P1-K1-G9
Method	BLASTN
NCBI GI	g2924728
BLAST score	71
E value	1.0e-31
Match length	365
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	150547
Seq. ID	LIB3175-042-P1-K1-H1
Method	BLASTN
NCBI GI	g4263753
BLAST score	200
E value	1.0e-108
Match length	357
% identity	90
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	150548
Seq. ID	LIB3175-042-P1-K1-H10
Method	BLASTX
NCBI GI	g462174
BLAST score	288
E value	6.0e-26
Match length	93
% identity	67
NCBI Description	GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP SYNTHETASE) (DIMETHYLALLYLTRANSFERASE / GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE >gi_413730 (L25813) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	150549
Seq. ID	LIB3175-042-P1-K1-H11
Method	BLASTX
NCBI GI	g2342685
BLAST score	182
E value	7.0e-14
Match length	72
% identity	50
NCBI Description	(AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595

come from this gene. [Arabidopsis thaliana]

Seq. No.	150550
Seq. ID	LIB3175-042-P1-K1-H12
Method	BLASTN
NCBI GI	g3449327
BLAST score	86
E value	5.0e-41
Match length	165
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	150551
Seq. ID	LIB3175-042-P1-K1-H2
Method	BLASTX
NCBI GI	g2244799
BLAST score	254
E value	8.0e-22
Match length	81
% identity	68
NCBI Description	(Z97336) carnitine racemase homolog [Arabidopsis thaliana]

Seq. No.	150552
Seq. ID	LIB3175-042-P1-K1-H3
Method	BLASTX
NCBI GI	g1402912
BLAST score	628
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	150553
Seq. ID	LIB3175-042-P1-K1-H4
Method	BLASTN
NCBI GI	g3128136
BLAST score	46
E value	1.0e-16
Match length	103
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	150554
Seq. ID	LIB3175-042-P1-K1-H5
Method	BLASTX
NCBI GI	g2119846
BLAST score	617
E value	2.0e-64
Match length	117
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis

thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150555
Seq. ID	LIB3175-042-P1-K1-H6
Method	BLASTX
NCBI GI	g3043415
BLAST score	287
E value	4.0e-26
Match length	54
% identity	100
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	150556
Seq. ID	LIB3175-042-P1-K1-H7
Method	BLASTN
NCBI GI	g547390
BLAST score	361
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	150557
Seq. ID	LIB3175-042-P1-K1-H8
Method	BLASTN
NCBI GI	g2264317
BLAST score	192
E value	1.0e-104
Match length	398
% identity	47
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	150558
Seq. ID	LIB3175-042-P1-K1-H9
Method	BLASTX
NCBI GI	g3063445
BLAST score	147
E value	2.0e-09
Match length	132
% identity	3
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	150559
Seq. ID	LIB3175-043-P1-K1-A10
Method	BLASTN
NCBI GI	g2815404
BLAST score	155
E value	1.0e-81
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	150560
Seq. ID	LIB3175-043-P1-K1-A12

Method	BLASTX
NCBI GI	g3355468
BLAST score	492
E value	1.0e-49
Match length	123
% identity	86
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	150561
Seq. ID	LIB3175-043-P1-K1-A3
Method	BLASTX
NCBI GI	g3063470
BLAST score	328
E value	7.0e-33
Match length	121
% identity	63
NCBI Description	(AC003981) F22O13.32 [Arabidopsis thaliana]

Seq. No.	150562
Seq. ID	LIB3175-043-P1-K1-A5
Method	BLASTN
NCBI GI	g547390
BLAST score	258
E value	1.0e-143
Match length	298
% identity	97
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	150563
Seq. ID	LIB3175-043-P1-K1-A6
Method	BLASTX
NCBI GI	g2642159
BLAST score	456
E value	9.0e-46
Match length	104
% identity	88
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	150564
Seq. ID	LIB3175-043-P1-K1-A7
Method	BLASTX
NCBI GI	g4218123
BLAST score	325
E value	3.0e-30
Match length	95
% identity	75
NCBI Description	(AL035353) photosystem I subunit PSI-E-like protein [Arabidopsis thaliana]

Seq. No.	150565
Seq. ID	LIB3175-043-P1-K1-A8
Method	BLASTX
NCBI GI	g2275202

BLAST score	419
E value	3.0e-41
Match length	78
% identity	100
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	150566
Seq. ID	LIB3175-043-P1-K1-A9
Method	BLASTN
NCBI GI	g4049332
BLAST score	170
E value	6.0e-91
Match length	185
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	150567
Seq. ID	LIB3175-043-P1-K1-B1
Method	BLASTN
NCBI GI	g2760167
BLAST score	65
E value	2.0e-28
Match length	101
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	150568
Seq. ID	LIB3175-043-P1-K1-B10
Method	BLASTN
NCBI GI	g2264305
BLAST score	278
E value	1.0e-155
Match length	320
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	150569
Seq. ID	LIB3175-043-P1-K1-B11
Method	BLASTX
NCBI GI	g2119846
BLAST score	576
E value	8.0e-60
Match length	110
% identity	96
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150570

Seq. ID	LIB3175-043-P1-K1-B12
Method	BLASTX
NCBI GI	g3157934
BLAST score	321
E value	1.0e-29
Match length	63
% identity	98
NCBI Description	(AC002131) Similar to hypothetical protein F09E5.8 gb_U37429 from C. elegans. ESTs gb_T42019 and gb_N97000 come from this gene. [Arabidopsis thaliana]

Seq. No.	150571
Seq. ID	LIB3175-043-P1-K1-B2
Method	BLASTX
NCBI GI	g730864
BLAST score	165
E value	2.0e-11
Match length	139
% identity	32
NCBI Description	SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN SPX19) >gi_2117442_pir__S50729 sporulation protein SPS19 - yeast (Saccharomyces cerevisiae) >gi_600063_emb_CAA55506_ (X78898) N1362 [Saccharomyces cerevisiae] >gi_1302205_emb_CAA96103_ (Z71479) ORF YNL202w [Saccharomyces cerevisiae]

Seq. No.	150572
Seq. ID	LIB3175-043-P1-K1-B3
Method	BLASTX
NCBI GI	g481132
BLAST score	369
E value	2.0e-35
Match length	87
% identity	83
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	150573
Seq. ID	LIB3175-043-P1-K1-B4
Method	BLASTN
NCBI GI	g2244991
BLAST score	333
E value	0.0e+00
Match length	390
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150574
Seq. ID	LIB3175-043-P1-K1-B5
Method	BLASTX
NCBI GI	g481914
BLAST score	264
E value	3.0e-55
Match length	127
% identity	85

NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica napus]
Seq. No.	150575
Seq. ID	LIB3175-043-P1-K1-B7
Method	BLASTX
NCBI GI	g3367516
BLAST score	586
E value	7.0e-61
Match length	118
% identity	96
NCBI Description	(AC004392) Similar to beta-glucosidase BGQ60 precursor gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]
Seq. No.	150576
Seq. ID	LIB3175-043-P1-K1-B8
Method	BLASTN
NCBI GI	g3702731
BLAST score	282
E value	1.0e-157
Match length	332
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.	150577
Seq. ID	LIB3175-043-P1-K1-C1
Method	BLASTX
NCBI GI	g3913418
BLAST score	796
E value	2.0e-85
Match length	154
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.	150578
Seq. ID	LIB3175-043-P1-K1-C10
Method	BLASTX
NCBI GI	g1916613
BLAST score	294
E value	1.0e-26
Match length	126
% identity	55
NCBI Description	(U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
Seq. No.	150579
Seq. ID	LIB3175-043-P1-K1-C11
Method	BLASTN
NCBI GI	g3080430
BLAST score	221
E value	1.0e-121
Match length	404
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19

(ESSAII project)

Seq. No.	150580
Seq. ID	LIB3175-043-P1-K1-C12
Method	BLASTX
NCBI GI	g2119846
BLAST score	657
E value	4.0e-69
Match length	138
% identity	91
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150581
Seq. ID	LIB3175-043-P1-K1-C3
Method	BLASTN
NCBI GI	g4757395
BLAST score	35
E value	4.0e-10
Match length	95
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	150582
Seq. ID	LIB3175-043-P1-K1-C5
Method	BLASTX
NCBI GI	g1175013
BLAST score	467
E value	6.0e-47
Match length	111
% identity	83
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	150583
Seq. ID	LIB3175-043-P1-K1-C6
Method	BLASTX
NCBI GI	g4467097
BLAST score	486
E value	3.0e-49
Match length	118
% identity	87
NCBI Description	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]

Seq. No.	150584
Seq. ID	LIB3175-043-P1-K1-C7
Method	BLASTN
NCBI GI	g2264305

BLAST score	325
E value	0.0e+00
Match length	325
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	150585
Seq. ID	LIB3175-043-P1-K1-C8
Method	BLASTN
NCBI GI	g4678196
BLAST score	362
E value	0.0e+00
Match length	494
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence, complete sequence

Seq. No.	150586
Seq. ID	LIB3175-043-P1-K1-C9
Method	BLASTX
NCBI GI	g3935181
BLAST score	808
E value	9.0e-87
Match length	153
% identity	96
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	150587
Seq. ID	LIB3175-043-P1-K1-D1
Method	BLASTN
NCBI GI	g2696018
BLAST score	62
E value	2.0e-26
Match length	235
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	150588
Seq. ID	LIB3175-043-P1-K1-D10
Method	BLASTN
NCBI GI	g950022
BLAST score	48
E value	6.0e-18
Match length	237
% identity	88
NCBI Description	A.thaliana psbW gene

Seq. No.	150589
Seq. ID	LIB3175-043-P1-K1-D11
Method	BLASTX
NCBI GI	g3298443
BLAST score	327
E value	2.0e-30
Match length	84
% identity	71

NCBI Description	(AB010880) chloroplast ribosomal protein L17 [Nicotiana tabacum]

Seq. No.	150590
Seq. ID	LIB3175-043-P1-K1-D12
Method	BLASTX
NCBI GI	g115783
BLAST score	341
E value	3.0e-32
Match length	91
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150591
Seq. ID	LIB3175-043-P1-K1-D2
Method	BLASTN
NCBI GI	g1402905
BLAST score	52
E value	5.0e-21
Match length	52
% identity	100
NCBI Description	A.thaliana mRNA for peroxidase, prxr2

Seq. No.	150592
Seq. ID	LIB3175-043-P1-K1-D3
Method	BLASTX
NCBI GI	g1709535
BLAST score	717
E value	5.0e-76
Match length	161
% identity	92
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	150593
Seq. ID	LIB3175-043-P1-K1-D4
Method	BLASTX
NCBI GI	g4678308
BLAST score	583
E value	1.0e-60
Match length	113
% identity	100
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	150594
Seq. ID	LIB3175-043-P1-K1-D7
Method	BLASTX
NCBI GI	g1402906

BLAST score	726
E value	4.0e-77
Match length	159
% identity	90
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	150595
Seq. ID	LIB3175-043-P1-K1-D8
Method	BLASTX
NCBI GI	g4567311
BLAST score	531
E value	3.0e-54
Match length	97
% identity	97
NCBI Description	(AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No.	150596
Seq. ID	LIB3175-043-P1-K1-D9
Method	BLASTN
NCBI GI	g2245031
BLAST score	430
E value	0.0e+00
Match length	451
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150597
Seq. ID	LIB3175-043-P1-K1-E1
Method	BLASTX
NCBI GI	g3540183
BLAST score	545
E value	7.0e-56
Match length	104
% identity	100
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	150598
Seq. ID	LIB3175-043-P1-K1-E10
Method	BLASTX
NCBI GI	g4056469
BLAST score	298
E value	3.0e-27
Match length	68
% identity	93
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	150599
Seq. ID	LIB3175-043-P1-K1-E11
Method	BLASTX

NCBI GI	g3287691
BLAST score	350
E value	2.0e-33
Match length	105
% identity	67
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	150600
Seq. ID	LIB3175-043-P1-K1-E12
Method	BLASTN
NCBI GI	g3449313
BLAST score	38
E value	1.0e-12
Match length	54
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	150601
Seq. ID	LIB3175-043-P1-K1-E3
Method	BLASTX
NCBI GI	g1504020
BLAST score	308
E value	4.0e-28
Match length	147
% identity	28
NCBI Description	(D86973) similar to Yeast translation activator GCN1 (P1:A48126) [Homo sapiens]

Seq. No.	150602
Seq. ID	LIB3175-043-P1-K1-E4
Method	BLASTX
NCBI GI	g113782
BLAST score	802
E value	4.0e-86
Match length	147
% identity	99
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	150603
Seq. ID	LIB3175-043-P1-K1-E5
Method	BLASTX
NCBI GI	g3600058
BLAST score	570
E value	7.0e-59
Match length	118
% identity	99
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	150604
Seq. ID	LIB3175-043-P1-K1-E6

Method	BLASTN
NCBI GI	g2459406
BLAST score	139
E value	3.0e-72
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150605
Seq. ID	LIB3175-043-P1-K1-E7
Method	BLASTX
NCBI GI	g1351272
BLAST score	192
E value	3.0e-15
Match length	36
% identity	100
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	150606
Seq. ID	LIB3175-043-P1-K1-E9
Method	BLASTN
NCBI GI	g4733953
BLAST score	332
E value	0.0e+00
Match length	332
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	150607
Seq. ID	LIB3175-043-P1-K1-F1
Method	BLASTX
NCBI GI	g1702986
BLAST score	451
E value	5.0e-45
Match length	111
% identity	86
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	150608
Seq. ID	LIB3175-043-P1-K1-F11
Method	BLASTN
NCBI GI	g469109
BLAST score	35
E value	9.0e-11
Match length	63
% identity	89
NCBI Description	A.thaliana (Columbia) Di19 mRNA

Seq. No.	150609
Seq. ID	LIB3175-043-P1-K1-F12

Method	BLASTX
NCBI GI	g119975
BLAST score	172
E value	1.0e-17
Match length	83
% identity	70
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	150610
Seq. ID	LIB3175-043-P1-K1-F2
Method	BLASTX
NCBI GI	g121907
BLAST score	413
E value	2.0e-40
Match length	145
% identity	63
NCBI Description	HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 - Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459) Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215) histone H1-2C [Arabidopsis thaliana]

Seq. No.	150611
Seq. ID	LIB3175-043-P1-K1-F3
Method	BLASTX
NCBI GI	g2832625
BLAST score	558
E value	2.0e-57
Match length	157
% identity	69
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	150612
Seq. ID	LIB3175-043-P1-K1-F4
Method	BLASTX
NCBI GI	g2832625
BLAST score	90
E value	5.0e-14
Match length	105
% identity	47
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	150613
Seq. ID	LIB3175-043-P1-K1-F5
Method	BLASTN
NCBI GI	g3980374
BLAST score	142
E value	5.0e-74
Match length	279
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150614

Seq. ID	LIB3175-043-P1-K1-F6
Method	BLASTN
NCBI GI	g3510343
BLAST score	336
E value	0.0e+00
Match length	351
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	150615
Seq. ID	LIB3175-043-P1-K1-F7
Method	BLASTX
NCBI GI	g121907
BLAST score	349
E value	1.0e-33
Match length	136
% identity	64
NCBI Description	HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 - Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459) Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215) histone H1-2C [Arabidopsis thaliana]

Seq. No.	150616
Seq. ID	LIB3175-043-P1-K1-F8
Method	BLASTX
NCBI GI	g4581114
BLAST score	577
E value	1.0e-59
Match length	118
% identity	96
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	150617
Seq. ID	LIB3175-043-P1-K1-F9
Method	BLASTX
NCBI GI	g4154281
BLAST score	300
E value	2.0e-27
Match length	78
% identity	73
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	150618
Seq. ID	LIB3175-043-P1-K1-G1
Method	BLASTX
NCBI GI	g4006827
BLAST score	409
E value	6.0e-40
Match length	159
% identity	50
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	150619
Seq. ID	LIB3175-043-P1-K1-G10

Method	BLASTX
NCBI GI	g629692
BLAST score	418
E value	3.0e-41
Match length	93
% identity	84
NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No.	150620
Seq. ID	LIB3175-043-P1-K1-G11
Method	BLASTX
NCBI GI	g3860247
BLAST score	468
E value	7.0e-47
Match length	109
% identity	84
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	150621
Seq. ID	LIB3175-043-P1-K1-G12
Method	BLASTX
NCBI GI	g119975
BLAST score	514
E value	2.0e-52
Match length	120
% identity	88
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	150622
Seq. ID	LIB3175-043-P1-K1-G2
Method	BLASTN
NCBI GI	g4756967
BLAST score	149
E value	3.0e-78
Match length	209
% identity	95
NCBI Description	Arabidopsis thaliana partial mRNA for hypothetical protein, clone g19

Seq. No.	150623
Seq. ID	LIB3175-043-P1-K1-G4
Method	BLASTN
NCBI GI	g4733953
BLAST score	332
E value	0.0e+00
Match length	402
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	150624

Seq. ID	LIB3175-043-P1-K1-G6
Method	BLASTX
NCBI GI	g3738339
BLAST score	337
E value	1.0e-31
Match length	125
% identity	63
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	150625
Seq. ID	LIB3175-043-P1-K1-G7
Method	BLASTX
NCBI GI	g4337206
BLAST score	303
E value	1.0e-27
Match length	131
% identity	44
NCBI Description	(AC006403) putative replication factor-A protein [Arabidopsis thaliana]

Seq. No.	150626
Seq. ID	LIB3175-043-P1-K1-G8
Method	BLASTN
NCBI GI	g2244991
BLAST score	428
E value	0.0e+00
Match length	481
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150627
Seq. ID	LIB3175-043-P1-K1-G9
Method	BLASTX
NCBI GI	g2435519
BLAST score	512
E value	4.0e-52
Match length	123
% identity	83
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	150628
Seq. ID	LIB3175-043-P1-K1-H1
Method	BLASTX
NCBI GI	g2062167
BLAST score	261
E value	1.0e-25
Match length	59
% identity	100
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	150629
Seq. ID	LIB3175-043-P1-K1-H2
Method	BLASTX

NCBI GI	g2275196
BLAST score	329
E value	5.0e-31
Match length	69
% identity	96
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana] >gi_4630746_gb_AAD26596.1_AC007236_1 (AC007236) water stress-induced protein [Arabidopsis thaliana]

Seq. No.	150630
Seq. ID	LIB3175-043-P1-K1-H3
Method	BLASTN
NCBI GI	g4584841
BLAST score	280
E value	1.0e-156
Match length	328
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	150631
Seq. ID	LIB3175-043-P1-K1-H6
Method	BLASTX
NCBI GI	g1076348
BLAST score	551
E value	8.0e-57
Match length	109
% identity	98
NCBI Description	myosin MYA1, class V - Arabidopsis thaliana >gi_433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis thaliana]

Seq. No.	150632
Seq. ID	LIB3175-043-P1-K1-H7
Method	BLASTX
NCBI GI	g132074
BLAST score	618
E value	1.0e-64
Match length	117
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	150633
Seq. ID	LIB3175-044-P1-K1-A1
Method	BLASTX
NCBI GI	g2654122
BLAST score	202
E value	5.0e-16
Match length	59
% identity	66
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	150634

Seq. ID	LIB3175-044-P1-K1-A10
Method	BLASTX
NCBI GI	g2494299
BLAST score	341
E value	6.0e-32
Match length	145
% identity	52
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	150635
Seq. ID	LIB3175-044-P1-K1-A11
Method	BLASTX
NCBI GI	g1706186
BLAST score	224
E value	3.0e-18
Match length	138
% identity	37
NCBI Description	HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi_110721_pir__A32742 murine ecotropic retrovirus receptor protein - mouse >gi_532612 (M26687) ecotropic retrovirus receptor [Mus musculus]

Seq. No.	150636
Seq. ID	LIB3175-044-P1-K1-A12
Method	BLASTX
NCBI GI	g99699
BLAST score	373
E value	7.0e-36
Match length	101
% identity	68
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgsr1) - Arabidopsis thaliana

Seq. No.	150637
Seq. ID	LIB3175-044-P1-K1-A2
Method	BLASTX
NCBI GI	g3721926
BLAST score	410
E value	1.0e-40
Match length	125
% identity	72
NCBI Description	(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

Seq. No.	150638
Seq. ID	LIB3175-044-P1-K1-A4
Method	BLASTX
NCBI GI	g629557
BLAST score	554
E value	6.0e-57
Match length	144
% identity	50
NCBI Description	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi_510240_emb_CAA43420_ (X61108) RNA binding protein

[Arabidopsis thaliana]

Seq. No.	150639
Seq. ID	LIB3175-044-P1-K1-A5
Method	BLASTX
NCBI GI	g899608
BLAST score	728
E value	2.0e-77
Match length	146
% identity	22
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	150640
Seq. ID	LIB3175-044-P1-K1-A6
Method	BLASTX
NCBI GI	g2317906
BLAST score	867
E value	1.0e-93
Match length	169
% identity	99
NCBI Description	(U89959) ARA-5 [Arabidopsis thaliana]

Seq. No.	150641
Seq. ID	LIB3175-044-P1-K1-A7
Method	BLASTX
NCBI GI	g3046700
BLAST score	367
E value	2.0e-35
Match length	78
% identity	95
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	150642
Seq. ID	LIB3175-044-P1-K1-B10
Method	BLASTN
NCBI GI	g4206762
BLAST score	239
E value	1.0e-132
Match length	409
% identity	54
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	150643
Seq. ID	LIB3175-044-P1-K1-B12
Method	BLASTX
NCBI GI	g4262156
BLAST score	466
E value	1.0e-46
Match length	121
% identity	79
NCBI Description	(AC005275) putative component of cytochrome B6-F complex [Arabidopsis thaliana]

Seq. No.	150644
Seq. ID	LIB3175-044-P1-K1-B2
Method	BLASTX
NCBI GI	g2129650
BLAST score	520
E value	5.0e-53
Match length	109
% identity	87
NCBI Description	myb-related transcription factor 24,7K - Arabidopsis thaliana >gi_1197190_emb_CAA92280_ (Z68157) myb-related transcription factor [Arabidopsis thaliana]

Seq. No.	150645
Seq. ID	LIB3175-044-P1-K1-B3
Method	BLASTX
NCBI GI	g1169476
BLAST score	858
E value	2.0e-92
Match length	170
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	150646
Seq. ID	LIB3175-044-P1-K1-B4
Method	BLASTX
NCBI GI	g1170203
BLAST score	556
E value	3.0e-57
Match length	142
% identity	79
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	150647
Seq. ID	LIB3175-044-P1-K1-B5
Method	BLASTX
NCBI GI	g1931644
BLAST score	269
E value	1.0e-23
Match length	123
% identity	45
NCBI Description	(U95973) membrane protein PTM1 precursor isolog [Arabidopsis thaliana]

Seq. No.	150648
Seq. ID	LIB3175-044-P1-K1-B6
Method	BLASTN
NCBI GI	g3367567
BLAST score	258
E value	1.0e-143
Match length	500
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	150649
Seq. ID	LIB3175-044-P1-K1-B7
Method	BLASTX
NCBI GI	g3892712
BLAST score	340
E value	8.0e-32
Match length	66
% identity	100
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	150650
Seq. ID	LIB3175-044-P1-K1-C1
Method	BLASTN
NCBI GI	g2947056
BLAST score	239
E value	1.0e-132
Match length	299
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150651
Seq. ID	LIB3175-044-P1-K1-C10
Method	BLASTX
NCBI GI	g2765081
BLAST score	705
E value	1.0e-74
Match length	153
% identity	91
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	150652
Seq. ID	LIB3175-044-P1-K1-C11
Method	BLASTX
NCBI GI	g1532135
BLAST score	300
E value	3.0e-27
Match length	74
% identity	76
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]

Seq. No.	150653
Seq. ID	LIB3175-044-P1-K1-C12
Method	BLASTX
NCBI GI	g4741960
BLAST score	620
E value	1.0e-64
Match length	137
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	150654
Seq. ID	LIB3175-044-P1-K1-C3
Method	BLASTX
NCBI GI	g4581146

BLAST score	761
E value	4.0e-81
Match length	153
% identity	99
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	150655
Seq. ID	LIB3175-044-P1-K1-C4
Method	BLASTX
NCBI GI	g404668
BLAST score	142
E value	7.0e-09
Match length	88
% identity	42
NCBI Description	(L22568) cor78 [Arabidopsis thaliana]

Seq. No.	150656
Seq. ID	LIB3175-044-P1-K1-C5
Method	BLASTN
NCBI GI	g3201608
BLAST score	61
E value	2.0e-25
Match length	89
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150657
Seq. ID	LIB3175-044-P1-K1-C6
Method	BLASTN
NCBI GI	g4512656
BLAST score	35
E value	1.0e-10
Match length	83
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	150658
Seq. ID	LIB3175-044-P1-K1-C7
Method	BLASTX
NCBI GI	g4406767
BLAST score	393
E value	2.0e-38
Match length	75
% identity	100
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	150659
Seq. ID	LIB3175-044-P1-K1-C8
Method	BLASTN
NCBI GI	g3695400
BLAST score	94
E value	2.0e-45
Match length	302

% identity	83
NCBI Description	Arabidopsis thaliana BAC T9A4

Seq. No.	150660
Seq. ID	LIB3175-044-P1-K1-C9
Method	BLASTX
NCBI GI	g4586265
BLAST score	310
E value	2.0e-28
Match length	145
% identity	45
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150661
Seq. ID	LIB3175-044-P1-K1-D1
Method	BLASTX
NCBI GI	g1652297
BLAST score	210
E value	2.0e-16
Match length	131
% identity	37
NCBI Description	(D90904) hypothetical protein [Synechocystis sp.]

Seq. No.	150662
Seq. ID	LIB3175-044-P1-K1-D10
Method	BLASTN
NCBI GI	g2244747
BLAST score	134
E value	2.0e-69
Match length	142
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150663
Seq. ID	LIB3175-044-P1-K1-D11
Method	BLASTN
NCBI GI	g3341671
BLAST score	142
E value	6.0e-74
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150664
Seq. ID	LIB3175-044-P1-K1-D12
Method	BLASTX
NCBI GI	g3096931
BLAST score	360
E value	3.0e-34
Match length	112
% identity	58
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	150665

Seq. ID	LIB3175-044-P1-K1-D4
Method	BLASTX
NCBI GI	g3122673
BLAST score	407
E value	6.0e-40
Match length	96
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	150666
Seq. ID	LIB3175-044-P1-K1-D6
Method	BLASTX
NCBI GI	g2244896
BLAST score	47
E value	6.0e-70
Match length	138
% identity	94
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	150667
Seq. ID	LIB3175-044-P1-K1-D9
Method	BLASTX
NCBI GI	g1532167
BLAST score	181
E value	3.0e-13
Match length	64
% identity	48
NCBI Description	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No.	150668
Seq. ID	LIB3175-044-P1-K1-E1
Method	BLASTX
NCBI GI	g4503169
BLAST score	214
E value	5.0e-17
Match length	93
% identity	42
NCBI Description	cut (Drosophila)-like 1 (CCAAT displacement protein) >gi_457517 (L12579) alternatively spliced [Homo sapiens]

Seq. No.	150669
Seq. ID	LIB3175-044-P1-K1-E10
Method	BLASTN
NCBI GI	g4415928
BLAST score	97
E value	3.0e-47
Match length	331
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150670
Seq. ID	LIB3175-044-P1-K1-E12
Method	BLASTN
NCBI GI	g2245073
BLAST score	342
E value	0.0e+00
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150671
Seq. ID	LIB3175-044-P1-K1-E2
Method	BLASTX
NCBI GI	g2865394
BLAST score	180
E value	4.0e-13
Match length	50
% identity	60
NCBI Description	(AF036949) basic leucine zipper protein [Zea mays]

Seq. No.	150672
Seq. ID	LIB3175-044-P1-K1-E3
Method	BLASTN
NCBI GI	g3399678
BLAST score	152
E value	3.0e-80
Match length	212
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150673
Seq. ID	LIB3175-044-P1-K1-E4
Method	BLASTX
NCBI GI	g1353352
BLAST score	233
E value	1.0e-19
Match length	61
% identity	77
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	150674
Seq. ID	LIB3175-044-P1-K1-E5
Method	BLASTX
NCBI GI	g3600058
BLAST score	529
E value	4.0e-54
Match length	117
% identity	94
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	150675
Seq. ID	LIB3175-044-P1-K1-E6
Method	BLASTX

NCBI GI	g4115337
BLAST score	815
E value	2.0e-87
Match length	165
% identity	18
NCBI Description	(L81141) ubiquitin [Pisum sativum]

Seq. No.	150676
Seq. ID	LIB3175-044-P1-K1-E8
Method	BLASTN
NCBI GI	g4581138
BLAST score	393
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	150677
Seq. ID	LIB3175-044-P1-K1-F1
Method	BLASTN
NCBI GI	g3335356
BLAST score	79
E value	6.0e-37
Match length	123
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150678
Seq. ID	LIB3175-044-P1-K1-F10
Method	BLASTX
NCBI GI	g3135611
BLAST score	727
E value	3.0e-77
Match length	150
% identity	93
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	150679
Seq. ID	LIB3175-044-P1-K1-F11
Method	BLASTX
NCBI GI	g2501578
BLAST score	740
E value	1.0e-78
Match length	164
% identity	87
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	150680
Seq. ID	LIB3175-044-P1-K1-F2
Method	BLASTX
NCBI GI	g4406783
BLAST score	591

E value	2.0e-61
Match length	114
% identity	100
NCBI Description	(AC006532) putative glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	150681
Seq. ID	LIB3175-044-P1-K1-F3
Method	BLASTX
NCBI GI	g4006941
BLAST score	596
E value	6.0e-62
Match length	127
% identity	91
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	150682
Seq. ID	LIB3175-044-P1-K1-F5
Method	BLASTX
NCBI GI	g3451071
BLAST score	377
E value	1.0e-36
Match length	89
% identity	89
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	150683
Seq. ID	LIB3175-044-P1-K1-F6
Method	BLASTN
NCBI GI	g2351065
BLAST score	358
E value	0.0e+00
Match length	486
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	150684
Seq. ID	LIB3175-044-P1-K1-F7
Method	BLASTX
NCBI GI	g4586256
BLAST score	643
E value	2.0e-67
Match length	133
% identity	95
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	150685
Seq. ID	LIB3175-044-P1-K1-F8
Method	BLASTX
NCBI GI	g2894603
BLAST score	423
E value	1.0e-41
Match length	96

% identity	85
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	150686
Seq. ID	LIB3175-044-P1-K1-F9
Method	BLASTX
NCBI GI	g2160184
BLAST score	608
E value	3.0e-63
Match length	113
% identity	100
NCBI Description	(AC000132) ESTs gb_H37208,gb_H36853 come from this gene. [Arabidopsis thaliana]

Seq. No.	150687
Seq. ID	LIB3175-044-P1-K1-G1
Method	BLASTX
NCBI GI	g112741
BLAST score	58
E value	2.0e-68
Match length	164
% identity	84
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	150688
Seq. ID	LIB3175-044-P1-K1-G10
Method	BLASTX
NCBI GI	g2347098
BLAST score	337
E value	1.0e-31
Match length	80
% identity	81
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	150689
Seq. ID	LIB3175-044-P1-K1-G11
Method	BLASTN
NCBI GI	g2062153
BLAST score	48
E value	4.0e-18
Match length	125
% identity	90
NCBI Description	Arabidopsis thaliana chromosome III BAC T02004 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150690
Seq. ID	LIB3175-044-P1-K1-G2
Method	BLASTX
NCBI GI	g3785986

BLAST score	413
E value	2.0e-40
Match length	107
% identity	78
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	150691
Seq. ID	LIB3175-044-P1-K1-G3
Method	BLASTN
NCBI GI	g3790580
BLAST score	383
E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHB1a mRNA, complete cds

Seq. No.	150692
Seq. ID	LIB3175-044-P1-K1-G6
Method	BLASTN
NCBI GI	g4531433
BLAST score	478
E value	0.0e+00
Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	150693
Seq. ID	LIB3175-044-P1-K1-G7
Method	BLASTX
NCBI GI	g1495269
BLAST score	636
E value	1.0e-66
Match length	141
% identity	87
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	150694
Seq. ID	LIB3175-044-P1-K1-G9
Method	BLASTX
NCBI GI	g4204300
BLAST score	246
E value	8.0e-21
Match length	147
% identity	41
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	150695
Seq. ID	LIB3175-044-P1-K1-H10
Method	BLASTX
NCBI GI	g4185505
BLAST score	467
E value	8.0e-47

Match length	115
% identity	77
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	150696
Seq. ID	LIB3175-044-P1-K1-H11
Method	BLASTX
NCBI GI	g4689316
BLAST score	545
E value	5.0e-56
Match length	113
% identity	94
NCBI Description	(AF130973) peroxisomal targeting signal type 2 receptor [Arabidopsis thaliana]

Seq. No.	150697
Seq. ID	LIB3175-044-P1-K1-H3
Method	BLASTN
NCBI GI	g3098611
BLAST score	295
E value	1.0e-165
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds

Seq. No.	150698
Seq. ID	LIB3175-044-P1-K1-H4
Method	BLASTX
NCBI GI	g1432083
BLAST score	695
E value	2.0e-73
Match length	155
% identity	89
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	150699
Seq. ID	LIB3175-044-P1-K1-H5
Method	BLASTX
NCBI GI	g1419090
BLAST score	279
E value	1.0e-24
Match length	108
% identity	53
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	150700
Seq. ID	LIB3175-044-P1-K1-H6
Method	BLASTX
NCBI GI	g486784
BLAST score	338
E value	9.0e-32

Match length	107
% identity	58
NCBI Description	Golgi-associated particle 102K chain - human

Seq. No.	150701
Seq. ID	LIB3175-044-P1-K1-H7
Method	BLASTX
NCBI GI	g4063570
BLAST score	767
E value	6.0e-82
Match length	155
% identity	98
NCBI Description	(AF035917) ATP synthase beta subunit [Tropaeolum tricolor]

Seq. No.	150702
Seq. ID	LIB3175-044-P1-K1-H8
Method	BLASTX
NCBI GI	g3328231
BLAST score	87
E value	3.1e-02
Match length	112
% identity	19
NCBI Description	(AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus laevis]

Seq. No.	150703
Seq. ID	LIB3175-044-P1-K1-H9
Method	BLASTX
NCBI GI	g4689316
BLAST score	856
E value	3.0e-92
Match length	163
% identity	52
NCBI Description	(AF130973) peroxisomal targeting signal type 2 receptor [Arabidopsis thaliana]

Seq. No.	150704
Seq. ID	LIB3175-045-P1-K1-A10
Method	BLASTX
NCBI GI	g1172873
BLAST score	428
E value	3.0e-42
Match length	133
% identity	67
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150705
Seq. ID	LIB3175-045-P1-K1-A11
Method	BLASTX
NCBI GI	g1172873
BLAST score	438
E value	2.0e-43
Match length	135
% identity	67

NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.	150706
Seq. ID	LIB3175-045-P1-K1-A2
Method	BLASTX
NCBI GI	g266693
BLAST score	244
E value	4.0e-21
Match length	72
% identity	69
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.	150707
Seq. ID	LIB3175-045-P1-K1-A3
Method	BLASTX
NCBI GI	g4038037
BLAST score	239
E value	4.0e-20
Match length	48
% identity	100
NCBI Description	(AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.	150708
Seq. ID	LIB3175-045-P1-K1-A5
Method	BLASTN
NCBI GI	g1871173
BLAST score	367
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence
Seq. No.	150709
Seq. ID	LIB3175-045-P1-K1-A6
Method	BLASTX
NCBI GI	g585536
BLAST score	771
E value	2.0e-82
Match length	142
% identity	99
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]
Seq. No.	150710
Seq. ID	LIB3175-045-P1-K1-A7
Method	BLASTX
NCBI GI	g1172873

BLAST score	284
E value	1.0e-25
Match length	89
% identity	65
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150711
Seq. ID	LIB3175-045-P1-K1-A8
Method	BLASTN
NCBI GI	g2815404
BLAST score	103
E value	9.0e-51
Match length	339
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	150712
Seq. ID	LIB3175-045-P1-K1-A9
Method	BLASTX
NCBI GI	g1172873
BLAST score	208
E value	8.0e-17
Match length	80
% identity	57
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150713
Seq. ID	LIB3175-045-P1-K1-B10
Method	BLASTX
NCBI GI	g1172873
BLAST score	416
E value	7.0e-41
Match length	133
% identity	66
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150714
Seq. ID	LIB3175-045-P1-K1-B11
Method	BLASTN
NCBI GI	g2815404
BLAST score	60
E value	4.0e-25
Match length	188
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	150715
Seq. ID	LIB3175-045-P1-K1-B12
Method	BLASTX
NCBI GI	g2827143
BLAST score	287
E value	1.0e-54
Match length	132
% identity	78
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	150716
Seq. ID	LIB3175-045-P1-K1-B2
Method	BLASTX
NCBI GI	g1518540
BLAST score	180
E value	1.0e-13
Match length	45
% identity	82
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	150717
Seq. ID	LIB3175-045-P1-K1-B4
Method	BLASTX
NCBI GI	g1172873
BLAST score	178
E value	4.0e-39
Match length	135
% identity	61
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150718
Seq. ID	LIB3175-045-P1-K1-B6
Method	BLASTX
NCBI GI	g1172873
BLAST score	428
E value	3.0e-42
Match length	135
% identity	67
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150719
Seq. ID	LIB3175-045-P1-K1-B7
Method	BLASTX
NCBI GI	g1172873
BLAST score	436
E value	3.0e-43
Match length	135
% identity	67
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A

precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150720
Seq. ID	LIB3175-045-P1-K1-B8
Method	BLASTX
NCBI GI	g1172873
BLAST score	382
E value	6.0e-37
Match length	115
% identity	67
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150721
Seq. ID	LIB3175-045-P1-K1-B9
Method	BLASTX
NCBI GI	g1172873
BLAST score	325
E value	3.0e-30
Match length	118
% identity	56
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150722
Seq. ID	LIB3175-045-P1-K1-C1
Method	BLASTN
NCBI GI	g2337888
BLAST score	140
E value	5.0e-73
Match length	230
% identity	47
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	150723
Seq. ID	LIB3175-045-P1-K1-C10
Method	BLASTN
NCBI GI	g2245031
BLAST score	124
E value	3.0e-63
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150724
Seq. ID	LIB3175-045-P1-K1-C11
Method	BLASTX
NCBI GI	g1175014
BLAST score	557
E value	2.0e-57

Match length	124
% identity	89
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi_629543_pir__S44085 plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic protein 2b [Arabidopsis thaliana]

Seq. No.	150725
Seq. ID	LIB3175-045-P1-K1-C12
Method	BLASTX
NCBI GI	g4220535
BLAST score	489
E value	2.0e-49
Match length	97
% identity	98
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	150726
Seq. ID	LIB3175-045-P1-K1-C2
Method	BLASTX
NCBI GI	g1172873
BLAST score	239
E value	4.0e-20
Match length	97
% identity	55
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	150727
Seq. ID	LIB3175-045-P1-K1-C3
Method	BLASTN
NCBI GI	g4455229
BLAST score	407
E value	0.0e+00
Match length	425
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	150728
Seq. ID	LIB3175-045-P1-K1-C4
Method	BLASTX
NCBI GI	g1703115
BLAST score	223
E value	2.0e-18
Match length	81
% identity	57
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	150729
Seq. ID	LIB3175-045-P1-K1-C5

Method	BLASTX
NCBI GI	g2464899
BLAST score	390
E value	8.0e-38
Match length	112
% identity	73
NCBI Description	(Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	150730
Seq. ID	LIB3175-045-P1-K1-C6
Method	BLASTX
NCBI GI	g1172872
BLAST score	614
E value	4.0e-64
Match length	135
% identity	89
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	150731
Seq. ID	LIB3175-045-P1-K1-C7
Method	BLASTX
NCBI GI	g421826
BLAST score	403
E value	2.0e-39
Match length	78
% identity	100
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	150732
Seq. ID	LIB3175-045-P1-K1-C8
Method	BLASTX
NCBI GI	g2342688
BLAST score	411
E value	3.0e-40
Match length	90
% identity	98
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). [Arabidopsis thaliana]

Seq. No.	150733
Seq. ID	LIB3175-045-P1-K1-C9
Method	BLASTX
NCBI GI	g2244760
BLAST score	315
E value	3.0e-29
Match length	86
% identity	70
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	150734
Seq. ID	LIB3175-045-P1-K1-D1
Method	BLASTX
NCBI GI	g3128187
BLAST score	331
E value	6.0e-31
Match length	77
% identity	77
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	150735
Seq. ID	LIB3175-045-P1-K1-D3
Method	BLASTX
NCBI GI	g1345595
BLAST score	527
E value	6.0e-54
Match length	110
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	150736
Seq. ID	LIB3175-045-P1-K1-D5
Method	BLASTN
NCBI GI	g3449331
BLAST score	98
E value	4.0e-48
Match length	150
% identity	45
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	150737
Seq. ID	LIB3175-045-P1-K1-D6
Method	BLASTX
NCBI GI	g4544419
BLAST score	656
E value	5.0e-69
Match length	128
% identity	100
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	150738
Seq. ID	LIB3175-045-P1-K1-D7
Method	BLASTX
NCBI GI	g2213592
BLAST score	271
E value	6.0e-24
Match length	115
% identity	24
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	150739
Seq. ID	LIB3175-045-P1-K1-D8

Method	BLASTX
NCBI GI	g1076301
BLAST score	159
E value	1.0e-10
Match length	54
% identity	35
NCBI Description	CONSTANS protein - Arabidopsis thaliana >gi_1161514_emb_CAA64407_ (X94937) CONSTANS protein [Arabidopsis thaliana]

Seq. No.	150740
Seq. ID	LIB3175-045-P1-K1-E10
Method	BLASTX
NCBI GI	g399013
BLAST score	511
E value	5.0e-52
Match length	100
% identity	100
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	150741
Seq. ID	LIB3175-045-P1-K1-E12
Method	BLASTX
NCBI GI	g3021336
BLAST score	630
E value	6.0e-66
Match length	138
% identity	91
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	150742
Seq. ID	LIB3175-045-P1-K1-E2
Method	BLASTN
NCBI GI	g4757409
BLAST score	364
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	150743
Seq. ID	LIB3175-045-P1-K1-E3
Method	BLASTX
NCBI GI	g2213592
BLAST score	293
E value	2.0e-26
Match length	119
% identity	25
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	150744
Seq. ID	LIB3175-045-P1-K1-E4
Method	BLASTX
NCBI GI	g115767
BLAST score	680
E value	8.0e-72
Match length	134
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	150745
Seq. ID	LIB3175-045-P1-K1-E5
Method	BLASTX
NCBI GI	g2462929
BLAST score	554
E value	4.0e-57
Match length	116
% identity	93
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	150746
Seq. ID	LIB3175-045-P1-K1-E7
Method	BLASTX
NCBI GI	g1170028
BLAST score	518
E value	8.0e-53
Match length	118
% identity	86
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	150747
Seq. ID	LIB3175-045-P1-K1-E8
Method	BLASTX
NCBI GI	g2462748
BLAST score	622
E value	5.0e-65
Match length	122
% identity	99
NCBI Description	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No.	150748
Seq. ID	LIB3175-045-P1-K1-F1
Method	BLASTX
NCBI GI	g3123188
BLAST score	479
E value	2.0e-48

Match length	94
% identity	98
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	150749
Seq. ID	LIB3175-045-P1-K1-F11
Method	BLASTX
NCBI GI	g1402912
BLAST score	518
E value	6.0e-53
Match length	116
% identity	88
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	150750
Seq. ID	LIB3175-045-P1-K1-F12
Method	BLASTX
NCBI GI	g1076361
BLAST score	442
E value	3.0e-44
Match length	92
% identity	98
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129660_pir__S69197 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) (clone TE 1-7) - Arabidopsis thaliana >gi_804946_emb_CAA85389_ (Z36912) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	150751
Seq. ID	LIB3175-045-P1-K1-F2
Method	BLASTX
NCBI GI	g3024426
BLAST score	277
E value	5.0e-25
Match length	75
% identity	77
NCBI Description	PYRUVATE,PHOSPHATE DIKINASE PRECURSOR (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi_1084302_pir__S55478 pyruvate,orthophosphate dikinase (EC 2.7.9.1) - common ice plant >gi_854265_emb_CAA57872_ (X82489) pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum]

Seq. No.	150752
Seq. ID	LIB3175-045-P1-K1-F3
Method	BLASTX
NCBI GI	g2338712
BLAST score	262
E value	9.0e-23
Match length	69
% identity	74
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	150753
Seq. ID	LIB3175-045-P1-K1-F4
Method	BLASTN
NCBI GI	g3176693
BLAST score	49
E value	2.0e-18
Match length	57
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150754
Seq. ID	LIB3175-045-P1-K1-F5
Method	BLASTX
NCBI GI	g3834309
BLAST score	102
E value	7.0e-75
Match length	141
% identity	100
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	150755
Seq. ID	LIB3175-045-P1-K1-F6
Method	BLASTX
NCBI GI	g2088654
BLAST score	549
E value	2.0e-56
Match length	121
% identity	90
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	150756
Seq. ID	LIB3175-045-P1-K1-F8
Method	BLASTN
NCBI GI	g4757409
BLAST score	116
E value	2.0e-58
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	150757
Seq. ID	LIB3175-045-P1-K1-F9
Method	BLASTX
NCBI GI	g4581146
BLAST score	580
E value	4.0e-60
Match length	118
% identity	98
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	150758
Seq. ID	LIB3175-045-P1-K1-G1
Method	BLASTN
NCBI GI	g3297806
BLAST score	152
E value	7.0e-80
Match length	433
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	150759
Seq. ID	LIB3175-045-P1-K1-G11
Method	BLASTX
NCBI GI	g4586254
BLAST score	408
E value	4.0e-40
Match length	109
% identity	82
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	150760
Seq. ID	LIB3175-045-P1-K1-G12
Method	BLASTX
NCBI GI	g113782
BLAST score	490
E value	2.0e-49
Match length	110
% identity	89
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	150761
Seq. ID	LIB3175-045-P1-K1-G3
Method	BLASTX
NCBI GI	g4510424
BLAST score	203
E value	2.0e-27
Match length	71
% identity	96
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	150762
Seq. ID	LIB3175-045-P1-K1-G4
Method	BLASTX
NCBI GI	g3242730
BLAST score	656
E value	5.0e-69
Match length	128
% identity	99
NCBI Description	(AC003040) putative host response protein (Pir7) [Arabidopsis thaliana]

Seq. No.	150763

Seq. ID	LIB3175-045-P1-K1-G5
Method	BLASTN
NCBI GI	g3985955
BLAST score	377
E value	0.0e+00
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	150764
Seq. ID	LIB3175-045-P1-K1-G6
Method	BLASTX
NCBI GI	g4760577
BLAST score	186
E value	7.0e-14
Match length	111
% identity	32
NCBI Description	(AB019602) IDN3-B [Homo sapiens]

Seq. No.	150765
Seq. ID	LIB3175-045-P1-K1-G7
Method	BLASTX
NCBI GI	g2827621
BLAST score	405
E value	1.0e-39
Match length	134
% identity	60
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	150766
Seq. ID	LIB3175-045-P1-K1-G8
Method	BLASTX
NCBI GI	g1084335
BLAST score	543
E value	9.0e-56
Match length	114
% identity	89
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	150767
Seq. ID	LIB3175-045-P1-K1-G9
Method	BLASTX
NCBI GI	g114330
BLAST score	233
E value	7.0e-22
Match length	63
% identity	84
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35) type 1, plasma membrane - Arabidopsis thaliana >gi_166746 (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]

Seq. No.	150768

Seq. ID	LIB3175-045-P1-K1-H1
Method	BLASTX
NCBI GI	g115783
BLAST score	342
E value	1.0e-60
Match length	125
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	150769
Seq. ID	LIB3175-045-P1-K1-H10
Method	BLASTX
NCBI GI	g1769905
BLAST score	126
E value	3.0e-39
Match length	127
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	150770
Seq. ID	LIB3175-045-P1-K1-H11
Method	BLASTX
NCBI GI	g2129648
BLAST score	665
E value	5.0e-70
Match length	121
% identity	99
NCBI Description	MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana]

Seq. No.	150771
Seq. ID	LIB3175-045-P1-K1-H12
Method	BLASTX
NCBI GI	g2499811
BLAST score	533
E value	1.0e-57
Match length	116
% identity	98
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	150772
Seq. ID	LIB3175-045-P1-K1-H2
Method	BLASTX
NCBI GI	g3819710
BLAST score	463
E value	2.0e-46
Match length	84
% identity	99
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	150773
Seq. ID	LIB3175-045-P1-K1-H3
Method	BLASTX
NCBI GI	g4510346
BLAST score	198
E value	7.0e-58
Match length	125
% identity	97
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150774
Seq. ID	LIB3175-045-P1-K1-H4
Method	BLASTN
NCBI GI	g4587986
BLAST score	58
E value	5.0e-24
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	150775
Seq. ID	LIB3175-045-P1-K1-H5
Method	BLASTX
NCBI GI	g421826
BLAST score	424
E value	7.0e-42
Match length	122
% identity	68
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	150776
Seq. ID	LIB3175-045-P1-K1-H6
Method	BLASTX
NCBI GI	g3510254
BLAST score	233
E value	2.0e-19
Match length	54
% identity	87
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	150777
Seq. ID	LIB3175-045-P1-K1-H7
Method	BLASTX
NCBI GI	g3183185
BLAST score	231
E value	4.0e-19
Match length	62
% identity	73
NCBI Description	GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG >gi_2224766_emb_CAB09712_ (Z97025) product highly similar to elongation factor EF-G [Bacillus subtilis] >gi_2633848_emb_CAB13350_ (Z99111) similar to GTP-binding elongation factor [Bacillus subtilis]

Seq. No.	150778
Seq. ID	LIB3175-045-P1-K1-H8
Method	BLASTX
NCBI GI	g1076317
BLAST score	632
E value	3.0e-66
Match length	138
% identity	89
NCBI Description	dihydrodipicolinate synthase (EC 4.2.1.52) precursor - Arabidopsis thaliana

Seq. No.	150779
Seq. ID	LIB3175-046-P1-K1-A11
Method	BLASTN
NCBI GI	g1669388
BLAST score	137
E value	3.0e-71
Match length	238
% identity	97
NCBI Description	Arabidopsis thaliana actin 8 (ACT8) gene, complete cds

Seq. No.	150780
Seq. ID	LIB3175-046-P1-K1-A12
Method	BLASTN
NCBI GI	g2245073
BLAST score	414
E value	0.0e+00
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150781
Seq. ID	LIB3175-046-P1-K1-A2
Method	BLASTX
NCBI GI	g115767
BLAST score	398
E value	9.0e-39
Match length	80
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	150782
Seq. ID	LIB3175-046-P1-K1-A4
Method	BLASTN
NCBI GI	g2494110
BLAST score	408
E value	0.0e+00
Match length	420
% identity	90

NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	150783
Seq. ID	LIB3175-046-P1-K1-A5
Method	BLASTX
NCBI GI	g498038
BLAST score	400
E value	6.0e-39
Match length	142
% identity	51
NCBI Description	(L33792) lipid transfer protein [Senecio odorus]

Seq. No.	150784
Seq. ID	LIB3175-046-P1-K1-A6
Method	BLASTX
NCBI GI	g4337189
BLAST score	725
E value	4.0e-77
Match length	139
% identity	98
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	150785
Seq. ID	LIB3175-046-P1-K1-A7
Method	BLASTX
NCBI GI	g3641252
BLAST score	115
E value	7.0e-06
Match length	88
% identity	6
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	150786
Seq. ID	LIB3175-046-P1-K1-B1
Method	BLASTX
NCBI GI	g2052379
BLAST score	727
E value	2.0e-77
Match length	135
% identity	100
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No.	150787
Seq. ID	LIB3175-046-P1-K1-B10
Method	BLASTX
NCBI GI	g2129648
BLAST score	316
E value	3.0e-29
Match length	69
% identity	52
NCBI Description	MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana]

Seq. No.	150788
Seq. ID	LIB3175-046-P1-K1-B12
Method	BLASTX
NCBI GI	g4581116
BLAST score	463
E value	2.0e-46
Match length	121
% identity	61
NCBI Description	(AC005825) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	150789
Seq. ID	LIB3175-046-P1-K1-B2
Method	BLASTX
NCBI GI	g1465368
BLAST score	316
E value	4.0e-29
Match length	143
% identity	57
NCBI Description	(X99548) bHLH protein [Arabidopsis thaliana]

Seq. No.	150790
Seq. ID	LIB3175-046-P1-K1-B4
Method	BLASTX
NCBI GI	g4586265
BLAST score	506
E value	2.0e-51
Match length	138
% identity	73
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	150791
Seq. ID	LIB3175-046-P1-K1-B5
Method	BLASTX
NCBI GI	g267069
BLAST score	572
E value	4.0e-59
Match length	108
% identity	98
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	150792
Seq. ID	LIB3175-046-P1-K1-B6
Method	BLASTX
NCBI GI	g2462749
BLAST score	362
E value	2.0e-34
Match length	109
% identity	65
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	150793
Seq. ID	LIB3175-046-P1-K1-B8

Method	BLASTX
NCBI GI	g3184100
BLAST score	232
E value	3.0e-19
Match length	72
% identity	57
NCBI Description	(AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No.	150794
Seq. ID	LIB3175-046-P1-K1-C1
Method	BLASTX
NCBI GI	g3929364
BLAST score	455
E value	2.0e-45
Match length	96
% identity	91
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	150795
Seq. ID	LIB3175-046-P1-K1-C2
Method	BLASTX
NCBI GI	g2218152
BLAST score	77
E value	1.0e-65
Match length	131
% identity	91
NCBI Description	(AF005279) type IIIa membrane protein cp-wap13 [Vigna unguiculata]

Seq. No.	150796
Seq. ID	LIB3175-046-P1-K1-C3
Method	BLASTN
NCBI GI	g2281648
BLAST score	140
E value	8.0e-73
Match length	140
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	150797
Seq. ID	LIB3175-046-P1-K1-C4
Method	BLASTX
NCBI GI	g2723477
BLAST score	203
E value	7.0e-16
Match length	45
% identity	96
NCBI Description	(D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	150798
Seq. ID	LIB3175-046-P1-K1-C5
Method	BLASTX
NCBI GI	g2252857
BLAST score	276
E value	9.0e-25
Match length	63
% identity	94
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	150799
Seq. ID	LIB3175-046-P1-K1-C6
Method	BLASTX
NCBI GI	g1351272
BLAST score	95
E value	9.0e-58
Match length	140
% identity	87
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	150800
Seq. ID	LIB3175-046-P1-K1-C7
Method	BLASTX
NCBI GI	g3928134
BLAST score	474
E value	1.0e-47
Match length	130
% identity	45
NCBI Description	(AJ130956) annexin P38 [Capsicum annuum]

Seq. No.	150801
Seq. ID	LIB3175-046-P1-K1-C8
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	3.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	150802
Seq. ID	LIB3175-046-P1-K1-C9
Method	BLASTX
NCBI GI	g4522012
BLAST score	403
E value	8.0e-45
Match length	131
% identity	68
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150803
Seq. ID	LIB3175-046-P1-K1-D1
Method	BLASTX
NCBI GI	g1351272
BLAST score	562
E value	6.0e-58
Match length	129
% identity	87
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	150804
Seq. ID	LIB3175-046-P1-K1-D10
Method	BLASTX
NCBI GI	g21913
BLAST score	213
E value	5.0e-17
Match length	88
% identity	44
NCBI Description	(X62626) vicilin [Theobroma cacao]

Seq. No.	150805
Seq. ID	LIB3175-046-P1-K1-D11
Method	BLASTN
NCBI GI	g4220636
BLAST score	331
E value	0.0e+00
Match length	400
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	150806
Seq. ID	LIB3175-046-P1-K1-D2
Method	BLASTN
NCBI GI	g2351068
BLAST score	80
E value	2.0e-37
Match length	116
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	150807
Seq. ID	LIB3175-046-P1-K1-D3
Method	BLASTX
NCBI GI	g4006834
BLAST score	554
E value	4.0e-57
Match length	108
% identity	100
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	150808

Seq. ID	LIB3175-046-P1-K1-D4
Method	BLASTX
NCBI GI	g1737218
BLAST score	386
E value	3.0e-37
Match length	73
% identity	100
NCBI Description	(U79959) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	150809
Seq. ID	LIB3175-046-P1-K1-D5
Method	BLASTX
NCBI GI	g2887500
BLAST score	287
E value	1.0e-25
Match length	60
% identity	87
NCBI Description	(AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No.	150810
Seq. ID	LIB3175-046-P1-K1-D6
Method	BLASTX
NCBI GI	g2388578
BLAST score	718
E value	3.0e-76
Match length	144
% identity	100
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	150811
Seq. ID	LIB3175-046-P1-K1-D7
Method	BLASTX
NCBI GI	g3335365
BLAST score	595
E value	8.0e-62
Match length	145
% identity	83
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	150812
Seq. ID	LIB3175-046-P1-K1-D8
Method	BLASTN
NCBI GI	g3449321
BLAST score	223
E value	1.0e-122
Match length	366
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	150813
Seq. ID	LIB3175-046-P1-K1-D9

Method	BLASTX
NCBI GI	g1710581
BLAST score	491
E value	9.0e-50
Match length	105
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	150814
Seq. ID	LIB3175-046-P1-K1-E1
Method	BLASTX
NCBI GI	g4519671
BLAST score	251
E value	2.0e-21
Match length	80
% identity	65
NCBI Description	(AB017693) transfactor [Nicotiana tabacum]

Seq. No.	150815
Seq. ID	LIB3175-046-P1-K1-E10
Method	BLASTN
NCBI GI	g3402745
BLAST score	155
E value	1.0e-81
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	150816
Seq. ID	LIB3175-046-P1-K1-E11
Method	BLASTX
NCBI GI	g2829899
BLAST score	162
E value	2.0e-11
Match length	50
% identity	66
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	150817
Seq. ID	LIB3175-046-P1-K1-E12
Method	BLASTX
NCBI GI	g417073
BLAST score	546
E value	4.0e-56
Match length	120
% identity	86
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	150818

Seq. ID	LIB3175-046-P1-K1-E2
Method	BLASTN
NCBI GI	g2760165
BLAST score	53
E value	4.0e-21
Match length	161
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	150819
Seq. ID	LIB3175-046-P1-K1-E3
Method	BLASTX
NCBI GI	g3913518
BLAST score	358
E value	4.0e-34
Match length	77
% identity	97
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	150820
Seq. ID	LIB3175-046-P1-K1-E4
Method	BLASTN
NCBI GI	g3860243
BLAST score	268
E value	1.0e-149
Match length	346
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150821
Seq. ID	LIB3175-046-P1-K1-E5
Method	BLASTX
NCBI GI	g3287679
BLAST score	607
E value	3.0e-63
Match length	137
% identity	85
NCBI Description	(AC003979) T22J18.6 [Arabidopsis thaliana]

Seq. No.	150822
Seq. ID	LIB3175-046-P1-K1-E6
Method	BLASTX
NCBI GI	g2104957
BLAST score	605
E value	5.0e-63
Match length	112
% identity	100
NCBI Description	(U96924) immunophilin [Arabidopsis thaliana]

Seq. No.	150823
Seq. ID	LIB3175-046-P1-K1-E7
Method	BLASTN

NCBI GI	g3985952
BLAST score	46
E value	7.0e-17
Match length	123
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	150824
Seq. ID	LIB3175-046-P1-K1-E8
Method	BLASTX
NCBI GI	g3157924
BLAST score	291
E value	3.0e-26
Match length	56
% identity	100
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	150825
Seq. ID	LIB3175-046-P1-K1-E9
Method	BLASTX
NCBI GI	g4741960
BLAST score	769
E value	3.0e-82
Match length	141
% identity	99
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	150826
Seq. ID	LIB3175-046-P1-K1-F1
Method	BLASTX
NCBI GI	g4589398
BLAST score	394
E value	3.0e-38
Match length	86
% identity	81
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	150827
Seq. ID	LIB3175-046-P1-K1-F10
Method	BLASTX
NCBI GI	g4732123
BLAST score	331
E value	3.0e-34
Match length	93
% identity	83
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]

Seq. No.	150828
Seq. ID	LIB3175-046-P1-K1-F12
Method	BLASTX

NCBI GI	g2738248
BLAST score	196
E value	1.0e-15
Match length	46
% identity	89
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	150829
Seq. ID	LIB3175-046-P1-K1-F2
Method	BLASTN
NCBI GI	g1865682
BLAST score	240
E value	1.0e-132
Match length	404
% identity	95
NCBI Description	A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No.	150830
Seq. ID	LIB3175-046-P1-K1-F4
Method	BLASTX
NCBI GI	g3176874
BLAST score	249
E value	7.0e-22
Match length	56
% identity	91
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	150831
Seq. ID	LIB3175-046-P1-K1-F5
Method	BLASTX
NCBI GI	g2623295
BLAST score	252
E value	1.0e-21
Match length	68
% identity	71
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150832
Seq. ID	LIB3175-046-P1-K1-F6
Method	BLASTN
NCBI GI	g2245031
BLAST score	412
E value	0.0e+00
Match length	433
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150833
Seq. ID	LIB3175-046-P1-K1-F8
Method	BLASTX
NCBI GI	g2245144
BLAST score	265
E value	2.0e-23
Match length	63

% identity	81
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	150834
Seq. ID	LIB3175-046-P1-K1-F9
Method	BLASTX
NCBI GI	g3860420
BLAST score	208
E value	2.0e-16
Match length	53
% identity	75
NCBI Description	(AJ011047) exo galactanase [Lupinus angustifolius]

Seq. No.	150835
Seq. ID	LIB3175-046-P1-K1-G11
Method	BLASTN
NCBI GI	g4263774
BLAST score	52
E value	2.0e-20
Match length	132
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150836
Seq. ID	LIB3175-046-P1-K1-G12
Method	BLASTX
NCBI GI	g3953473
BLAST score	608
E value	2.0e-63
Match length	123
% identity	100
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	150837
Seq. ID	LIB3175-046-P1-K1-G2
Method	BLASTN
NCBI GI	g3785968
BLAST score	39
E value	5.0e-13
Match length	130
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150838
Seq. ID	LIB3175-046-P1-K1-G4
Method	BLASTX
NCBI GI	g4538963
BLAST score	534
E value	1.0e-54
Match length	131
% identity	62
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	150839
Seq. ID	LIB3175-046-P1-K1-G5
Method	BLASTX
NCBI GI	g4263711
BLAST score	208
E value	2.0e-16
Match length	45
% identity	84
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	150840
Seq. ID	LIB3175-046-P1-K1-G6
Method	BLASTX
NCBI GI	g731529
BLAST score	189
E value	3.0e-14
Match length	127
% identity	37
NCBI Description	HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION >gi_1077719_pir__S50660 hypothetical protein YER157w - yeast (Saccharomyces cerevisiae) >gi_603397 (U18917) Yer157wp [Saccharomyces cerevisiae]

Seq. No.	150841
Seq. ID	LIB3175-046-P1-K1-G7
Method	BLASTN
NCBI GI	g4376087
BLAST score	314
E value	1.0e-176
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	150842
Seq. ID	LIB3175-046-P1-K1-G8
Method	BLASTX
NCBI GI	g3928103
BLAST score	481
E value	2.0e-48
Match length	102
% identity	94
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	150843
Seq. ID	LIB3175-046-P1-K1-H10
Method	BLASTX
NCBI GI	g1708420
BLAST score	349
E value	3.0e-33
Match length	107
% identity	72
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase

homologue [Arabidopsis thaliana]

Seq. No.	150844
Seq. ID	LIB3175-046-P1-K1-H11
Method	BLASTX
NCBI GI	g122781
BLAST score	183
E value	1.0e-13
Match length	47
% identity	68
NCBI Description	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi_82210_pir__A05198 hypothetical protein 229 - common tobacco chloroplast >gi_11844_emb_CAA77364_ (Z00044) hypothetical protein [Nicotiana tabacum] >gi_225212_prf__1211235AT ORF 229 [Nicotiana tabacum]

Seq. No.	150845
Seq. ID	LIB3175-046-P1-K1-H12
Method	BLASTN
NCBI GI	g4544381
BLAST score	65
E value	3.0e-28
Match length	88
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	150846
Seq. ID	LIB3175-046-P1-K1-H3
Method	BLASTX
NCBI GI	g1351411
BLAST score	144
E value	6.0e-25
Match length	92
% identity	61
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir__S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir__S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]

Seq. No.	150847
Seq. ID	LIB3175-046-P1-K1-H4
Method	BLASTX
NCBI GI	g4325346
BLAST score	586
E value	9.0e-61
Match length	134
% identity	88
NCBI Description	(AF128393) similar to N-ethylmaleimide sensitive fusion proteins; contains similarity to ATPases (Pfam: PF00004, Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana]

Seq. No.	150848
Seq. ID	LIB3175-046-P1-K1-H5
Method	BLASTX
NCBI GI	g2842469

BLAST score	168
E value	9.0e-12
Match length	80
% identity	40
NCBI Description	(AL021747) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	150849
Seq. ID	LIB3175-046-P1-K1-H7
Method	BLASTX
NCBI GI	g2160135
BLAST score	349
E value	5.0e-33
Match length	91
% identity	79
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.1,F19K23.15. EST gb_ATTS0156 comes from this gene. [Arabidopsis thaliana]

Seq. No.	150850
Seq. ID	LIB3175-047-P1-K1-A5
Method	BLASTN
NCBI GI	g2842474
BLAST score	46
E value	3.0e-17
Match length	103
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	150851
Seq. ID	LIB3175-047-P1-K1-A8
Method	BLASTN
NCBI GI	g16375
BLAST score	50
E value	2.0e-19
Match length	169
% identity	79
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	150852
Seq. ID	LIB3175-047-P1-K1-B2
Method	BLASTX
NCBI GI	g2129672
BLAST score	192
E value	8.0e-15
Match length	89
% identity	52
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	150853
Seq. ID	LIB3175-047-P1-K1-B6
Method	BLASTN
NCBI GI	g4559375

BLAST score	164
E value	3.0e-87
Match length	194
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	150854
Seq. ID	LIB3175-047-P1-K1-D11
Method	BLASTN
NCBI GI	g2564049
BLAST score	50
E value	2.0e-19
Match length	165
% identity	78
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	150855
Seq. ID	LIB3175-047-P1-K1-D4
Method	BLASTN
NCBI GI	g1184164
BLAST score	37
E value	1.0e-11
Match length	130
% identity	78
NCBI Description	Arabidopsis thaliana syntaxin-related knolle mRNA, complete cds

Seq. No.	150856
Seq. ID	LIB3175-047-P1-K1-D6
Method	BLASTN
NCBI GI	g905390
BLAST score	45
E value	1.0e-16
Match length	141
% identity	79
NCBI Description	Arabidopsis thaliana serine acetyltransferase (Sat-52) mRNA, complete cds

Seq. No.	150857
Seq. ID	LIB3175-047-P1-K1-E2
Method	BLASTX
NCBI GI	g3342804
BLAST score	107
E value	9.0e-18
Match length	59
% identity	75
NCBI Description	(AF061839) putative 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	150858
Seq. ID	LIB3175-047-P1-K1-E3
Method	BLASTX
NCBI GI	g3548811
BLAST score	218
E value	5.0e-18

Match length	86
% identity	53
NCBI Description	(AC005313) kinetochore (SKP1p)-like protein [Arabidopsis thaliana]

Seq. No.	150859
Seq. ID	LIB3175-047-P1-K1-E4
Method	BLASTN
NCBI GI	g4159700
BLAST score	58
E value	4.0e-24
Match length	204
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	150860
Seq. ID	LIB3175-047-P1-K1-E7
Method	BLASTN
NCBI GI	g2961335
BLAST score	44
E value	1.0e-15
Match length	99
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	150861
Seq. ID	LIB3175-047-P1-K1-E8
Method	BLASTN
NCBI GI	g4220633
BLAST score	161
E value	1.0e-85
Match length	167
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	150862
Seq. ID	LIB3175-047-P1-K1-F10
Method	BLASTN
NCBI GI	g4490291
BLAST score	155
E value	6.0e-82
Match length	231
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	150863
Seq. ID	LIB3175-047-P1-K1-F7
Method	BLASTX
NCBI GI	g2119046
BLAST score	463
E value	2.0e-46
Match length	101
% identity	92

NCBI Description	small nuclear ribonucleoprotein U1A - Arabidopsis thaliana >gi_1050430_emb_CAA90283_ (Z49991) U1snRNP-specific protein [Arabidopsis thaliana] >gi_2529669 (AC002535) U1snRNP-specific protein, U1A [Arabidopsis thaliana]
Seq. No.	150864
Seq. ID	LIB3175-047-P1-K1-F9
Method	BLASTX
NCBI GI	g4753655
BLAST score	284
E value	1.0e-25
Match length	80
% identity	66
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]
Seq. No.	150865
Seq. ID	LIB3175-047-P1-K1-G1
Method	BLASTN
NCBI GI	g4519192
BLAST score	107
E value	4.0e-53
Match length	206
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence
Seq. No.	150866
Seq. ID	LIB3175-047-P1-K1-G2
Method	BLASTX
NCBI GI	g3834312
BLAST score	492
E value	6.0e-50
Match length	114
% identity	81
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an
Seq. No.	150867
Seq. ID	LIB3175-047-P1-K1-G6
Method	BLASTN
NCBI GI	g2245126
BLAST score	45
E value	1.0e-16
Match length	126
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	150868
Seq. ID	LIB3175-047-P1-K1-G9
Method	BLASTX
NCBI GI	g4512675
BLAST score	254

E value	2.0e-22
Match length	63
% identity	83
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	150869
Seq. ID	LIB3175-047-P1-K1-H1
Method	BLASTN
NCBI GI	g2924257
BLAST score	65
E value	3.0e-28
Match length	159
% identity	43
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	150870
Seq. ID	LIB3175-047-P1-K1-H3
Method	BLASTN
NCBI GI	g4757403
BLAST score	94
E value	2.0e-45
Match length	303
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	150871
Seq. ID	LIB3175-048-P1-K1-A1
Method	BLASTX
NCBI GI	g2981620
BLAST score	138
E value	7.0e-09
Match length	27
% identity	100
NCBI Description	(AB008856) mutated 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	150872
Seq. ID	LIB3175-048-P1-K1-A4
Method	BLASTN
NCBI GI	g4733984
BLAST score	42
E value	7.0e-15
Match length	60
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F14O4 genomic sequence, complete sequence

Seq. No.	150873
Seq. ID	LIB3175-048-P1-K1-A5
Method	BLASTX
NCBI GI	g4056469
BLAST score	348
E value	5.0e-33
Match length	71
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation

factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	150874
Seq. ID	LIB3175-048-P1-K1-A7
Method	BLASTN
NCBI GI	g2842474
BLAST score	260
E value	1.0e-144
Match length	295
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	150875
Seq. ID	LIB3175-048-P1-K1-A8
Method	BLASTN
NCBI GI	g4455262
BLAST score	157
E value	3.0e-83
Match length	181
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	150876
Seq. ID	LIB3175-048-P1-K1-A9
Method	BLASTN
NCBI GI	g4584531
BLAST score	163
E value	1.0e-86
Match length	314
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	150877
Seq. ID	LIB3175-048-P1-K1-B1
Method	BLASTX
NCBI GI	g3319349
BLAST score	176
E value	3.0e-13
Match length	38
% identity	95
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	150878
Seq. ID	LIB3175-048-P1-K1-B10
Method	BLASTX
NCBI GI	g602764
BLAST score	240
E value	8.0e-21
Match length	51
% identity	92
NCBI Description	(D43783) beta-amylase [Arabidopsis thaliana]

>gi_998369_bbs_163908 (S77076) beta-amylase {EC 3.2.1.2} [Arabidopsis thaliana=thale cress, Heynh., Peptide, 498 aa] [Arabidopsis thaliana]

Seq. No.	150879
Seq. ID	LIB3175-048-P1-K1-B11
Method	BLASTN
NCBI GI	g2618605
BLAST score	113
E value	9.0e-57
Match length	262
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	150880
Seq. ID	LIB3175-048-P1-K1-B3
Method	BLASTX
NCBI GI	g120667
BLAST score	275
E value	5.0e-41
Match length	97
% identity	89
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	150881
Seq. ID	LIB3175-048-P1-K1-B4
Method	BLASTX
NCBI GI	g1922944
BLAST score	155
E value	7.0e-11
Match length	32
% identity	100
NCBI Description	(AC000106) Strong similarity to Picea histone H2A (gb_X67819). ESTs gb_ATTS3874,gb_T46627,gb_T14194 come from this gene. [Arabidopsis thaliana]

Seq. No.	150882
Seq. ID	LIB3175-048-P1-K1-B5
Method	BLASTX
NCBI GI	g542157
BLAST score	254
E value	2.0e-22
Match length	62
% identity	81
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	150883
Seq. ID	LIB3175-048-P1-K1-B6
Method	BLASTX
NCBI GI	g3395425

BLAST score	444
E value	2.0e-44
Match length	96
% identity	54
NCBI Description	(AC004683) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	150884
Seq. ID	LIB3175-048-P1-K1-C1
Method	BLASTN
NCBI GI	g4662640
BLAST score	275
E value	1.0e-153
Match length	324
% identity	25
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	150885
Seq. ID	LIB3175-048-P1-K1-C10
Method	BLASTX
NCBI GI	g557472
BLAST score	163
E value	4.0e-11
Match length	94
% identity	40
NCBI Description	(U15178) arabinosidase [Bacteroides ovatus]

Seq. No.	150886
Seq. ID	LIB3175-048-P1-K1-C4
Method	BLASTN
NCBI GI	g16363
BLAST score	32
E value	1.0e-08
Match length	96
% identity	82
NCBI Description	A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b binding protein

Seq. No.	150887
Seq. ID	LIB3175-048-P1-K1-C5
Method	BLASTN
NCBI GI	g4522002
BLAST score	78
E value	4.0e-36
Match length	98
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T23K3 genomic sequence, complete sequence

Seq. No.	150888
Seq. ID	LIB3175-048-P1-K1-C7
Method	BLASTX
NCBI GI	g399013
BLAST score	444
E value	2.0e-44
Match length	105

% identity	50
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	150889
Seq. ID	LIB3175-048-P1-K1-D1
Method	BLASTX
NCBI GI	g115767
BLAST score	295
E value	6.0e-27
Match length	81
% identity	74
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	150890
Seq. ID	LIB3175-048-P1-K1-D11
Method	BLASTX
NCBI GI	g1172635
BLAST score	466
E value	5.0e-47
Match length	97
% identity	96
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	150891
Seq. ID	LIB3175-048-P1-K1-D12
Method	BLASTN
NCBI GI	g2529657
BLAST score	42
E value	1.0e-14
Match length	135
% identity	78
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150892
Seq. ID	LIB3175-048-P1-K1-D4
Method	BLASTN
NCBI GI	g4519192
BLAST score	112
E value	4.0e-56
Match length	334
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MBK21, complete sequence

Seq. No.	150893
Seq. ID	LIB3175-048-P1-K1-D6
Method	BLASTX
NCBI GI	g3913651
BLAST score	227
E value	7.0e-19
Match length	104
% identity	46
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR (FNR) >gi_2225993_emb_CAA74359_ (Y14032) ferredoxin--NADP(+) reductase [Nicotiana tabacum]

Seq. No.	150894
Seq. ID	LIB3175-048-P1-K1-D7
Method	BLASTX
NCBI GI	g2181180
BLAST score	178
E value	4.0e-13
Match length	91
% identity	42
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	150895
Seq. ID	LIB3175-048-P1-K1-E1
Method	BLASTX
NCBI GI	g2832661
BLAST score	265
E value	2.0e-23
Match length	101
% identity	59
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	150896
Seq. ID	LIB3175-048-P1-K1-E2
Method	BLASTN
NCBI GI	g4063730
BLAST score	73
E value	2.0e-33
Match length	119
% identity	97
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	150897
Seq. ID	LIB3175-048-P1-K1-E5
Method	BLASTN
NCBI GI	g4454587
BLAST score	39
E value	5.0e-13
Match length	109
% identity	89
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	150898
Seq. ID	LIB3175-048-P1-K1-E8
Method	BLASTN
NCBI GI	g3785968
BLAST score	163
E value	1.0e-86
Match length	280
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150899
Seq. ID	LIB3175-048-P1-K1-F10
Method	BLASTN
NCBI GI	g2244950
BLAST score	318
E value	1.0e-179
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150900
Seq. ID	LIB3175-048-P1-K1-F12
Method	BLASTN
NCBI GI	g472876
BLAST score	52
E value	2.0e-20
Match length	119
% identity	82
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	150901
Seq. ID	LIB3175-048-P1-K1-F3
Method	BLASTN
NCBI GI	g2749918
BLAST score	33
E value	6.0e-09
Match length	124
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150902
Seq. ID	LIB3175-048-P1-K1-F4
Method	BLASTN
NCBI GI	g3327922
BLAST score	60
E value	2.0e-25
Match length	124
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150903
Seq. ID	LIB3175-048-P1-K1-F5

Method	BLASTX
NCBI GI	g2499610
BLAST score	537
E value	4.0e-55
Match length	120
% identity	88
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6) (ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457404_dbj_BAA04869_ (D21842) MAP kinase [Arabidopsis thaliana] >gi_2281091 (AC002333) MAP Kinase 6 [Arabidopsis thaliana]

Seq. No.	150904
Seq. ID	LIB3175-048-P1-K1-F7
Method	BLASTN
NCBI GI	g3033373
BLAST score	101
E value	1.0e-49
Match length	309
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150905
Seq. ID	LIB3175-048-P1-K1-G1
Method	BLASTN
NCBI GI	g531378
BLAST score	58
E value	2.0e-24
Match length	149
% identity	81
NCBI Description	A.thaliana RCI1B mRNA

Seq. No.	150906
Seq. ID	LIB3175-048-P1-K1-G8
Method	BLASTX
NCBI GI	g3983125
BLAST score	214
E value	9.0e-18
Match length	52
% identity	85
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	150907
Seq. ID	LIB3175-048-P1-K1-H1
Method	BLASTN
NCBI GI	g4165340
BLAST score	90
E value	4.0e-43
Match length	266
% identity	80
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150908

Seq. ID	LIB3175-048-P1-K1-H2
Method	BLASTX
NCBI GI	g2119846
BLAST score	526
E value	5.0e-54
Match length	98
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	150909
Seq. ID	LIB3175-048-P1-K1-H5
Method	BLASTN
NCBI GI	g2656031
BLAST score	67
E value	2.0e-29
Match length	139
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	150910
Seq. ID	LIB3175-048-P1-K1-H7
Method	BLASTX
NCBI GI	g3763932
BLAST score	333
E value	3.0e-31
Match length	94
% identity	66
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	150911
Seq. ID	LIB3175-049-P1-K1-A10
Method	BLASTN
NCBI GI	g4376087
BLAST score	65
E value	3.0e-28
Match length	153
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	150912
Seq. ID	LIB3175-049-P1-K1-A12
Method	BLASTN
NCBI GI	g4467094
BLAST score	39
E value	5.0e-13
Match length	117
% identity	78
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	150913
Seq. ID	LIB3175-049-P1-K1-A2
Method	BLASTX
NCBI GI	g2832717
BLAST score	470
E value	3.0e-47
Match length	118
% identity	75
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	150914
Seq. ID	LIB3175-049-P1-K1-A3
Method	BLASTX
NCBI GI	g1345595
BLAST score	386
E value	2.0e-37
Match length	110
% identity	62
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	150915
Seq. ID	LIB3175-049-P1-K1-A6
Method	BLASTN
NCBI GI	g4454004
BLAST score	318
E value	1.0e-179
Match length	345
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	150916
Seq. ID	LIB3175-049-P1-K1-A7
Method	BLASTN
NCBI GI	g4646229
BLAST score	82
E value	2.0e-38
Match length	209
% identity	81
NCBI Description	Arabidopsis thaliana chromosome II BAC F27A10 genomic sequence, complete sequence

Seq. No.	150917
Seq. ID	LIB3175-049-P1-K1-B11
Method	BLASTN
NCBI GI	g4510338
BLAST score	88
E value	6.0e-42
Match length	259
% identity	79
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	150918
Seq. ID	LIB3175-049-P1-K1-B3
Method	BLASTX
NCBI GI	g3915823
BLAST score	159
E value	3.0e-11
Match length	30
% identity	100
NCBI Description	[Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	150919
Seq. ID	LIB3175-049-P1-K1-B5
Method	BLASTX
NCBI GI	g2306917
BLAST score	425
E value	4.0e-42
Match length	96
% identity	86
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	150920
Seq. ID	LIB3175-049-P1-K1-B6
Method	BLASTN
NCBI GI	g2924505
BLAST score	252
E value	1.0e-139
Match length	349
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	150921
Seq. ID	LIB3175-049-P1-K1-B9
Method	BLASTN
NCBI GI	g1628582
BLAST score	50
E value	3.0e-19
Match length	116
% identity	48
NCBI Description	Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds

Seq. No.	150922
Seq. ID	LIB3175-049-P1-K1-C12
Method	BLASTN
NCBI GI	g2894557
BLAST score	48
E value	4.0e-18
Match length	119
% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	150923
Seq. ID	LIB3175-049-P1-K1-D2

Method	BLASTN
NCBI GI	g4589427
BLAST score	116
E value	1.0e-58
Match length	136
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	150924
Seq. ID	LIB3175-049-P1-K1-D3
Method	BLASTX
NCBI GI	g2145358
BLAST score	388
E value	8.0e-38
Match length	95
% identity	81
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	150925
Seq. ID	LIB3175-049-P1-K1-E10
Method	BLASTX
NCBI GI	g2842477
BLAST score	481
E value	1.0e-48
Match length	111
% identity	79
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	150926
Seq. ID	LIB3175-049-P1-K1-E11
Method	BLASTN
NCBI GI	g16446
BLAST score	38
E value	3.0e-12
Match length	151
% identity	85
NCBI Description	A.thaliana gene for photosystem II 10 kDa polypeptide

Seq. No.	150927
Seq. ID	LIB3175-049-P1-K1-F7
Method	BLASTN
NCBI GI	g3510343
BLAST score	36
E value	6.0e-11
Match length	132
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	150928
Seq. ID	LIB3175-049-P1-K1-F8
Method	BLASTN
NCBI GI	g4006885
BLAST score	61
E value	6.0e-26

Match length	104
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	150929
Seq. ID	LIB3175-049-P1-K1-G5
Method	BLASTN
NCBI GI	g2244991
BLAST score	47
E value	2.0e-17
Match length	182
% identity	79
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	150930
Seq. ID	LIB3175-049-P1-K1-G8
Method	BLASTN
NCBI GI	g58298
BLAST score	38
E value	2.0e-12
Match length	154
% identity	79
NCBI Description	Synthetic DNA for A.thaliana ats1A leader spliced to B.thuringiensis CryIA(c)

Seq. No.	150931
Seq. ID	LIB3175-049-P1-K1-H11
Method	BLASTN
NCBI GI	g2924652
BLAST score	74
E value	5.0e-34
Match length	80
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	150932
Seq. ID	LIB3175-049-P1-K1-H12
Method	BLASTX
NCBI GI	g99688
BLAST score	299
E value	2.0e-27
Match length	94
% identity	67
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	150933
Seq. ID	LIB3175-049-P1-K1-H3
Method	BLASTN
NCBI GI	g3250673
BLAST score	46
E value	3.0e-17
Match length	109

% identity	82
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	150934
Seq. ID	LIB3175-050-P1-K1-A11
Method	BLASTN
NCBI GI	g3309276
BLAST score	63
E value	2.0e-27
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3 cM, complete sequence

Seq. No.	150935
Seq. ID	LIB3175-050-P1-K1-A2
Method	BLASTX
NCBI GI	g1527221
BLAST score	576
E value	3.0e-60
Match length	114
% identity	97
NCBI Description	(U68219) catalase [Brassica napus]

Seq. No.	150936
Seq. ID	LIB3175-050-P1-K1-A3
Method	BLASTX
NCBI GI	g3451065
BLAST score	530
E value	2.0e-54
Match length	104
% identity	98
NCBI Description	(AL031326) water channel - like protein [Arabidopsis thaliana]

Seq. No.	150937
Seq. ID	LIB3175-050-P1-K1-A9
Method	BLASTN
NCBI GI	g3849811
BLAST score	174
E value	2.0e-93
Match length	178
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150938
Seq. ID	LIB3175-050-P1-K1-B6
Method	BLASTX
NCBI GI	g1076387
BLAST score	439
E value	1.0e-43
Match length	100
% identity	88
NCBI Description	protein kinase homolog - Arabidopsis thaliana >gi_717180_emb_CAA55866_ (X79279) protein kinase homologous

to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]

Seq. No.	150939
Seq. ID	LIB3175-050-P1-K1-C12
Method	BLASTN
NCBI GI	g4220638
BLAST score	62
E value	9.0e-27
Match length	85
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	150940
Seq. ID	LIB3175-050-P1-K1-C6
Method	BLASTN
NCBI GI	g1490552
BLAST score	265
E value	1.0e-147
Match length	284
% identity	99
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	150941
Seq. ID	LIB3175-050-P1-K1-E11
Method	BLASTN
NCBI GI	g4519192
BLAST score	62
E value	2.0e-26
Match length	173
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	150942
Seq. ID	LIB3175-050-P1-K1-E3
Method	BLASTN
NCBI GI	g2584827
BLAST score	360
E value	0.0e+00
Match length	453
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150943
Seq. ID	LIB3175-050-P1-K1-E4
Method	BLASTX
NCBI GI	g3776559
BLAST score	232
E value	7.0e-20
Match length	58
% identity	71
NCBI Description	(AC005388) Strong similarity to gene F14J9.26 gi_3482933 cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]

Seq. No.	150944
Seq. ID	LIB3175-050-P1-K1-E5
Method	BLASTX
NCBI GI	g115480
BLAST score	434
E value	3.0e-43
Match length	88
% identity	53
NCBI Description	CALMODULIN-1 >gi_166649 (M38379) calmodulin-1 [Arabidopsis thaliana]

Seq. No.	150945
Seq. ID	LIB3175-050-P1-K1-E6
Method	BLASTN
NCBI GI	g4199934
BLAST score	167
E value	4.0e-89
Match length	229
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	150946
Seq. ID	LIB3175-050-P1-K1-E8
Method	BLASTX
NCBI GI	g99699
BLAST score	606
E value	3.0e-63
Match length	116
% identity	96
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgsr1) - Arabidopsis thaliana

Seq. No.	150947
Seq. ID	LIB3175-050-P1-K1-E9
Method	BLASTN
NCBI GI	g4757404
BLAST score	73
E value	3.0e-33
Match length	77
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	150948
Seq. ID	LIB3175-050-P1-K1-F1
Method	BLASTN
NCBI GI	g4519193
BLAST score	139
E value	4.0e-72
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	150949
Seq. ID	LIB3175-050-P1-K1-F10
Method	BLASTX
NCBI GI	g1778141
BLAST score	220
E value	4.0e-18
Match length	55
% identity	80
NCBI Description	(U66321) phosphate/phosphoenolpyruvate translocator precursor; PPT [Arabidopsis thaliana]

Seq. No.	150950
Seq. ID	LIB3175-050-P1-K1-F3
Method	BLASTX
NCBI GI	g553038
BLAST score	268
E value	6.0e-24
Match length	62
% identity	85
NCBI Description	(M58464) beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	150951
Seq. ID	LIB3175-050-P1-K1-F6
Method	BLASTN
NCBI GI	g4757405
BLAST score	75
E value	3.0e-34
Match length	245
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	150952
Seq. ID	LIB3175-050-P1-K1-G11
Method	BLASTX
NCBI GI	g1175011
BLAST score	518
E value	5.0e-53
Match length	102
% identity	97
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	150953
Seq. ID	LIB3175-050-P1-K1-G12
Method	BLASTX
NCBI GI	g2618723
BLAST score	87
E value	5.0e-41
Match length	115
% identity	82
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	150954
Seq. ID	LIB3175-050-P1-K1-G2
Method	BLASTN
NCBI GI	g469109
BLAST score	154
E value	3.0e-81
Match length	241
% identity	94
NCBI Description	A.thaliana (Columbia) Di19 mRNA

Seq. No.	150955
Seq. ID	LIB3175-050-P1-K1-G6
Method	BLASTX
NCBI GI	g3402751
BLAST score	504
E value	2.0e-62
Match length	121
% identity	48
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]

Seq. No.	150956
Seq. ID	LIB3175-050-P1-K1-H12
Method	BLASTX
NCBI GI	g3184281
BLAST score	418
E value	3.0e-41
Match length	101
% identity	86
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	150957
Seq. ID	LIB3175-050-P1-K1-H2
Method	BLASTX
NCBI GI	g1495273
BLAST score	482
E value	7.0e-49
Match length	97
% identity	97
NCBI Description	(Z50752) sugar transporter [Arabidopsis thaliana]

Seq. No.	150958
Seq. ID	LIB3175-050-P1-K1-H4
Method	BLASTX
NCBI GI	g4581146
BLAST score	632
E value	3.0e-66
Match length	125
% identity	99
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	150959
Seq. ID	LIB3175-050-P1-K1-H6

Method	BLASTX
NCBI GI	g3522945
BLAST score	325
E value	5.0e-32
Match length	114
% identity	71
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	150960
Seq. ID	LIB3175-050-P1-K1-H8
Method	BLASTN
NCBI GI	g2924730
BLAST score	49
E value	1.0e-18
Match length	65
% identity	73
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	150961
Seq. ID	LIB3175-051-P1-K1-A11
Method	BLASTX
NCBI GI	g3176874
BLAST score	480
E value	3.0e-63
Match length	148
% identity	89
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	150962
Seq. ID	LIB3175-051-P1-K1-A12
Method	BLASTN
NCBI GI	g3063438
BLAST score	424
E value	0.0e+00
Match length	459
% identity	98
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	150963
Seq. ID	LIB3175-051-P1-K1-A2
Method	BLASTN
NCBI GI	g3128134
BLAST score	106
E value	1.0e-52
Match length	272
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	150964
Seq. ID	LIB3175-051-P1-K1-A3
Method	BLASTN
NCBI GI	g2182285
BLAST score	346

E value	0.0e+00
Match length	411
% identity	98
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	150965
Seq. ID	LIB3175-051-P1-K1-A6
Method	BLASTN
NCBI GI	g3702735
BLAST score	298
E value	1.0e-167
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	150966
Seq. ID	LIB3175-051-P1-K1-A7
Method	BLASTX
NCBI GI	g3334659
BLAST score	232
E value	3.0e-19
Match length	100
% identity	50
NCBI Description	(Y10489) putative cytochrome P450 [Glycine max]

Seq. No.	150967
Seq. ID	LIB3175-051-P1-K1-A8
Method	BLASTN
NCBI GI	g3869067
BLAST score	146
E value	2.0e-76
Match length	405
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	150968
Seq. ID	LIB3175-051-P1-K1-A9
Method	BLASTN
NCBI GI	g4589969
BLAST score	194
E value	1.0e-105
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	150969
Seq. ID	LIB3175-051-P1-K1-B1
Method	BLASTN
NCBI GI	g2570223
BLAST score	43
E value	5.0e-15
Match length	107
% identity	90

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150970
Seq. ID	LIB3175-051-P1-K1-B11
Method	BLASTX
NCBI GI	g3925363
BLAST score	534
E value	1.0e-54
Match length	137
% identity	74
NCBI Description	(AF067961) homeodomain protein [Malus domestica]

Seq. No.	150971
Seq. ID	LIB3175-051-P1-K1-B12
Method	BLASTN
NCBI GI	g2088638
BLAST score	394
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150972
Seq. ID	LIB3175-051-P1-K1-B3
Method	BLASTX
NCBI GI	g4689386
BLAST score	355
E value	1.0e-33
Match length	139
% identity	55
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	150973
Seq. ID	LIB3175-051-P1-K1-B4
Method	BLASTX
NCBI GI	g3157928
BLAST score	142
E value	4.0e-09
Match length	52
% identity	58
NCBI Description	(AC002131) Similar to fumarylacetoacetate hydrolase, gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No.	150974
Seq. ID	LIB3175-051-P1-K1-B5
Method	BLASTX
NCBI GI	g1171059
BLAST score	156
E value	2.0e-10
Match length	29
% identity	93
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 1A (MT-1A) (MT-Q) >gi_1361995_pir__S57858 metallothionein 1a - Arabidopsis thaliana >gi_555978 (U15130) metallothionein-like protein

[Arabidopsis thaliana] >gi_1086457 (U11253) metallothionein [Arabidopsis thaliana] >gi_1580893_prf__2116236B metallothionein 2 [Arabidopsis thaliana]

Seq. No.	150975
Seq. ID	LIB3175-051-P1-K1-B7
Method	BLASTX
NCBI GI	g2194132
BLAST score	246
E value	7.0e-21
Match length	80
% identity	33
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	150976
Seq. ID	LIB3175-051-P1-K1-B9
Method	BLASTN
NCBI GI	g3128142
BLAST score	380
E value	0.0e+00
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	150977
Seq. ID	LIB3175-051-P1-K1-C12
Method	BLASTX
NCBI GI	g3329368
BLAST score	451
E value	3.0e-47
Match length	106
% identity	92
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	150978
Seq. ID	LIB3175-051-P1-K1-C2
Method	BLASTX
NCBI GI	g3892050
BLAST score	393
E value	4.0e-38
Match length	112
% identity	68
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	150979
Seq. ID	LIB3175-051-P1-K1-C4
Method	BLASTN
NCBI GI	g2088638
BLAST score	156
E value	2.0e-82
Match length	280
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	150980

Seq. ID	LIB3175-051-P1-K1-C5
Method	BLASTX
NCBI GI	g4585882
BLAST score	110
E value	2.0e-30
Match length	88
% identity	78
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	150981
Seq. ID	LIB3175-051-P1-K1-C6
Method	BLASTN
NCBI GI	g3702735
BLAST score	346
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	150982
Seq. ID	LIB3175-051-P1-K1-C7
Method	BLASTX
NCBI GI	g2129659
BLAST score	477
E value	6.0e-48
Match length	142
% identity	72
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	150983
Seq. ID	LIB3175-051-P1-K1-C8
Method	BLASTX
NCBI GI	g510880
BLAST score	395
E value	2.0e-38
Match length	138
% identity	57
NCBI Description	(X80067) putative aspartic protease [Brassica oleracea]

Seq. No.	150984
Seq. ID	LIB3175-051-P1-K1-C9
Method	BLASTX
NCBI GI	g135627
BLAST score	333
E value	4.0e-31
Match length	66
% identity	100
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2) (TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2) >gi_99764_pir__S10945 transcription initiation factor IID (clone At-1) - Arabidopsis thaliana >gi_16546_emb_CAA38742_ (X54995) transcription initiation factor II [Arabidopsis thaliana] >gi_4204264 (AC005223) 43453 [Arabidopsis thaliana] >gi_227073_prf__1613452A transcription initiation

factor TFIID-1 [Arabidopsis thaliana]

Seq. No.	150985
Seq. ID	LIB3175-051-P1-K1-D10
Method	BLASTX
NCBI GI	g4033469
BLAST score	405
E value	1.0e-48
Match length	129
% identity	59
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	150986
Seq. ID	LIB3175-051-P1-K1-D3
Method	BLASTN
NCBI GI	g4455168
BLAST score	253
E value	1.0e-140
Match length	455
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	150987
Seq. ID	LIB3175-051-P1-K1-D4
Method	BLASTN
NCBI GI	g4713943
BLAST score	427
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	150988
Seq. ID	LIB3175-051-P1-K1-D5
Method	BLASTN
NCBI GI	g4159701
BLAST score	348
E value	0.0e+00
Match length	453
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence

Seq. No.	150989
Seq. ID	LIB3175-051-P1-K1-D7
Method	BLASTX
NCBI GI	g4580394
BLAST score	254
E value	8.0e-22
Match length	107
% identity	43
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	150990
Seq. ID	LIB3175-051-P1-K1-D9
Method	BLASTX
NCBI GI	g730526
BLAST score	644
E value	2.0e-67
Match length	132
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	150991
Seq. ID	LIB3175-051-P1-K1-E11
Method	BLASTX
NCBI GI	g2983997
BLAST score	226
E value	1.0e-18
Match length	96
% identity	47
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	150992
Seq. ID	LIB3175-051-P1-K1-E12
Method	BLASTN
NCBI GI	g4519192
BLAST score	223
E value	1.0e-122
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	150993
Seq. ID	LIB3175-051-P1-K1-E2
Method	BLASTX
NCBI GI	g1931640
BLAST score	158
E value	1.0e-10
Match length	98
% identity	53
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	150994
Seq. ID	LIB3175-051-P1-K1-E5
Method	BLASTX
NCBI GI	g3639089
BLAST score	741
E value	6.0e-79
Match length	151
% identity	94
NCBI Description	(AF090445) phospholipase D1 [Brassica oleracea] >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1 [Brassica oleracea var. capitata]

Seq. No.	150995
Seq. ID	LIB3175-051-P1-K1-E6
Method	BLASTN
NCBI GI	g972928
BLAST score	210
E value	1.0e-114
Match length	353
% identity	92
NCBI Description	Arabidopsis thaliana IAA13 (IAA13) gene, complete cds

Seq. No.	150996
Seq. ID	LIB3175-051-P1-K1-E7
Method	BLASTX
NCBI GI	g4586109
BLAST score	423
E value	9.0e-42
Match length	79
% identity	100
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	150997
Seq. ID	LIB3175-051-P1-K1-E8
Method	BLASTX
NCBI GI	g2791834
BLAST score	455
E value	2.0e-47
Match length	104
% identity	95
NCBI Description	(AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No.	150998
Seq. ID	LIB3175-051-P1-K1-E9
Method	BLASTX
NCBI GI	g4417280
BLAST score	689
E value	8.0e-73
Match length	143
% identity	97
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	150999
Seq. ID	LIB3175-051-P1-K1-F10
Method	BLASTX
NCBI GI	g1346520
BLAST score	372
E value	1.0e-42
Match length	101
% identity	90
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_790978_emb_CAA56590_ (X80362) S-adenosyl-L-methionine synthetase [Brassica juncea]

Seq. No.	151000
Seq. ID	LIB3175-051-P1-K1-F11
Method	BLASTN

NCBI GI	g4662640
BLAST score	406
E value	0.0e+00
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	151001
Seq. ID	LIB3175-051-P1-K1-F12
Method	BLASTX
NCBI GI	g131360
BLAST score	201
E value	2.0e-15
Match length	40
% identity	100
NCBI Description	PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR >gi_81727_pir__S02115 photosystem II protein psbK precursor - white mustard chloroplast >gi_12209_emb_CAA31909_ (X13558) K preprotein (AA -24 to 37) [Sinapis alba]

Seq. No.	151002
Seq. ID	LIB3175-051-P1-K1-F2
Method	BLASTX
NCBI GI	g3193316
BLAST score	119
E value	2.0e-59
Match length	149
% identity	85
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	151003
Seq. ID	LIB3175-051-P1-K1-F3
Method	BLASTX
NCBI GI	g2341035
BLAST score	319
E value	2.0e-29
Match length	61
% identity	95
NCBI Description	(AC000104) Match to Arabidopsis photolysase (PHH1) gene (gb_X99061) and cryptochrome 2 apoprotein (CRY2) (gb_U43397). ESTs gb_W43661 and gb_Z25638 come from this gene. [Arabidopsis thaliana]

Seq. No.	151004
Seq. ID	LIB3175-051-P1-K1-F4
Method	BLASTN
NCBI GI	g4519192
BLAST score	79
E value	2.0e-36
Match length	229
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	151005

Seq. ID	LIB3175-051-P1-K1-F5
Method	BLASTN
NCBI GI	g3449321
BLAST score	371
E value	0.0e+00
Match length	431
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	151006
Seq. ID	LIB3175-051-P1-K1-F6
Method	BLASTX
NCBI GI	g4580392
BLAST score	452
E value	3.0e-45
Match length	112
% identity	88
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151007
Seq. ID	LIB3175-051-P1-K1-F7
Method	BLASTX
NCBI GI	g1076316
BLAST score	184
E value	1.0e-15
Match length	61
% identity	56
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	151008
Seq. ID	LIB3175-051-P1-K1-F9
Method	BLASTN
NCBI GI	g4159706
BLAST score	60
E value	5.0e-26
Match length	60
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	151009
Seq. ID	LIB3175-051-P1-K1-G1
Method	BLASTN
NCBI GI	g4335711
BLAST score	277
E value	1.0e-154
Match length	289
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151010
Seq. ID	LIB3175-051-P1-K1-G10
Method	BLASTX

NCBI GI	g3193285
BLAST score	570
E value	7.0e-59
Match length	131
% identity	82
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	151011
Seq. ID	LIB3175-051-P1-K1-G11
Method	BLASTX
NCBI GI	g2494112
BLAST score	801
E value	6.0e-86
Match length	152
% identity	99
NCBI Description	(AC002376) Match to Arabidopsis ATHKCP (gb_L40948). ESTs gb_ATTS0764, gb_R90646, gb_AA389809, gb_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana]

Seq. No.	151012
Seq. ID	LIB3175-051-P1-K1-G12
Method	BLASTN
NCBI GI	g4757409
BLAST score	116
E value	2.0e-58
Match length	464
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	151013
Seq. ID	LIB3175-051-P1-K1-G5
Method	BLASTX
NCBI GI	g1709804
BLAST score	458
E value	9.0e-46
Match length	136
% identity	63
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	151014
Seq. ID	LIB3175-051-P1-K1-G7
Method	BLASTN
NCBI GI	g2924728
BLAST score	118
E value	1.0e-59
Match length	457
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	151015
Seq. ID	LIB3175-051-P1-K1-G8
Method	BLASTN
NCBI GI	g2351073
BLAST score	213
E value	1.0e-116
Match length	431
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	151016
Seq. ID	LIB3175-051-P1-K1-G9
Method	BLASTN
NCBI GI	g4454447
BLAST score	379
E value	0.0e+00
Match length	439
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151017
Seq. ID	LIB3175-051-P1-K1-H10
Method	BLASTX
NCBI GI	g2119846
BLAST score	729
E value	2.0e-77
Match length	141
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151018
Seq. ID	LIB3175-051-P1-K1-H11
Method	BLASTX
NCBI GI	g2760320
BLAST score	599
E value	3.0e-62
Match length	127
% identity	94
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	151019
Seq. ID	LIB3175-051-P1-K1-H12
Method	BLASTN
NCBI GI	g2656029
BLAST score	180
E value	1.0e-96
Match length	421
% identity	75
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

09604705.100000

Seq. No.	151020
Seq. ID	LIB3175-051-P1-K1-H2
Method	BLASTX
NCBI GI	g2494113
BLAST score	323
E value	4.0e-30
Match length	108
% identity	56
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	151021
Seq. ID	LIB3175-051-P1-K1-H9
Method	BLASTX
NCBI GI	g4191783
BLAST score	206
E value	3.0e-16
Match length	131
% identity	44
NCBI Description	(AC005917) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151022
Seq. ID	LIB3175-052-P1-K1-A1
Method	BLASTX
NCBI GI	g3953465
BLAST score	450
E value	8.0e-45
Match length	110
% identity	86
NCBI Description	(AC002328) F20N2.10 [Arabidopsis thaliana]

Seq. No.	151023
Seq. ID	LIB3175-052-P1-K1-A10
Method	BLASTN
NCBI GI	g511080
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	A.thaliana HEM15 mRNA for ferrochelatase

Seq. No.	151024
Seq. ID	LIB3175-052-P1-K1-A11
Method	BLASTX
NCBI GI	g282865
BLAST score	635
E value	2.0e-66
Match length	128
% identity	70
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll

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a/b-binding protein [Arabidopsis thaliana]

Seq. No.	151025
Seq. ID	LIB3175-052-P1-K1-A12
Method	BLASTX
NCBI GI	g4585993
BLAST score	162
E value	5.0e-11
Match length	40
% identity	75
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	151026
Seq. ID	LIB3175-052-P1-K1-A6
Method	BLASTN
NCBI GI	g431259
BLAST score	43
E value	5.0e-15
Match length	109
% identity	83
NCBI Description	Arabidopsis thaliana 16kDa ubiquitin conjugating enzyme (UBC1) gene, complete cds

Seq. No.	151027
Seq. ID	LIB3175-052-P1-K1-A8
Method	BLASTN
NCBI GI	g2335089
BLAST score	61
E value	2.0e-26
Match length	92
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151028
Seq. ID	LIB3175-052-P1-K1-B1
Method	BLASTN
NCBI GI	g2281081
BLAST score	244
E value	1.0e-135
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151029
Seq. ID	LIB3175-052-P1-K1-B10
Method	BLASTX
NCBI GI	g4586265
BLAST score	549
E value	2.0e-56
Match length	126
% identity	80
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 151030

Seq. ID	LIB3175-052-P1-K1-B12
Method	BLASTX
NCBI GI	g4039152
BLAST score	212
E value	6.0e-17
Match length	44
% identity	93
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	151031
Seq. ID	LIB3175-052-P1-K1-B3
Method	BLASTN
NCBI GI	g3985957
BLAST score	44
E value	5.0e-16
Match length	82
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	151032
Seq. ID	LIB3175-052-P1-K1-B7
Method	BLASTX
NCBI GI	g4056506
BLAST score	610
E value	1.0e-63
Match length	124
% identity	98
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	151033
Seq. ID	LIB3175-052-P1-K1-B8
Method	BLASTX
NCBI GI	g115783
BLAST score	629
E value	8.0e-66
Match length	119
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	151034
Seq. ID	LIB3175-052-P1-K1-B9
Method	BLASTN
NCBI GI	g16174
BLAST score	51
E value	8.0e-20
Match length	212
% identity	76
NCBI Description	A.thaliana ANT1 mRNA for adenylate translocator

Seq. No.	151035
Seq. ID	LIB3175-052-P1-K1-C1

Method	BLASTX
NCBI GI	g2894574
BLAST score	202
E value	6.0e-16
Match length	74
% identity	59
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	151036
Seq. ID	LIB3175-052-P1-K1-C11
Method	BLASTX
NCBI GI	g2529682
BLAST score	300
E value	2.0e-27
Match length	113
% identity	57
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	151037
Seq. ID	LIB3175-052-P1-K1-C7
Method	BLASTX
NCBI GI	g1710780
BLAST score	377
E value	3.0e-36
Match length	111
% identity	68
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	151038
Seq. ID	LIB3175-052-P1-K1-C8
Method	BLASTX
NCBI GI	g4415907
BLAST score	474
E value	1.0e-47
Match length	134
% identity	72
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	151039
Seq. ID	LIB3175-052-P1-K1-D10
Method	BLASTX
NCBI GI	g3386565
BLAST score	408
E value	7.0e-40
Match length	148
% identity	58
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	151040
Seq. ID	LIB3175-052-P1-K1-D11

Method	BLASTN
NCBI GI	g3228389
BLAST score	156
E value	3.0e-82
Match length	470
% identity	86
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	151041
Seq. ID	LIB3175-052-P1-K1-D12
Method	BLASTX
NCBI GI	g2827528
BLAST score	381
E value	1.0e-36
Match length	121
% identity	61
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	151042
Seq. ID	LIB3175-052-P1-K1-D2
Method	BLASTN
NCBI GI	g1483217
BLAST score	396
E value	0.0e+00
Match length	457
% identity	99
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	151043
Seq. ID	LIB3175-052-P1-K1-D3
Method	BLASTX
NCBI GI	g425194
BLAST score	687
E value	1.0e-72
Match length	146
% identity	92
NCBI Description	(L26243) heat shock protein [Spinacia oleracea] >gi_2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No.	151044
Seq. ID	LIB3175-052-P1-K1-D5
Method	BLASTX
NCBI GI	g3914740
BLAST score	472
E value	2.0e-47
Match length	134
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	151045
Seq. ID	LIB3175-052-P1-K1-D7
Method	BLASTN
NCBI GI	g14342
BLAST score	78

E value	6.0e-36
Match length	164
% identity	84
NCBI Description	A.thaliana mRNA for carbonic anhydrase

Seq. No.	151046
Seq. ID	LIB3175-052-P1-K1-D8
Method	BLASTX
NCBI GI	g4567273
BLAST score	546
E value	3.0e-56
Match length	106
% identity	99
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	151047
Seq. ID	LIB3175-052-P1-K1-E1
Method	BLASTX
NCBI GI	g99735
BLAST score	773
E value	1.0e-82
Match length	147
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	151048
Seq. ID	LIB3175-052-P1-K1-E10
Method	BLASTX
NCBI GI	g3540185
BLAST score	248
E value	4.0e-21
Match length	78
% identity	56
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	151049
Seq. ID	LIB3175-052-P1-K1-E12
Method	BLASTX
NCBI GI	g3831459
BLAST score	534
E value	1.0e-66
Match length	136
% identity	94
NCBI Description	(AC005700) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	151050
Seq. ID	LIB3175-052-P1-K1-E2
Method	BLASTN
NCBI GI	g3757512
BLAST score	242
E value	1.0e-133
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12A24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151051
Seq. ID	LIB3175-052-P1-K1-E3
Method	BLASTX
NCBI GI	g1172873
BLAST score	618
E value	2.0e-64
Match length	138
% identity	88
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	151052
Seq. ID	LIB3175-052-P1-K1-E7
Method	BLASTX
NCBI GI	g2129659
BLAST score	303
E value	1.0e-27
Match length	104
% identity	62
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	151053
Seq. ID	LIB3175-052-P1-K1-E8
Method	BLASTX
NCBI GI	g4539405
BLAST score	631
E value	5.0e-66
Match length	127
% identity	98
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	151054
Seq. ID	LIB3175-052-P1-K1-E9
Method	BLASTX
NCBI GI	g3759184
BLAST score	257
E value	4.0e-22
Match length	107
% identity	58
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	151055
Seq. ID	LIB3175-052-P1-K1-F1
Method	BLASTX
NCBI GI	g3979940
BLAST score	192
E value	1.0e-14
Match length	74
% identity	51
NCBI Description	(AL034393) Y18D10A.3 [Caenorhabditis elegans]

Seq. No.	151056
Seq. ID	LIB3175-052-P1-K1-F10
Method	BLASTX
NCBI GI	g4455180
BLAST score	655
E value	8.0e-69
Match length	150
% identity	88
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	151057
Seq. ID	LIB3175-052-P1-K1-F12
Method	BLASTN
NCBI GI	g3152602
BLAST score	58
E value	6.0e-24
Match length	181
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151058
Seq. ID	LIB3175-052-P1-K1-F2
Method	BLASTX
NCBI GI	g4586265
BLAST score	495
E value	4.0e-50
Match length	112
% identity	81
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	151059
Seq. ID	LIB3175-052-P1-K1-F3
Method	BLASTX
NCBI GI	g1363489
BLAST score	570
E value	7.0e-59
Match length	133
% identity	83
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	151060
Seq. ID	LIB3175-052-P1-K1-F4
Method	BLASTX
NCBI GI	g4220473
BLAST score	646
E value	8.0e-68
Match length	129
% identity	97
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151061
Seq. ID	LIB3175-052-P1-K1-F5
Method	BLASTN
NCBI GI	g1154626

BLAST score	71
E value	1.0e-31
Match length	330
% identity	76
NCBI Description	A.thaliana CHLH gene

Seq. No.	151062
Seq. ID	LIB3175-052-P1-K1-F9
Method	BLASTX
NCBI GI	g2129538
BLAST score	568
E value	1.0e-58
Match length	112
% identity	100
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	151063
Seq. ID	LIB3175-052-P1-K1-G1
Method	BLASTX
NCBI GI	g2160133
BLAST score	360
E value	3.0e-34
Match length	90
% identity	86
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	151064
Seq. ID	LIB3175-052-P1-K1-G10
Method	BLASTX
NCBI GI	g2264378
BLAST score	612
E value	7.0e-64
Match length	133
% identity	89
NCBI Description	(AC002354) putative bZIP-like transcription factor [Arabidopsis thaliana]

Seq. No.	151065
Seq. ID	LIB3175-052-P1-K1-G12
Method	BLASTN
NCBI GI	g1041701
BLAST score	74
E value	9.0e-34
Match length	90
% identity	96
NCBI Description	Arabidopsis thaliana expansin At-EXP1 (At-EXP1) mRNA, partial cds

Seq. No.	151066
Seq. ID	LIB3175-052-P1-K1-G5
Method	BLASTN
NCBI GI	g886427
BLAST score	54

E value	2.0e-21
Match length	322
% identity	76
NCBI Description	A.thaliana mRNA for zeta-crystallin homologue

Seq. No.	151067
Seq. ID	LIB3175-052-P1-K1-G7
Method	BLASTN
NCBI GI	g3449313
BLAST score	164
E value	3.0e-87
Match length	299
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	151068
Seq. ID	LIB3175-052-P1-K1-G8
Method	BLASTX
NCBI GI	g4455253
BLAST score	685
E value	2.0e-72
Match length	149
% identity	89
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	151069
Seq. ID	LIB3175-052-P1-K1-G9
Method	BLASTX
NCBI GI	g2341034
BLAST score	600
E value	2.0e-62
Match length	125
% identity	97
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	151070
Seq. ID	LIB3175-052-P1-K1-H1
Method	BLASTX
NCBI GI	g2677828
BLAST score	324
E value	4.0e-30
Match length	84
% identity	74
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	151071
Seq. ID	LIB3175-052-P1-K1-H10
Method	BLASTX
NCBI GI	g3873710
BLAST score	274
E value	2.0e-24
Match length	67
% identity	67
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this

gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No.	151072
Seq. ID	LIB3175-052-P1-K1-H11
Method	BLASTX
NCBI GI	g3873710
BLAST score	246
E value	6.0e-21
Match length	82
% identity	54
NCBI Description	(Z73102) predicted using Genefinder; similar to Zinc finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No.	151073
Seq. ID	LIB3175-052-P1-K1-H12
Method	BLASTX
NCBI GI	g3924603
BLAST score	506
E value	2.0e-51
Match length	149
% identity	70
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	151074
Seq. ID	LIB3175-052-P1-K1-H2
Method	BLASTX
NCBI GI	g1514649
BLAST score	82
E value	3.0e-42
Match length	123
% identity	80
NCBI Description	(X86021) potassium channel [Solanum tuberosum]

Seq. No.	151075
Seq. ID	LIB3175-052-P1-K1-H5
Method	BLASTN
NCBI GI	g2828278
BLAST score	231
E value	1.0e-127
Match length	442
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	151076
Seq. ID	LIB3175-052-P1-K1-H7
Method	BLASTX
NCBI GI	g115767
BLAST score	742
E value	5.0e-79
Match length	143

% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	151077
Seq. ID	LIB3175-052-P1-K1-H8
Method	BLASTX
NCBI GI	g1345595
BLAST score	687
E value	1.0e-72
Match length	138
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	151078
Seq. ID	LIB3175-052-P1-K1-H9
Method	BLASTX
NCBI GI	g2160147
BLAST score	441
E value	8.0e-44
Match length	108
% identity	84
NCBI Description	(AC000375) EST gb_ATTS3706 comes from this gene. [Arabidopsis thaliana]

Seq. No.	151079
Seq. ID	LIB3175-053-P1-K1-A10
Method	BLASTX
NCBI GI	g70644
BLAST score	309
E value	3.0e-28
Match length	84
% identity	16
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	151080
Seq. ID	LIB3175-053-P1-K1-A11
Method	BLASTX
NCBI GI	g2677828
BLAST score	435
E value	5.0e-43
Match length	114
% identity	71
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	151081
Seq. ID	LIB3175-053-P1-K1-A12
Method	BLASTX

NCBI GI	g4544399
BLAST score	529
E value	4.0e-54
Match length	146
% identity	66
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	151082
Seq. ID	LIB3175-053-P1-K1-A2
Method	BLASTX
NCBI GI	g4741940
BLAST score	494
E value	5.0e-50
Match length	93
% identity	98
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	151083
Seq. ID	LIB3175-053-P1-K1-A5
Method	BLASTX
NCBI GI	g132110
BLAST score	103
E value	2.0e-04
Match length	83
% identity	28
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	151084
Seq. ID	LIB3175-053-P1-K1-B1
Method	BLASTX
NCBI GI	g1518540
BLAST score	581
E value	4.0e-60
Match length	120
% identity	86
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	151085
Seq. ID	LIB3175-053-P1-K1-B11
Method	BLASTN
NCBI GI	g4757394
BLAST score	179
E value	4.0e-96
Match length	229
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence

Seq. No.	151086
Seq. ID	LIB3175-053-P1-K1-B12
Method	BLASTX

NCBI GI	g3522945
BLAST score	631
E value	4.0e-66
Match length	119
% identity	99
NCBI Description	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	151087
Seq. ID	LIB3175-053-P1-K1-B2
Method	BLASTX
NCBI GI	g4741952
BLAST score	421
E value	2.0e-41
Match length	108
% identity	58
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	151088
Seq. ID	LIB3175-053-P1-K1-B3
Method	BLASTX
NCBI GI	g135467
BLAST score	708
E value	5.0e-75
Match length	152
% identity	88
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	151089
Seq. ID	LIB3175-053-P1-K1-B8
Method	BLASTX
NCBI GI	g3776558
BLAST score	598
E value	4.0e-62
Match length	136
% identity	93
NCBI Description	(AC005388) Identical to gb_L14814 DNA for tissue-specific acyl carrier protein isoform 2 from A. thaliana. ESTs gb_AA597351, gb_T41805, gb_H36871, gb_R30210, gb_AA042549, gb_Z47650, gb_H76304 and gb_AA597348 come from this gene. [Arabidopsi

Seq. No.	151090
Seq. ID	LIB3175-053-P1-K1-B9
Method	BLASTX
NCBI GI	g2194139
BLAST score	295
E value	7.0e-27
Match length	98
% identity	68
NCBI Description	(AC002062) EST gb_ATTS0887 comes from this gene. [Arabidopsis thaliana]

Seq. No.	151091
Seq. ID	LIB3175-053-P1-K1-C2
Method	BLASTX

NCBI GI	g2651305
BLAST score	338
E value	1.0e-31
Match length	147
% identity	52
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151092
Seq. ID	LIB3175-053-P1-K1-C3
Method	BLASTX
NCBI GI	g4006893
BLAST score	624
E value	4.0e-65
Match length	125
% identity	97
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	151093
Seq. ID	LIB3175-053-P1-K1-C4
Method	BLASTX
NCBI GI	g3386612
BLAST score	217
E value	2.0e-25
Match length	121
% identity	53
NCBI Description	(AC004665) DNA-binding protein, dbp [Arabidopsis thaliana]

Seq. No.	151094
Seq. ID	LIB3175-053-P1-K1-C5
Method	BLASTN
NCBI GI	g2924732
BLAST score	279
E value	1.0e-156
Match length	310
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	151095
Seq. ID	LIB3175-053-P1-K1-C6
Method	BLASTN
NCBI GI	g4220632
BLAST score	141
E value	2.0e-73
Match length	287
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	151096
Seq. ID	LIB3175-053-P1-K1-D11
Method	BLASTX
NCBI GI	g2511594
BLAST score	50
E value	1.0e-12
Match length	80
% identity	60

NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	151097
Seq. ID	LIB3175-053-P1-K1-D4
Method	BLASTN
NCBI GI	g4589410
BLAST score	294
E value	1.0e-164
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	151098
Seq. ID	LIB3175-053-P1-K1-D5
Method	BLASTX
NCBI GI	g3212869
BLAST score	591
E value	2.0e-61
Match length	121
% identity	88
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	151099
Seq. ID	LIB3175-053-P1-K1-D8
Method	BLASTX
NCBI GI	g1706958
BLAST score	270
E value	9.0e-24
Match length	136
% identity	47
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	151100
Seq. ID	LIB3175-053-P1-K1-E10
Method	BLASTX
NCBI GI	g112743
BLAST score	286
E value	3.0e-26
Match length	66
% identity	86
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	151101
Seq. ID	LIB3175-053-P1-K1-E12
Method	BLASTX

NCBI GI	g401169
BLAST score	277
E value	5.0e-25
Match length	53
% identity	100
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	151102
Seq. ID	LIB3175-053-P1-K1-E2
Method	BLASTX
NCBI GI	g2894598
BLAST score	154
E value	2.0e-31
Match length	121
% identity	49
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	151103
Seq. ID	LIB3175-053-P1-K1-E3
Method	BLASTX
NCBI GI	g266829
BLAST score	682
E value	5.0e-72
Match length	131
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1 >gi_81655_pir__S20882 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis thaliana >gi_16431_emb_CAA45611_ (X64328) protein phosphatase-1 [Arabidopsis thaliana] >gi_166572 (M93408) phosphoprotein phosphatase 1 [Arabidopsis thaliana] >gi_3980395 (AC004561) phosphoprotein phosphatase-type 1 catalytic subunit [Arabidopsis thaliana]

Seq. No.	151104
Seq. ID	LIB3175-053-P1-K1-E4
Method	BLASTX
NCBI GI	g115385
BLAST score	681
E value	7.0e-72
Match length	130
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151105
Seq. ID	LIB3175-053-P1-K1-E9
Method	BLASTN
NCBI GI	g2833627
BLAST score	72
E value	3.0e-32
Match length	233
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	151106
Seq. ID	LIB3175-053-P1-K1-F1
Method	BLASTN
NCBI GI	g3242970
BLAST score	46
E value	4.0e-17
Match length	90
% identity	88
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151107
Seq. ID	LIB3175-053-P1-K1-F10
Method	BLASTN
NCBI GI	g4406790
BLAST score	213
E value	1.0e-116
Match length	303
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1O16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151108
Seq. ID	LIB3175-053-P1-K1-F2
Method	BLASTX
NCBI GI	g4585935
BLAST score	157
E value	4.0e-11
Match length	38
% identity	87
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	151109
Seq. ID	LIB3175-053-P1-K1-F3
Method	BLASTX
NCBI GI	g1353352
BLAST score	282
E value	3.0e-46
Match length	149
% identity	59
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	151110
Seq. ID	LIB3175-053-P1-K1-F4
Method	BLASTX
NCBI GI	g4538963
BLAST score	633
E value	1.0e-74
Match length	143
% identity	78
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	151111
Seq. ID	LIB3175-053-P1-K1-F8
Method	BLASTX
NCBI GI	g1345592
BLAST score	161
E value	3.0e-11
Match length	59
% identity	63
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	151112
Seq. ID	LIB3175-053-P1-K1-G10
Method	BLASTX
NCBI GI	g2341034
BLAST score	396
E value	2.0e-38
Match length	86
% identity	94
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	151113
Seq. ID	LIB3175-053-P1-K1-G11
Method	BLASTX
NCBI GI	g2129562
BLAST score	157
E value	7.0e-11
Match length	48
% identity	69
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	151114
Seq. ID	LIB3175-053-P1-K1-G3
Method	BLASTX
NCBI GI	g2118220
BLAST score	296
E value	6.0e-27
Match length	77
% identity	49
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	151115
Seq. ID	LIB3175-053-P1-K1-G4

Method	BLASTX
NCBI GI	g4689382
BLAST score	282
E value	2.0e-39
Match length	147
% identity	60
NCBI Description	(AF139466) chlorophyll a/b binding protein CP29 [Vigna radiata]

Seq. No.	151116
Seq. ID	LIB3175-053-P1-K1-G5
Method	BLASTX
NCBI GI	g2760830
BLAST score	144
E value	3.0e-09
Match length	63
% identity	40
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	151117
Seq. ID	LIB3175-053-P1-K1-G6
Method	BLASTX
NCBI GI	g1076660
BLAST score	264
E value	5.0e-23
Match length	85
% identity	71
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	151118
Seq. ID	LIB3175-053-P1-K1-G7
Method	BLASTN
NCBI GI	g4263753
BLAST score	200
E value	1.0e-108
Match length	351
% identity	97
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151119
Seq. ID	LIB3175-053-P1-K1-G8
Method	BLASTN
NCBI GI	g4115370
BLAST score	42
E value	1.0e-14
Match length	117
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151120
Seq. ID	LIB3175-053-P1-K1-G9

Method	BLASTX
NCBI GI	g4371282
BLAST score	257
E value	2.0e-22
Match length	70
% identity	76
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	151121
Seq. ID	LIB3175-053-P1-K1-H10
Method	BLASTX
NCBI GI	g4585997
BLAST score	286
E value	6.0e-26
Match length	91
% identity	67
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	151122
Seq. ID	LIB3175-053-P1-K1-H2
Method	BLASTN
NCBI GI	g16202
BLAST score	103
E value	4.0e-51
Match length	147
% identity	93
NCBI Description	A.thaliana of bcb gene encoding blue copper-binding protein

Seq. No.	151123
Seq. ID	LIB3175-053-P1-K1-H3
Method	BLASTN
NCBI GI	g4589414
BLAST score	182
E value	7.0e-98
Match length	344
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	151124
Seq. ID	LIB3175-053-P1-K1-H4
Method	BLASTX
NCBI GI	g417103
BLAST score	46
E value	5.0e-63
Match length	136
% identity	92
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	151125
Seq. ID	LIB3175-053-P1-K1-H5
Method	BLASTX
NCBI GI	g3511285
BLAST score	150
E value	3.0e-10
Match length	46
% identity	63
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	151126
Seq. ID	LIB3175-053-P1-K1-H6
Method	BLASTX
NCBI GI	g1706958
BLAST score	479
E value	2.0e-48
Match length	101
% identity	89
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	151127
Seq. ID	LIB3175-054-P1-K1-A1
Method	BLASTN
NCBI GI	g1483219
BLAST score	33
E value	2.0e-09
Match length	65
% identity	88
NCBI Description	A.thaliana mRNA for peroxidase ATP1a, clone EST 103m21t7

Seq. No.	151128
Seq. ID	LIB3175-054-P1-K1-A10
Method	BLASTN
NCBI GI	g4580744
BLAST score	266
E value	1.0e-148
Match length	401
% identity	96
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	151129
Seq. ID	LIB3175-054-P1-K1-A12
Method	BLASTX
NCBI GI	g1362007

BLAST score	683
E value	4.0e-72
Match length	143
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	151130
Seq. ID	LIB3175-054-P1-K1-A2
Method	BLASTX
NCBI GI	g1351271
BLAST score	343
E value	3.0e-32
Match length	131
% identity	58
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	151131
Seq. ID	LIB3175-054-P1-K1-A4
Method	BLASTX
NCBI GI	g4835226
BLAST score	291
E value	4.0e-26
Match length	84
% identity	68
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	151132
Seq. ID	LIB3175-054-P1-K1-A5
Method	BLASTX
NCBI GI	g629602
BLAST score	267
E value	2.0e-23
Match length	81
% identity	58
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	151133
Seq. ID	LIB3175-054-P1-K1-A6
Method	BLASTX
NCBI GI	g416758
BLAST score	141
E value	1.0e-69
Match length	145
% identity	91
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	151134
Seq. ID	LIB3175-054-P1-K1-A7
Method	BLASTN
NCBI GI	g4580365
BLAST score	181
E value	3.0e-97
Match length	361
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	151135
Seq. ID	LIB3175-054-P1-K1-B1
Method	BLASTX
NCBI GI	g2894574
BLAST score	626
E value	2.0e-65
Match length	121
% identity	98
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	151136
Seq. ID	LIB3175-054-P1-K1-B10
Method	BLASTX
NCBI GI	g1402912
BLAST score	628
E value	9.0e-66
Match length	121
% identity	98
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	151137
Seq. ID	LIB3175-054-P1-K1-B11
Method	BLASTN
NCBI GI	g2264317
BLAST score	142
E value	4.0e-74
Match length	288
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	151138
Seq. ID	LIB3175-054-P1-K1-B12
Method	BLASTX
NCBI GI	g133938
BLAST score	568
E value	1.0e-58
Match length	145
% identity	77
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70866_pir__R3SP3 ribosomal protein S3 - spinach chloroplast >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3 [Spinacia oleracea]

Seq. No.	151139
Seq. ID	LIB3175-054-P1-K1-B2
Method	BLASTN
NCBI GI	g4335711
BLAST score	159
E value	4.0e-84
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151140
Seq. ID	LIB3175-054-P1-K1-B3
Method	BLASTN
NCBI GI	g3426063
BLAST score	386
E value	0.0e+00
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for monooxygenase

Seq. No.	151141
Seq. ID	LIB3175-054-P1-K1-B4
Method	BLASTN
NCBI GI	g4567300
BLAST score	219
E value	1.0e-120
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	151142
Seq. ID	LIB3175-054-P1-K1-B6
Method	BLASTN
NCBI GI	g4512656
BLAST score	164
E value	4.0e-87
Match length	359
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	151143
Seq. ID	LIB3175-054-P1-K1-B7
Method	BLASTX
NCBI GI	g2501296
BLAST score	255
E value	6.0e-22
Match length	126
% identity	40
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]

Seq. No.	151144
Seq. ID	LIB3175-054-P1-K1-B8
Method	BLASTN

NCBI GI	g3046847
BLAST score	204
E value	1.0e-111
Match length	348
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	151145
Seq. ID	LIB3175-054-P1-K1-B9
Method	BLASTX
NCBI GI	g2384671
BLAST score	709
E value	3.0e-75
Match length	143
% identity	94
NCBI Description	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No.	151146
Seq. ID	LIB3175-054-P1-K1-C10
Method	BLASTN
NCBI GI	g2980757
BLAST score	341
E value	0.0e+00
Match length	390
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	151147
Seq. ID	LIB3175-054-P1-K1-C11
Method	BLASTX
NCBI GI	g1345973
BLAST score	332
E value	1.0e-53
Match length	102
% identity	100
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	151148
Seq. ID	LIB3175-054-P1-K1-C12
Method	BLASTX
NCBI GI	g4204267
BLAST score	617
E value	2.0e-64
Match length	148
% identity	86
NCBI Description	(AC005223) 55585 [Arabidopsis thaliana]

Seq. No.	151149
Seq. ID	LIB3175-054-P1-K1-C3
Method	BLASTX
NCBI GI	g116229
BLAST score	478
E value	3.0e-48
Match length	107
% identity	91
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR >gi_99676_pir__S20876 chaperonin hsp60 precursor - Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547) chaperonin hsp60 [Arabidopsis thaliana]

Seq. No.	151150
Seq. ID	LIB3175-054-P1-K1-C4
Method	BLASTX
NCBI GI	g1169598
BLAST score	484
E value	8.0e-49
Match length	100
% identity	88
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	151151
Seq. ID	LIB3175-054-P1-K1-C5
Method	BLASTX
NCBI GI	g2245066
BLAST score	581
E value	3.0e-60
Match length	106
% identity	99
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	151152
Seq. ID	LIB3175-054-P1-K1-C6
Method	BLASTX
NCBI GI	g2924520
BLAST score	620
E value	9.0e-65
Match length	124
% identity	95
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	151153
Seq. ID	LIB3175-054-P1-K1-C9
Method	BLASTX
NCBI GI	g4164578
BLAST score	611
E value	1.0e-63
Match length	135
% identity	92
NCBI Description	(AF098947) CTF2B [Arabidopsis thaliana]

Seq. No.	151154
Seq. ID	LIB3175-054-P1-K1-D1
Method	BLASTX
NCBI GI	g2271477
BLAST score	469
E value	5.0e-47
Match length	108
% identity	84
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	151155
Seq. ID	LIB3175-054-P1-K1-D10
Method	BLASTX
NCBI GI	g4539370
BLAST score	152
E value	7.0e-10
Match length	48
% identity	65
NCBI Description	(AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	151156
Seq. ID	LIB3175-054-P1-K1-D11
Method	BLASTX
NCBI GI	g4559321
BLAST score	537
E value	5.0e-55
Match length	135
% identity	80
NCBI Description	(AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151157
Seq. ID	LIB3175-054-P1-K1-D12
Method	BLASTX
NCBI GI	g4539418
BLAST score	126
E value	6.0e-66
Match length	134
% identity	95
NCBI Description	(AL049171) caffeoyl-CoA O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	151158
Seq. ID	LIB3175-054-P1-K1-D2
Method	BLASTN
NCBI GI	g4732169
BLAST score	397
E value	0.0e+00
Match length	432
% identity	87
NCBI Description	Arabidopsis thaliana BAC T3E15

Seq. No.	151159
Seq. ID	LIB3175-054-P1-K1-D3
Method	BLASTX
NCBI GI	g4467099
BLAST score	616

E value	2.0e-64
Match length	122
% identity	98
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	151160
Seq. ID	LIB3175-054-P1-K1-D4
Method	BLASTX
NCBI GI	g4539324
BLAST score	170
E value	5.0e-12
Match length	69
% identity	52
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.	151161
Seq. ID	LIB3175-054-P1-K1-D5
Method	BLASTX
NCBI GI	g520478
BLAST score	372
E value	2.0e-42
Match length	95
% identity	94
NCBI Description	(U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate dehydrogenase [Arabidopsis thaliana]

Seq. No.	151162
Seq. ID	LIB3175-054-P1-K1-D6
Method	BLASTX
NCBI GI	g3915847
BLAST score	43
E value	7.0e-51
Match length	113
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	151163
Seq. ID	LIB3175-054-P1-K1-D7
Method	BLASTX
NCBI GI	g2739373
BLAST score	245
E value	8.0e-21
Match length	139
% identity	40
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	151164
Seq. ID	LIB3175-054-P1-K1-D8
Method	BLASTX
NCBI GI	g4678328
BLAST score	479
E value	3.0e-48
Match length	94

% identity	99
NCBI Description	(AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]

Seq. No.	151165
Seq. ID	LIB3175-054-P1-K1-D9
Method	BLASTX
NCBI GI	g2739389
BLAST score	82
E value	3.0e-45
Match length	126
% identity	73
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	151166
Seq. ID	LIB3175-054-P1-K1-E1
Method	BLASTX
NCBI GI	g166708
BLAST score	106
E value	9.0e-45
Match length	98
% identity	95
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	151167
Seq. ID	LIB3175-054-P1-K1-E11
Method	BLASTN
NCBI GI	g4803835
BLAST score	275
E value	1.0e-153
Match length	295
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No.	151168
Seq. ID	LIB3175-054-P1-K1-E12
Method	BLASTX
NCBI GI	g4538912
BLAST score	236
E value	1.0e-19
Match length	89
% identity	72
NCBI Description	(AL049482) putative protein [Arabidopsis thaliana]

Seq. No.	151169
Seq. ID	LIB3175-054-P1-K1-E2
Method	BLASTN
NCBI GI	g2642152
BLAST score	231
E value	1.0e-127
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151170
Seq. ID	LIB3175-054-P1-K1-E4
Method	BLASTX
NCBI GI	g115385
BLAST score	293
E value	3.0e-29
Match length	69
% identity	84
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151171
Seq. ID	LIB3175-054-P1-K1-E7
Method	BLASTN
NCBI GI	g1237123
BLAST score	363
E value	0.0e+00
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana photosystem I PSI-N mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	151172
Seq. ID	LIB3175-054-P1-K1-E9
Method	BLASTN
NCBI GI	g4467131
BLAST score	108
E value	6.0e-54
Match length	192
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	151173
Seq. ID	LIB3175-054-P1-K1-F1
Method	BLASTX
NCBI GI	g4734009
BLAST score	125
E value	6.0e-10
Match length	90
% identity	46
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151174
Seq. ID	LIB3175-054-P1-K1-F11
Method	BLASTN
NCBI GI	g3869066
BLAST score	186
E value	1.0e-100
Match length	358
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	151175
Seq. ID	LIB3175-054-P1-K1-F12

Method	BLASTX
NCBI GI	g4204285
BLAST score	419
E value	4.0e-41
Match length	134
% identity	59
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	151176
Seq. ID	LIB3175-054-P1-K1-F2
Method	BLASTX
NCBI GI	g4758946
BLAST score	186
E value	7.0e-14
Match length	71
% identity	55
NCBI Description	POP2 (yeast homolog) >gi_4106061_gb_AAD02685_ (AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	151177
Seq. ID	LIB3175-054-P1-K1-F3
Method	BLASTX
NCBI GI	g4206207
BLAST score	160
E value	7.0e-11
Match length	93
% identity	33
NCBI Description	(AF071527) putative reverse transcriptase [Arabidopsis thaliana] >gi_4263040_gb_AAD15309_ (AC005142) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	151178
Seq. ID	LIB3175-054-P1-K1-F4
Method	BLASTX
NCBI GI	g1652892
BLAST score	247
E value	5.0e-21
Match length	148
% identity	26
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	151179
Seq. ID	LIB3175-054-P1-K1-F5
Method	BLASTX
NCBI GI	g1076708
BLAST score	602
E value	1.0e-62
Match length	123
% identity	25
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana]

	>gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]
Seq. No.	151180
Seq. ID	LIB3175-054-P1-K1-F9
Method	BLASTX
NCBI GI	g3914826
BLAST score	461
E value	3.0e-46
Match length	110
% identity	85
NCBI Description	DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR >gi_2330560_emb_CAA69972_ (Y08722) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_4115372 (AC005967) chloroplast single subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]
Seq. No.	151181
Seq. ID	LIB3175-054-P1-K1-G10
Method	BLASTX
NCBI GI	g99735
BLAST score	789
E value	1.0e-84
Match length	149
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)
Seq. No.	151182
Seq. ID	LIB3175-054-P1-K1-G11
Method	BLASTN
NCBI GI	g4757392
BLAST score	224
E value	1.0e-123
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence
Seq. No.	151183
Seq. ID	LIB3175-054-P1-K1-G2
Method	BLASTX
NCBI GI	g1402904
BLAST score	657
E value	4.0e-69
Match length	130
% identity	97
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]
Seq. No.	151184
Seq. ID	LIB3175-054-P1-K1-G3
Method	BLASTX
NCBI GI	g4585882
BLAST score	625
E value	2.0e-65

Match length	126
% identity	98
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	151185
Seq. ID	LIB3175-054-P1-K1-G4
Method	BLASTX
NCBI GI	g3157944
BLAST score	748
E value	9.0e-80
Match length	148
% identity	98
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge

Seq. No.	151186
Seq. ID	LIB3175-054-P1-K1-G7
Method	BLASTX
NCBI GI	g267069
BLAST score	609
E value	2.0e-63
Match length	114
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	151187
Seq. ID	LIB3175-054-P1-K1-G8
Method	BLASTN
NCBI GI	g2245073
BLAST score	306
E value	1.0e-172
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	151188
Seq. ID	LIB3175-054-P1-K1-G9
Method	BLASTX
NCBI GI	g3914658
BLAST score	568
E value	1.0e-58
Match length	110
% identity	100
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	151189
Seq. ID	LIB3175-054-P1-K1-H10

Method	BLASTN
NCBI GI	g3128143
BLAST score	42
E value	2.0e-14
Match length	126
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	151190
Seq. ID	LIB3175-054-P1-K1-H11
Method	BLASTX
NCBI GI	g4115364
BLAST score	528
E value	5.0e-54
Match length	109
% identity	94
NCBI Description	(AC005957) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	151191
Seq. ID	LIB3175-054-P1-K1-H4
Method	BLASTX
NCBI GI	g4586253
BLAST score	567
E value	2.0e-58
Match length	150
% identity	66
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	151192
Seq. ID	LIB3175-054-P1-K1-H5
Method	BLASTX
NCBI GI	g2129640
BLAST score	641
E value	4.0e-67
Match length	149
% identity	87
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	151193
Seq. ID	LIB3175-054-P1-K1-H6
Method	BLASTX
NCBI GI	g4539460
BLAST score	99
E value	1.0e-03
Match length	136
% identity	4
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	151194
Seq. ID	LIB3175-054-P1-K1-H7
Method	BLASTX
NCBI GI	g2129672
BLAST score	222

E value	1.0e-18
Match length	57
% identity	84
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	151195
Seq. ID	LIB3175-054-P1-K1-H8
Method	BLASTN
NCBI GI	g4567259
BLAST score	354
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	151196
Seq. ID	LIB3175-054-P1-K1-H9
Method	BLASTX
NCBI GI	g4585935
BLAST score	646
E value	8.0e-68
Match length	123
% identity	98
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	151197
Seq. ID	LIB3175-055-P1-K1-A1
Method	BLASTX
NCBI GI	g4314378
BLAST score	512
E value	2.0e-52
Match length	98
% identity	99
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	151198
Seq. ID	LIB3175-055-P1-K1-A10
Method	BLASTN
NCBI GI	g3702724
BLAST score	275
E value	1.0e-153
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	151199
Seq. ID	LIB3175-055-P1-K1-A4
Method	BLASTN
NCBI GI	g1732569
BLAST score	60

E value	9.0e-26
Match length	84
% identity	93
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	151200
Seq. ID	LIB3175-055-P1-K1-A5
Method	BLASTN
NCBI GI	g3985958
BLAST score	138
E value	6.0e-72
Match length	186
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	151201
Seq. ID	LIB3175-055-P1-K1-A6
Method	BLASTN
NCBI GI	g3335356
BLAST score	320
E value	1.0e-180
Match length	426
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151202
Seq. ID	LIB3175-055-P1-K1-A8
Method	BLASTX
NCBI GI	g2146733
BLAST score	445
E value	3.0e-44
Match length	75
% identity	100
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	151203
Seq. ID	LIB3175-055-P1-K1-A9
Method	BLASTX
NCBI GI	g3819710
BLAST score	526
E value	1.0e-53
Match length	96
% identity	100
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	151204
Seq. ID	LIB3175-055-P1-K1-B1
Method	BLASTN
NCBI GI	g4063730
BLAST score	409
E value	0.0e+00
Match length	429
% identity	99

NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151205
Seq. ID	LIB3175-055-P1-K1-B10
Method	BLASTN
NCBI GI	g633027
BLAST score	373
E value	0.0e+00
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for protein phosphatase 2C

Seq. No.	151206
Seq. ID	LIB3175-055-P1-K1-B12
Method	BLASTN
NCBI GI	g4220645
BLAST score	217
E value	1.0e-118
Match length	443
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	151207
Seq. ID	LIB3175-055-P1-K1-B2
Method	BLASTX
NCBI GI	g267077
BLAST score	749
E value	7.0e-80
Match length	138
% identity	99
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	151208
Seq. ID	LIB3175-055-P1-K1-B3
Method	BLASTX
NCBI GI	g2281093
BLAST score	687
E value	1.0e-72
Match length	137
% identity	96
NCBI Description	(AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No.	151209
Seq. ID	LIB3175-055-P1-K1-B4
Method	BLASTN
NCBI GI	g3510339
BLAST score	178
E value	1.0e-95
Match length	210
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	151210
Seq. ID	LIB3175-055-P1-K1-B6
Method	BLASTN
NCBI GI	g4662628
BLAST score	185
E value	1.0e-99
Match length	381
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	151211
Seq. ID	LIB3175-055-P1-K1-B7
Method	BLASTN
NCBI GI	g4262221
BLAST score	372
E value	0.0e+00
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151212
Seq. ID	LIB3175-055-P1-K1-B8
Method	BLASTN
NCBI GI	g2828188
BLAST score	242
E value	1.0e-133
Match length	455
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K3, complete sequence [Arabidopsis thaliana]

Seq. No.	151213
Seq. ID	LIB3175-055-P1-K1-C1
Method	BLASTX
NCBI GI	g4580389
BLAST score	709
E value	4.0e-75
Match length	147
% identity	89
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	151214
Seq. ID	LIB3175-055-P1-K1-C10
Method	BLASTN
NCBI GI	g2696018
BLAST score	208
E value	1.0e-113
Match length	381
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	151215
Seq. ID	LIB3175-055-P1-K1-C2

Method	BLASTN
NCBI GI	g3688169
BLAST score	42
E value	3.0e-15
Match length	42
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	151216
Seq. ID	LIB3175-055-P1-K1-C3
Method	BLASTX
NCBI GI	g2529229
BLAST score	383
E value	6.0e-37
Match length	106
% identity	70
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	151217
Seq. ID	LIB3175-055-P1-K1-C6
Method	BLASTX
NCBI GI	g1931640
BLAST score	145
E value	3.0e-09
Match length	67
% identity	46
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	151218
Seq. ID	LIB3175-055-P1-K1-C7
Method	BLASTX
NCBI GI	g1351272
BLAST score	422
E value	1.0e-41
Match length	103
% identity	82
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	151219
Seq. ID	LIB3175-055-P1-K1-C8
Method	BLASTX
NCBI GI	g1695717
BLAST score	712
E value	2.0e-75
Match length	147
% identity	95
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	151220
Seq. ID	LIB3175-055-P1-K1-D11
Method	BLASTX
NCBI GI	g3402487

BLAST score	678
E value	1.0e-71
Match length	139
% identity	98
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	151221
Seq. ID	LIB3175-055-P1-K1-D12
Method	BLASTX
NCBI GI	g2738248
BLAST score	569
E value	9.0e-59
Match length	109
% identity	100
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	151222
Seq. ID	LIB3175-055-P1-K1-D2
Method	BLASTN
NCBI GI	g4757405
BLAST score	319
E value	1.0e-179
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	151223
Seq. ID	LIB3175-055-P1-K1-D3
Method	BLASTX
NCBI GI	g3047125
BLAST score	591
E value	2.0e-61
Match length	124
% identity	89
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	151224
Seq. ID	LIB3175-055-P1-K1-D4
Method	BLASTN
NCBI GI	g3510342
BLAST score	34
E value	6.0e-10
Match length	46
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	151225
Seq. ID	LIB3175-055-P1-K1-D6
Method	BLASTX
NCBI GI	g4371284
BLAST score	661
E value	1.0e-69
Match length	133

% identity	96
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	151226
Seq. ID	LIB3175-055-P1-K1-D7
Method	BLASTX
NCBI GI	g1931640
BLAST score	141
E value	1.0e-08
Match length	71
% identity	39
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	151227
Seq. ID	LIB3175-055-P1-K1-D8
Method	BLASTN
NCBI GI	g3650026
BLAST score	348
E value	0.0e+00
Match length	436
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151228
Seq. ID	LIB3175-055-P1-K1-D9
Method	BLASTX
NCBI GI	g4185505
BLAST score	309
E value	3.0e-28
Match length	100
% identity	62
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	151229
Seq. ID	LIB3175-055-P1-K1-E1
Method	BLASTX
NCBI GI	g4490737
BLAST score	96
E value	3.0e-03
Match length	67
% identity	70
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	151230
Seq. ID	LIB3175-055-P1-K1-E2
Method	BLASTN
NCBI GI	g4544435
BLAST score	139
E value	4.0e-72
Match length	403
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	151231
Seq. ID	LIB3175-055-P1-K1-E3
Method	BLASTN
NCBI GI	g2264314
BLAST score	34
E value	2.0e-09
Match length	170
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	151232
Seq. ID	LIB3175-055-P1-K1-E4
Method	BLASTX
NCBI GI	g4531442
BLAST score	200
E value	5.0e-16
Match length	77
% identity	56
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151233
Seq. ID	LIB3175-055-P1-K1-E5
Method	BLASTX
NCBI GI	g4531442
BLAST score	500
E value	1.0e-50
Match length	136
% identity	79
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151234
Seq. ID	LIB3175-055-P1-K1-E7
Method	BLASTN
NCBI GI	g4519184
BLAST score	215
E value	1.0e-117
Match length	425
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16F13, complete sequence

Seq. No.	151235
Seq. ID	LIB3175-055-P1-K1-F2
Method	BLASTN
NCBI GI	g2642152
BLAST score	360
E value	0.0e+00
Match length	381
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151236
Seq. ID	LIB3175-055-P1-K1-F3
Method	BLASTX

NCBI GI	g3341690
BLAST score	563
E value	4.0e-58
Match length	123
% identity	88
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151237
Seq. ID	LIB3175-055-P1-K1-F4
Method	BLASTN
NCBI GI	g4531433
BLAST score	63
E value	6.0e-27
Match length	251
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	151238
Seq. ID	LIB3175-055-P1-K1-F5
Method	BLASTX
NCBI GI	g4531442
BLAST score	612
E value	7.0e-64
Match length	137
% identity	92
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151239
Seq. ID	LIB3175-055-P1-K1-F7
Method	BLASTN
NCBI GI	g4220640
BLAST score	64
E value	1.0e-27
Match length	200
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	151240
Seq. ID	LIB3175-055-P1-K1-F9
Method	BLASTX
NCBI GI	g4185505
BLAST score	451
E value	6.0e-45
Match length	115
% identity	75
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	151241
Seq. ID	LIB3175-055-P1-K1-G10
Method	BLASTX
NCBI GI	g1170203
BLAST score	540
E value	2.0e-55
Match length	143

% identity	77
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	151242
Seq. ID	LIB3175-055-P1-K1-G11
Method	BLASTN
NCBI GI	g4531433
BLAST score	117
E value	5.0e-59
Match length	342
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	151243
Seq. ID	LIB3175-055-P1-K1-G2
Method	BLASTX
NCBI GI	g2129759
BLAST score	557
E value	2.0e-57
Match length	108
% identity	96
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	151244
Seq. ID	LIB3175-055-P1-K1-G3
Method	BLASTN
NCBI GI	g4531433
BLAST score	33
E value	3.0e-09
Match length	89
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	151245
Seq. ID	LIB3175-055-P1-K1-G6
Method	BLASTX
NCBI GI	g4531442
BLAST score	225
E value	1.0e-31
Match length	142
% identity	56
NCBI Description	(AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151246
Seq. ID	LIB3175-055-P1-K1-G9
Method	BLASTN
NCBI GI	g4406752
BLAST score	40
E value	3.0e-13
Match length	60
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151247
Seq. ID	LIB3175-055-P1-K1-H10
Method	BLASTX
NCBI GI	g4734010
BLAST score	325
E value	4.0e-30
Match length	144
% identity	44
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151248
Seq. ID	LIB3175-055-P1-K1-H11
Method	BLASTX
NCBI GI	g1864017
BLAST score	541
E value	1.0e-55
Match length	104
% identity	98
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	151249
Seq. ID	LIB3175-055-P1-K1-H12
Method	BLASTN
NCBI GI	g2058281
BLAST score	48
E value	3.0e-18
Match length	108
% identity	94
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	151250
Seq. ID	LIB3175-055-P1-K1-H3
Method	BLASTX
NCBI GI	g2654440
BLAST score	266
E value	3.0e-23
Match length	124
% identity	52
NCBI Description	(U70076) Lemir [Lycopersicon esculentum]

Seq. No.	151251
Seq. ID	LIB3175-055-P1-K1-H4
Method	BLASTX
NCBI GI	g4734010
BLAST score	277
E value	1.0e-24
Match length	122
% identity	44
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151252
Seq. ID	LIB3175-055-P1-K1-H5
Method	BLASTX
NCBI GI	g4734009
BLAST score	61

E value	1.0e-09
Match length	107
% identity	31
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151253
Seq. ID	LIB3175-055-P1-K1-H6
Method	BLASTX
NCBI GI	g3893822
BLAST score	501
E value	6.0e-51
Match length	116
% identity	84
NCBI Description	(U96498) ATPase beta subunit [Nicotiana sylvestris]

Seq. No.	151254
Seq. ID	LIB3175-055-P1-K1-H8
Method	BLASTX
NCBI GI	g3421102
BLAST score	652
E value	1.0e-68
Match length	133
% identity	95
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	151255
Seq. ID	LIB3175-055-P1-K1-H9
Method	BLASTX
NCBI GI	g2191177
BLAST score	625
E value	2.0e-65
Match length	128
% identity	100
NCBI Description	(AF007270) belongs to the SPOU family of rRNA methylases. [Arabidopsis thaliana]

Seq. No.	151256
Seq. ID	LIB3175-056-P1-K1-A1
Method	BLASTN
NCBI GI	g3449326
BLAST score	447
E value	0.0e+00
Match length	463
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	151257
Seq. ID	LIB3175-056-P1-K1-A11
Method	BLASTX
NCBI GI	g4469003
BLAST score	179
E value	4.0e-13
Match length	120
% identity	46
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	151258
Seq. ID	LIB3175-056-P1-K1-A12
Method	BLASTN
NCBI GI	g4589418
BLAST score	192
E value	1.0e-104
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	151259
Seq. ID	LIB3175-056-P1-K1-A3
Method	BLASTX
NCBI GI	g3286693
BLAST score	568
E value	1.0e-58
Match length	122
% identity	93
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	151260
Seq. ID	LIB3175-056-P1-K1-A4
Method	BLASTX
NCBI GI	g3043415
BLAST score	761
E value	3.0e-81
Match length	151
% identity	99
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	151261
Seq. ID	LIB3175-056-P1-K1-A5
Method	BLASTN
NCBI GI	g2244991
BLAST score	268
E value	1.0e-149
Match length	456
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	151262
Seq. ID	LIB3175-056-P1-K1-A7
Method	BLASTX
NCBI GI	g4204260
BLAST score	225
E value	2.0e-18
Match length	57
% identity	81
NCBI Description	(AC005223) 25568 [Arabidopsis thaliana]

Seq. No.	151263
Seq. ID	LIB3175-056-P1-K1-B10
Method	BLASTX

NCBI GI	g3928134
BLAST score	536
E value	7.0e-55
Match length	147
% identity	29
NCBI Description	(AJ130956) annexin P38 [Capsicum annuum]

Seq. No.	151264
Seq. ID	LIB3175-056-P1-K1-B11
Method	BLASTX
NCBI GI	g4099088
BLAST score	509
E value	1.0e-51
Match length	101
% identity	100
NCBI Description	(U83177) SNF1 family protein kinase [Arabidopsis thaliana]

Seq. No.	151265
Seq. ID	LIB3175-056-P1-K1-B12
Method	BLASTN
NCBI GI	g4049332
BLAST score	342
E value	0.0e+00
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	151266
Seq. ID	LIB3175-056-P1-K1-B2
Method	BLASTX
NCBI GI	g1931639
BLAST score	255
E value	6.0e-22
Match length	110
% identity	43
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	151267
Seq. ID	LIB3175-056-P1-K1-B3
Method	BLASTX
NCBI GI	g1703108
BLAST score	672
E value	8.0e-71
Match length	125
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	151268
Seq. ID	LIB3175-056-P1-K1-B4
Method	BLASTX
NCBI GI	g1705620
BLAST score	788

E value	2.0e-84
Match length	147
% identity	100
NCBI Description	CATALASE 2 >gi_1246399_emb_CAA64220_ (X94447) catalase [Arabidopsis thaliana]

Seq. No.	151269
Seq. ID	LIB3175-056-P1-K1-B6
Method	BLASTX
NCBI GI	g3582340
BLAST score	189
E value	3.0e-14
Match length	88
% identity	49
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	151270
Seq. ID	LIB3175-056-P1-K1-C1
Method	BLASTX
NCBI GI	g3913648
BLAST score	376
E value	4.0e-36
Match length	122
% identity	60
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)

Seq. No.	151271
Seq. ID	LIB3175-056-P1-K1-C4
Method	BLASTN
NCBI GI	g3241923
BLAST score	245
E value	1.0e-135
Match length	461
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	151272
Seq. ID	LIB3175-056-P1-K1-C5
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	151273
Seq. ID	LIB3175-056-P1-K1-C7
Method	BLASTX
NCBI GI	g4235093
BLAST score	143
E value	9.0e-09
Match length	102
% identity	36
NCBI Description	(AF108944) beta-xylosidase [Aspergillus niger]

Seq. No.	151274
Seq. ID	LIB3175-056-P1-K1-C9
Method	BLASTX
NCBI GI	g927428
BLAST score	637
E value	1.0e-66
Match length	152
% identity	79
NCBI Description	(X86733) fis1 [Linum usitatissimum]

Seq. No.	151275
Seq. ID	LIB3175-056-P1-K1-D10
Method	BLASTX
NCBI GI	g3641837
BLAST score	620
E value	1.0e-64
Match length	125
% identity	99
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	151276
Seq. ID	LIB3175-056-P1-K1-D11
Method	BLASTN
NCBI GI	g4159707
BLAST score	273
E value	1.0e-152
Match length	454
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	151277
Seq. ID	LIB3175-056-P1-K1-D2
Method	BLASTX
NCBI GI	g1922937
BLAST score	644
E value	1.0e-67
Match length	126
% identity	100
NCBI Description	(AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs gb_H76869,gb_T21700,gb_ATTS5089 come from this gene. [Arabidopsis thaliana]

Seq. No.	151278
Seq. ID	LIB3175-056-P1-K1-D3
Method	BLASTX
NCBI GI	g2160169
BLAST score	349
E value	6.0e-33
Match length	126
% identity	56
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	151279
Seq. ID	LIB3175-056-P1-K1-D4

Method	BLASTX
NCBI GI	g3292829
BLAST score	209
E value	2.0e-16
Match length	82
% identity	55
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	151280
Seq. ID	LIB3175-056-P1-K1-D5
Method	BLASTX
NCBI GI	g112681
BLAST score	647
E value	7.0e-68
Match length	151
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	151281
Seq. ID	LIB3175-056-P1-K1-D7
Method	BLASTN
NCBI GI	g3510343
BLAST score	428
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	151282
Seq. ID	LIB3175-056-P1-K1-D9
Method	BLASTX
NCBI GI	g4678349
BLAST score	678
E value	2.0e-71
Match length	151
% identity	29
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	151283
Seq. ID	LIB3175-056-P1-K1-E1
Method	BLASTX
NCBI GI	g3668175
BLAST score	677
E value	2.0e-71
Match length	145
% identity	89
NCBI Description	(AB006778) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	151284
Seq. ID	LIB3175-056-P1-K1-E10
Method	BLASTX

NCBI GI	g4725950
BLAST score	274
E value	4.0e-24
Match length	129
% identity	50
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana] >gi_4725951_emb_CAB41722.1_ (AL049730) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	151285
Seq. ID	LIB3175-056-P1-K1-E11
Method	BLASTX
NCBI GI	g2623962
BLAST score	668
E value	2.0e-70
Match length	144
% identity	86
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	151286
Seq. ID	LIB3175-056-P1-K1-E12
Method	BLASTX
NCBI GI	g4033467
BLAST score	189
E value	3.0e-14
Match length	36
% identity	100
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	151287
Seq. ID	LIB3175-056-P1-K1-E4
Method	BLASTX
NCBI GI	g2979559
BLAST score	276
E value	2.0e-24
Match length	60
% identity	87
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	151288
Seq. ID	LIB3175-056-P1-K1-E5
Method	BLASTX
NCBI GI	g4567269
BLAST score	607
E value	3.0e-63
Match length	133
% identity	91
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	151289
Seq. ID	LIB3175-056-P1-K1-E6
Method	BLASTX
NCBI GI	g464986

BLAST score	733
E value	6.0e-78
Match length	137
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	151290
Seq. ID	LIB3175-056-P1-K1-E7
Method	BLASTX
NCBI GI	g3947448
BLAST score	346
E value	1.0e-32
Match length	151
% identity	47
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	151291
Seq. ID	LIB3175-056-P1-K1-E9
Method	BLASTX
NCBI GI	g2244981
BLAST score	262
E value	9.0e-23
Match length	113
% identity	49
NCBI Description	(Z97340) similarity to proline-rich protein APG - Arabidopsis [Arabidopsis thaliana]

Seq. No.	151292
Seq. ID	LIB3175-056-P1-K1-F1
Method	BLASTN
NCBI GI	g3406034
BLAST score	213
E value	1.0e-116
Match length	418
% identity	98
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151293

Seq. ID	LIB3175-056-P1-K1-F10
Method	BLASTX
NCBI GI	g2505874
BLAST score	705
E value	9.0e-75
Match length	137
% identity	99
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	151294
Seq. ID	LIB3175-056-P1-K1-F11
Method	BLASTX
NCBI GI	g3451077
BLAST score	146
E value	2.0e-09
Match length	36
% identity	69
NCBI Description	(AL031326) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	151295
Seq. ID	LIB3175-056-P1-K1-F12
Method	BLASTN
NCBI GI	g4220633
BLAST score	362
E value	0.0e+00
Match length	398
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	151296
Seq. ID	LIB3175-056-P1-K1-F3
Method	BLASTX
NCBI GI	g3668086
BLAST score	223
E value	4.0e-18
Match length	64
% identity	64
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	151297
Seq. ID	LIB3175-056-P1-K1-F4
Method	BLASTX
NCBI GI	g4503161
BLAST score	196
E value	5.0e-15
Match length	141
% identity	30
NCBI Description	cullin 1 >gi_2493906_sp_Q13616_CUL1_HUMAN CULLIN HOMOLOG 1 (CUL-1) >gi_1381142 (U58087) Hs-CUL-1 [Homo sapiens]

Seq. No.	151298
Seq. ID	LIB3175-056-P1-K1-F5
Method	BLASTN
NCBI GI	g3193282
BLAST score	452

E value	0.0e+00
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	151299
Seq. ID	LIB3175-056-P1-K1-F6
Method	BLASTN
NCBI GI	g3702729
BLAST score	140
E value	9.0e-73
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A11, complete sequence [Arabidopsis thaliana]

Seq. No.	151300
Seq. ID	LIB3175-056-P1-K1-F7
Method	BLASTX
NCBI GI	g4539465
BLAST score	138
E value	1.0e-31
Match length	72
% identity	91
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	151301
Seq. ID	LIB3175-056-P1-K1-F8
Method	BLASTX
NCBI GI	g1755162
BLAST score	640
E value	4.0e-67
Match length	138
% identity	90
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	151302
Seq. ID	LIB3175-056-P1-K1-F9
Method	BLASTX
NCBI GI	g4741952
BLAST score	679
E value	1.0e-71
Match length	128
% identity	76
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	151303
Seq. ID	LIB3175-056-P1-K1-G1
Method	BLASTX
NCBI GI	g3914658
BLAST score	645
E value	1.0e-67
Match length	146
% identity	87
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	151304
Seq. ID	LIB3175-056-P1-K1-G11
Method	BLASTX
NCBI GI	g4741952
BLAST score	709
E value	4.0e-75
Match length	136
% identity	75
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	151305
Seq. ID	LIB3175-056-P1-K1-G2
Method	BLASTX
NCBI GI	g1706772
BLAST score	788
E value	2.0e-84
Match length	148
% identity	100
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	151306
Seq. ID	LIB3175-056-P1-K1-G3
Method	BLASTX
NCBI GI	g2497886
BLAST score	289
E value	6.0e-26
Match length	53
% identity	98
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	151307
Seq. ID	LIB3175-056-P1-K1-G4
Method	BLASTX
NCBI GI	g2494275
BLAST score	250
E value	2.0e-21
Match length	75
% identity	60
NCBI Description	ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No.	151308

Seq. ID	LIB3175-056-P1-K1-G6
Method	BLASTN
NCBI GI	g3059018
BLAST score	41
E value	1.0e-13
Match length	453
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	151309
Seq. ID	LIB3175-056-P1-K1-G8
Method	BLASTX
NCBI GI	g2781394
BLAST score	239
E value	5.0e-20
Match length	108
% identity	52
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	151310
Seq. ID	LIB3175-056-P1-K1-H1
Method	BLASTN
NCBI GI	g3985958
BLAST score	312
E value	1.0e-175
Match length	428
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	151311
Seq. ID	LIB3175-056-P1-K1-H10
Method	BLASTX
NCBI GI	g4544399
BLAST score	475
E value	8.0e-48
Match length	132
% identity	64
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	151312
Seq. ID	LIB3175-056-P1-K1-H11
Method	BLASTX
NCBI GI	g1107501
BLAST score	402
E value	4.0e-39
Match length	99
% identity	83
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	151313
Seq. ID	LIB3175-056-P1-K1-H12

Method	BLASTX
NCBI GI	g1363487
BLAST score	422
E value	8.0e-42
Match length	85
% identity	100
NCBI Description	IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) IAA7 [Arabidopsis thaliana]

Seq. No.	151314
Seq. ID	LIB3175-056-P1-K1-H2
Method	BLASTX
NCBI GI	g2462749
BLAST score	147
E value	3.0e-09
Match length	107
% identity	32
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	151315
Seq. ID	LIB3175-056-P1-K1-H3
Method	BLASTX
NCBI GI	g2911057
BLAST score	636
E value	1.0e-66
Match length	124
% identity	100
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	151316
Seq. ID	LIB3175-056-P1-K1-H5
Method	BLASTX
NCBI GI	g1107501
BLAST score	199
E value	1.0e-15
Match length	84
% identity	46
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	151317
Seq. ID	LIB3175-056-P1-K1-H7
Method	BLASTX
NCBI GI	g481914
BLAST score	608
E value	2.0e-63
Match length	120
% identity	93
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica napus]

Seq. No.	151318

Seq. ID	LIB3175-056-P1-K1-H9
Method	BLASTX
NCBI GI	g4587549
BLAST score	320
E value	1.0e-29
Match length	59
% identity	100
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	151319
Seq. ID	LIB3175-057-P1-K1-A1
Method	BLASTX
NCBI GI	g2146727
BLAST score	515
E value	2.0e-55
Match length	123
% identity	97
NCBI Description	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	151320
Seq. ID	LIB3175-057-P1-K1-A10
Method	BLASTX
NCBI GI	g1871185
BLAST score	232
E value	3.0e-19
Match length	62
% identity	77
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	151321
Seq. ID	LIB3175-057-P1-K1-A11
Method	BLASTN
NCBI GI	g4249393
BLAST score	266
E value	1.0e-148
Match length	274
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151322
Seq. ID	LIB3175-057-P1-K1-A12
Method	BLASTX
NCBI GI	g1707013
BLAST score	222
E value	4.0e-18
Match length	90
% identity	50
NCBI Description	(U78721) Brassica napus hypothetical protein 2 isolog [Arabidopsis thaliana]

Seq. No.	151323

Seq. ID	LIB3175-057-P1-K1-A2
Method	BLASTN
NCBI GI	g598070
BLAST score	51
E value	4.0e-20
Match length	83
% identity	90
NCBI Description	Arabidopsis thaliana cinnamyl alcohol dehydrogenase (CAD1) gene, complete cds

Seq. No.	151324
Seq. ID	LIB3175-057-P1-K1-A4
Method	BLASTX
NCBI GI	g1001294
BLAST score	264
E value	5.0e-23
Match length	104
% identity	42
NCBI Description	(D64006) hypothetical protein [Synechocystis sp.]

Seq. No.	151325
Seq. ID	LIB3175-057-P1-K1-A6
Method	BLASTX
NCBI GI	g3269293
BLAST score	259
E value	2.0e-22
Match length	95
% identity	57
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	151326
Seq. ID	LIB3175-057-P1-K1-A7
Method	BLASTX
NCBI GI	g2146727
BLAST score	328
E value	7.0e-31
Match length	67
% identity	100
NCBI Description	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	151327
Seq. ID	LIB3175-057-P1-K1-A8
Method	BLASTX
NCBI GI	g3033400
BLAST score	402
E value	3.0e-39
Match length	78
% identity	91
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	151328
Seq. ID	LIB3175-057-P1-K1-B1
Method	BLASTX
NCBI GI	g3212879

BLAST score	593
E value	1.0e-61
Match length	142
% identity	85
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	151329
Seq. ID	LIB3175-057-P1-K1-B10
Method	BLASTX
NCBI GI	g1168256
BLAST score	679
E value	1.0e-71
Match length	142
% identity	94
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	151330
Seq. ID	LIB3175-057-P1-K1-B2
Method	BLASTN
NCBI GI	g472876
BLAST score	75
E value	2.0e-34
Match length	123
% identity	90
NCBI Description	A.thaliana mRNA for plasma membrane intrinsic protein 2a

Seq. No.	151331
Seq. ID	LIB3175-057-P1-K1-B3
Method	BLASTX
NCBI GI	g115783
BLAST score	619
E value	1.0e-64
Match length	128
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	151332
Seq. ID	LIB3175-057-P1-K1-B4
Method	BLASTN
NCBI GI	g2462076
BLAST score	443
E value	0.0e+00
Match length	451
% identity	100
NCBI Description	A.thaliana mRNA for oxa1-like gene

Seq. No.	151333
Seq. ID	LIB3175-057-P1-K1-B6
Method	BLASTX

NCBI GI	g1184075
BLAST score	251
E value	2.0e-21
Match length	148
% identity	3
NCBI Description	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No.	151334
Seq. ID	LIB3175-057-P1-K1-B8
Method	BLASTX
NCBI GI	g2499236
BLAST score	314
E value	2.0e-40
Match length	113
% identity	77
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis thaliana]

Seq. No.	151335
Seq. ID	LIB3175-057-P1-K1-B9
Method	BLASTX
NCBI GI	g4505337
BLAST score	281
E value	3.0e-25
Match length	92
% identity	59
NCBI Description	nucleotide binding protein 1 (E.coli MinD like) >gi_1709232_sp_P53384_NBP_HUMAN NUCLEOTIDE-BINDING PROTEIN (NBP) >gi_1082661_pir__JC4010 nucleotide-binding protein - human >gi_515644 (U01833) putative nucleotide-binding protein [Homo sapiens]

Seq. No.	151336
Seq. ID	LIB3175-057-P1-K1-C1
Method	BLASTX
NCBI GI	g3273751
BLAST score	617
E value	2.0e-64
Match length	143
% identity	85
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	151337
Seq. ID	LIB3175-057-P1-K1-C10
Method	BLASTX
NCBI GI	g1170897
BLAST score	400
E value	7.0e-58
Match length	146
% identity	83
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1076276_pir__S52039 NAD-malate dehydrogenase - cucumber >gi_695311 (L31900) glyoxysomal malate dehydrogenase

[Cucumis sativus]

Seq. No.	151338
Seq. ID	LIB3175-057-P1-K1-C2
Method	BLASTX
NCBI GI	g1762150
BLAST score	729
E value	2.0e-77
Match length	150
% identity	87
NCBI Description	(U49919) lupeol synthase [Arabidopsis thaliana]

Seq. No.	151339
Seq. ID	LIB3175-057-P1-K1-C3
Method	BLASTX
NCBI GI	g4204285
BLAST score	408
E value	5.0e-40
Match length	98
% identity	73
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	151340
Seq. ID	LIB3175-057-P1-K1-C4
Method	BLASTX
NCBI GI	g3068713
BLAST score	632
E value	4.0e-66
Match length	145
% identity	90
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	151341
Seq. ID	LIB3175-057-P1-K1-C5
Method	BLASTX
NCBI GI	g4455223
BLAST score	381
E value	1.0e-36
Match length	73
% identity	51
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	151342
Seq. ID	LIB3175-057-P1-K1-C6
Method	BLASTX
NCBI GI	g2454182
BLAST score	537
E value	5.0e-55
Match length	146
% identity	75
NCBI Description	(U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	151343
Seq. ID	LIB3175-057-P1-K1-C7

Method	BLASTX
NCBI GI	g3859560
BLAST score	176
E value	1.0e-12
Match length	96
% identity	41
NCBI Description	(AF098668) acyl-protein thioesterase [Homo sapiens] >gi_4581413_emb_CAB40158.1_ (AL031295) dJ886K2.4 (acyl-protein thioesterase) [Homo sapiens]

Seq. No.	151344
Seq. ID	LIB3175-057-P1-K1-D1
Method	BLASTX
NCBI GI	g3702321
BLAST score	727
E value	3.0e-77
Match length	139
% identity	56
NCBI Description	(AC005397) putative TGF-beta receptor interacting protein [Arabidopsis thaliana]

Seq. No.	151345
Seq. ID	LIB3175-057-P1-K1-D10
Method	BLASTN
NCBI GI	g2160132
BLAST score	56
E value	6.0e-23
Match length	112
% identity	88
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	151346
Seq. ID	LIB3175-057-P1-K1-D12
Method	BLASTX
NCBI GI	g2623962
BLAST score	379
E value	1.0e-36
Match length	81
% identity	90
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	151347
Seq. ID	LIB3175-057-P1-K1-D3
Method	BLASTX
NCBI GI	g4063751
BLAST score	217
E value	2.0e-17
Match length	118
% identity	40
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	151348
Seq. ID	LIB3175-057-P1-K1-D4

Method	BLASTX
NCBI GI	g4581156
BLAST score	702
E value	2.0e-74
Match length	148
% identity	95
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No.	151349
Seq. ID	LIB3175-057-P1-K1-D5
Method	BLASTX
NCBI GI	g3023848
BLAST score	529
E value	4.0e-54
Match length	116
% identity	33
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	151350
Seq. ID	LIB3175-057-P1-K1-D6
Method	BLASTX
NCBI GI	g4512675
BLAST score	591
E value	2.0e-61
Match length	135
% identity	81
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	151351
Seq. ID	LIB3175-057-P1-K1-D7
Method	BLASTX
NCBI GI	g4204274
BLAST score	631
E value	5.0e-66
Match length	120
% identity	95
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	151352
Seq. ID	LIB3175-057-P1-K1-E11
Method	BLASTN
NCBI GI	g4159710
BLAST score	180
E value	1.0e-96
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	151353
Seq. ID	LIB3175-057-P1-K1-E12
Method	BLASTN
NCBI GI	g4335744

BLAST score	262
E value	1.0e-145
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151354
Seq. ID	LIB3175-057-P1-K1-E2
Method	BLASTX
NCBI GI	g3337095
BLAST score	447
E value	2.0e-44
Match length	141
% identity	62
NCBI Description	(AB016206) polygalacturonase inhibitor (PGIP) [Citrus iyo]

Seq. No.	151355
Seq. ID	LIB3175-057-P1-K1-E3
Method	BLASTN
NCBI GI	g2656024
BLAST score	180
E value	1.0e-96
Match length	408
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	151356
Seq. ID	LIB3175-057-P1-K1-E4
Method	BLASTX
NCBI GI	g2129579
BLAST score	718
E value	3.0e-76
Match length	137
% identity	99
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	151357
Seq. ID	LIB3175-057-P1-K1-E7
Method	BLASTX
NCBI GI	g2160133
BLAST score	384
E value	5.0e-37
Match length	91
% identity	87
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	151358
Seq. ID	LIB3175-057-P1-K1-E8
Method	BLASTX
NCBI GI	g3894183
BLAST score	458

E value	9.0e-46
Match length	130
% identity	74
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	151359
Seq. ID	LIB3175-057-P1-K1-E9
Method	BLASTX
NCBI GI	g3511285
BLAST score	311
E value	2.0e-28
Match length	113
% identity	51
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	151360
Seq. ID	LIB3175-057-P1-K1-F1
Method	BLASTX
NCBI GI	g120669
BLAST score	314
E value	3.0e-29
Match length	64
% identity	91
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No.	151361
Seq. ID	LIB3175-057-P1-K1-F10
Method	BLASTN
NCBI GI	g4510360
BLAST score	271
E value	1.0e-151
Match length	372
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	151362
Seq. ID	LIB3175-057-P1-K1-F11
Method	BLASTX
NCBI GI	g4538897
BLAST score	659
E value	3.0e-69
Match length	130
% identity	100
NCBI Description	(AL049482) AX110P-like protein [Arabidopsis thaliana]

Seq. No.	151363
Seq. ID	LIB3175-057-P1-K1-F2
Method	BLASTX
NCBI GI	g115783
BLAST score	686
E value	2.0e-72

Match length	137
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	151364
Seq. ID	LIB3175-057-P1-K1-F4
Method	BLASTX
NCBI GI	g1666171
BLAST score	592
E value	2.0e-61
Match length	130
% identity	82
NCBI Description	(Y09105) unknown [Nicotiana plumbaginifolia]

Seq. No.	151365
Seq. ID	LIB3175-057-P1-K1-F5
Method	BLASTN
NCBI GI	g2351062
BLAST score	145
E value	6.0e-76
Match length	220
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	151366
Seq. ID	LIB3175-057-P1-K1-F9
Method	BLASTN
NCBI GI	g4757392
BLAST score	159
E value	3.0e-84
Match length	187
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	151367
Seq. ID	LIB3175-057-P1-K1-G1
Method	BLASTX
NCBI GI	g3395938
BLAST score	578
E value	8.0e-60
Match length	126
% identity	90
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	151368
Seq. ID	LIB3175-057-P1-K1-G2
Method	BLASTX
NCBI GI	g2129609
BLAST score	372
E value	1.0e-35
Match length	123

% identity	67
NCBI Description	HD-ZIP protein - Arabidopsis thaliana >gi_1212757_emb_CAA91183_ (Z54356) HD-ZIP [Arabidopsis thaliana]
Seq. No.	151369
Seq. ID	LIB3175-057-P1-K1-G3
Method	BLASTX
NCBI GI	g1170505
BLAST score	547
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]
Seq. No.	151370
Seq. ID	LIB3175-057-P1-K1-G6
Method	BLASTX
NCBI GI	g542157
BLAST score	631
E value	5.0e-66
Match length	148
% identity	81
NCBI Description	ribosomal 5S RNA-binding protein - Rice
Seq. No.	151371
Seq. ID	LIB3175-057-P1-K1-G7
Method	BLASTN
NCBI GI	g4589446
BLAST score	120
E value	6.0e-61
Match length	302
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence
Seq. No.	151372
Seq. ID	LIB3175-057-P1-K1-G8
Method	BLASTN
NCBI GI	g3687221
BLAST score	382
E value	0.0e+00
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	151373
Seq. ID	LIB3175-057-P1-K1-G9
Method	BLASTX
NCBI GI	g4432856

BLAST score	60
E value	1.0e-77
Match length	149
% identity	98
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	151374
Seq. ID	LIB3175-057-P1-K1-H11
Method	BLASTN
NCBI GI	g4589950
BLAST score	46
E value	6.0e-17
Match length	82
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	151375
Seq. ID	LIB3175-057-P1-K1-H12
Method	BLASTX
NCBI GI	g2981475
BLAST score	335
E value	2.0e-31
Match length	95
% identity	66
NCBI Description	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]

Seq. No.	151376
Seq. ID	LIB3175-057-P1-K1-H2
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	3.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	151377
Seq. ID	LIB3175-057-P1-K1-H4
Method	BLASTX
NCBI GI	g4193388
BLAST score	503
E value	5.0e-51
Match length	134
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	151378
Seq. ID	LIB3175-057-P1-K1-H8
Method	BLASTX
NCBI GI	g2335099
BLAST score	385

E value	3.0e-37
Match length	115
% identity	61
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	151379
Seq. ID	LIB3175-058-P1-K1-A1
Method	BLASTX
NCBI GI	g4581109
BLAST score	444
E value	2.0e-45
Match length	111
% identity	86
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	151380
Seq. ID	LIB3175-058-P1-K1-A2
Method	BLASTX
NCBI GI	g3386597
BLAST score	403
E value	2.0e-39
Match length	79
% identity	96
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana] >gi_3702347 (AC005397) putative permease [Arabidopsis thaliana]

Seq. No.	151381
Seq. ID	LIB3175-058-P1-K1-A3
Method	BLASTN
NCBI GI	g2342717
BLAST score	124
E value	2.0e-63
Match length	218
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151382
Seq. ID	LIB3175-058-P1-K1-A5
Method	BLASTX
NCBI GI	g4063751
BLAST score	214
E value	4.0e-17
Match length	131
% identity	42
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	151383
Seq. ID	LIB3175-058-P1-K1-A7
Method	BLASTN
NCBI GI	g3461810
BLAST score	308
E value	1.0e-173
Match length	395

% identity 98
NCBI Description Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 151384
Seq. ID LIB3175-058-P1-K1-A8
Method BLASTX
NCBI GI g529353
BLAST score 196
E value 4.0e-15
Match length 56
% identity 59
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No. 151385
Seq. ID LIB3175-058-P1-K1-B1
Method BLASTX
NCBI GI g3851636
BLAST score 495
E value 4.0e-50
Match length 124
% identity 74
NCBI Description (AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 151386
Seq. ID LIB3175-058-P1-K1-B10
Method BLASTX
NCBI GI g4206206
BLAST score 657
E value 4.0e-69
Match length 139
% identity 91
NCBI Description (AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No. 151387
Seq. ID LIB3175-058-P1-K1-B11
Method BLASTX
NCBI GI g464662
BLAST score 213
E value 5.0e-17
Match length 105
% identity 48
NCBI Description CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	151388
Seq. ID	LIB3175-058-P1-K1-B12
Method	BLASTX
NCBI GI	g99735
BLAST score	743
E value	3.0e-79
Match length	145
% identity	97
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	151389
Seq. ID	LIB3175-058-P1-K1-B2
Method	BLASTX
NCBI GI	g3212866
BLAST score	260
E value	1.0e-22
Match length	78
% identity	67
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	151390
Seq. ID	LIB3175-058-P1-K1-B3
Method	BLASTX
NCBI GI	g1172872
BLAST score	455
E value	2.0e-45
Match length	88
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	151391
Seq. ID	LIB3175-058-P1-K1-B4
Method	BLASTX
NCBI GI	g2832359
BLAST score	306
E value	7.0e-28
Match length	79
% identity	82
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	151392
Seq. ID	LIB3175-058-P1-K1-B5
Method	BLASTX
NCBI GI	g4056469
BLAST score	608
E value	3.0e-63
Match length	119
% identity	99
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	151393
Seq. ID	LIB3175-058-P1-K1-B6
Method	BLASTX
NCBI GI	g544425
BLAST score	417
E value	6.0e-41
Match length	82
% identity	99
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	151394
Seq. ID	LIB3175-058-P1-K1-B7
Method	BLASTX
NCBI GI	g3935156
BLAST score	399
E value	3.0e-43
Match length	110
% identity	77
NCBI Description	(AC005106) T25N20.20 [Arabidopsis thaliana]

Seq. No.	151395
Seq. ID	LIB3175-058-P1-K1-B8
Method	BLASTN
NCBI GI	g3510343
BLAST score	196
E value	1.0e-106
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	151396
Seq. ID	LIB3175-058-P1-K1-B9
Method	BLASTX
NCBI GI	g2827143
BLAST score	274
E value	2.0e-24
Match length	79
% identity	73
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	151397
Seq. ID	LIB3175-058-P1-K1-C1
Method	BLASTX
NCBI GI	g1709798
BLAST score	508
E value	1.0e-51
Match length	133

% identity	81
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi_1155334 (U43398) POTATP1 [Solanum tuberosum]

Seq. No.	151398
Seq. ID	LIB3175-058-P1-K1-C10
Method	BLASTX
NCBI GI	g4580460
BLAST score	280
E value	8.0e-33
Match length	111
% identity	77
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	151399
Seq. ID	LIB3175-058-P1-K1-C11
Method	BLASTX
NCBI GI	g2342735
BLAST score	372
E value	7.0e-36
Match length	90
% identity	83
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	151400
Seq. ID	LIB3175-058-P1-K1-C12
Method	BLASTN
NCBI GI	g4587641
BLAST score	44
E value	1.0e-15
Match length	68
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	151401
Seq. ID	LIB3175-058-P1-K1-C2
Method	BLASTX
NCBI GI	g4185505
BLAST score	461
E value	4.0e-46
Match length	112
% identity	78
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	151402
Seq. ID	LIB3175-058-P1-K1-C4
Method	BLASTX
NCBI GI	g2244749
BLAST score	671
E value	1.0e-70
Match length	132
% identity	99
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	151403
Seq. ID	LIB3175-058-P1-K1-C5
Method	BLASTN
NCBI GI	g4757415
BLAST score	201
E value	1.0e-109
Match length	365
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	151404
Seq. ID	LIB3175-058-P1-K1-C6
Method	BLASTX
NCBI GI	g2119846
BLAST score	657
E value	4.0e-69
Match length	138
% identity	90
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151405
Seq. ID	LIB3175-058-P1-K1-D1
Method	BLASTX
NCBI GI	g2950210
BLAST score	308
E value	3.0e-28
Match length	62
% identity	100
NCBI Description	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	151406
Seq. ID	LIB3175-058-P1-K1-D10
Method	BLASTX
NCBI GI	g4741952
BLAST score	631
E value	4.0e-66
Match length	119
% identity	74
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	151407
Seq. ID	LIB3175-058-P1-K1-D12
Method	BLASTX
NCBI GI	g2500193
BLAST score	90
E value	1.0e-12
Match length	49
% identity	88
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC4 (GTP BINDING PROTEIN ROP2) >gi_1304417 (U45236) Description: rac-like protein;

GTP binding protein; Method: conceptual translation supplied by author. [Arabidopsis thaliana] >gi_1777764 (U49972) GTP binding protein Rop2At [Arabidopsis thaliana]

Seq. No.	151408
Seq. ID	LIB3175-058-P1-K1-D2
Method	BLASTN
NCBI GI	g4589412
BLAST score	111
E value	1.0e-55
Match length	250
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	151409
Seq. ID	LIB3175-058-P1-K1-D3
Method	BLASTX
NCBI GI	g4589398
BLAST score	431
E value	1.0e-42
Match length	104
% identity	74
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	151410
Seq. ID	LIB3175-058-P1-K1-D4
Method	BLASTN
NCBI GI	g4589969
BLAST score	307
E value	1.0e-172
Match length	368
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	151411
Seq. ID	LIB3175-058-P1-K1-D5
Method	BLASTX
NCBI GI	g4758520
BLAST score	191
E value	1.0e-14
Match length	104
% identity	3
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	151412
Seq. ID	LIB3175-058-P1-K1-D6
Method	BLASTX
NCBI GI	g2459445
BLAST score	299
E value	4.0e-27
Match length	94
% identity	30
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	151413
Seq. ID	LIB3175-058-P1-K1-D7
Method	BLASTX
NCBI GI	g4220480
BLAST score	299
E value	4.0e-27
Match length	136
% identity	49
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	151414
Seq. ID	LIB3175-058-P1-K1-D8
Method	BLASTX
NCBI GI	g1769905
BLAST score	477
E value	6.0e-48
Match length	136
% identity	68
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	151415
Seq. ID	LIB3175-058-P1-K1-E1
Method	BLASTX
NCBI GI	g1935914
BLAST score	182
E value	2.0e-13
Match length	69
% identity	49
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	151416
Seq. ID	LIB3175-058-P1-K1-E10
Method	BLASTX
NCBI GI	g2961384
BLAST score	623
E value	4.0e-65
Match length	127
% identity	96
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	151417
Seq. ID	LIB3175-058-P1-K1-E11
Method	BLASTX
NCBI GI	g2435519
BLAST score	615
E value	3.0e-64
Match length	143
% identity	83
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	151418
Seq. ID	LIB3175-058-P1-K1-E12

Method	BLASTX
NCBI GI	g1170089
BLAST score	425
E value	4.0e-42
Match length	87
% identity	97
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	151419
Seq. ID	LIB3175-058-P1-K1-E2
Method	BLASTN
NCBI GI	g2760165
BLAST score	280
E value	1.0e-156
Match length	316
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	151420
Seq. ID	LIB3175-058-P1-K1-E4
Method	BLASTX
NCBI GI	g3372233
BLAST score	494
E value	5.0e-50
Match length	97
% identity	100
NCBI Description	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]

Seq. No.	151421
Seq. ID	LIB3175-058-P1-K1-E6
Method	BLASTX
NCBI GI	g3925277
BLAST score	217
E value	1.0e-17
Match length	111
% identity	47
NCBI Description	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	151422
Seq. ID	LIB3175-058-P1-K1-E7
Method	BLASTX
NCBI GI	g3925277
BLAST score	202
E value	9.0e-16
Match length	130
% identity	38
NCBI Description	(AL032643) similar to Uncharacterized protein family

UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	151423
Seq. ID	LIB3175-058-P1-K1-E8
Method	BLASTX
NCBI GI	g1669389
BLAST score	740
E value	9.0e-79
Match length	150
% identity	94
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	151424
Seq. ID	LIB3175-058-P1-K1-E9
Method	BLASTX
NCBI GI	g1352463
BLAST score	566
E value	2.0e-58
Match length	114
% identity	96
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	151425
Seq. ID	LIB3175-058-P1-K1-F1
Method	BLASTX
NCBI GI	g1353352
BLAST score	447
E value	2.0e-44
Match length	154
% identity	60
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	151426
Seq. ID	LIB3175-058-P1-K1-F10
Method	BLASTX
NCBI GI	g1172977
BLAST score	44
E value	3.0e-57
Match length	135
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	151427
Seq. ID	LIB3175-058-P1-K1-F11
Method	BLASTX
NCBI GI	g2244949
BLAST score	576
E value	1.0e-59
Match length	122
% identity	98
NCBI Description	(Z97339) similarity to ORF - Lilium longiflorum

[Arabidopsis thaliana]

Seq. No.	151428
Seq. ID	LIB3175-058-P1-K1-F12
Method	BLASTX
NCBI GI	g1076678
BLAST score	299
E value	1.0e-27
Match length	61
% identity	98
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	151429
Seq. ID	LIB3175-058-P1-K1-F2
Method	BLASTN
NCBI GI	g3600029
BLAST score	175
E value	7.0e-94
Match length	243
% identity	93
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	151430
Seq. ID	LIB3175-058-P1-K1-F3
Method	BLASTX
NCBI GI	g4567282
BLAST score	296
E value	1.0e-26
Match length	59
% identity	98
NCBI Description	(AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	151431
Seq. ID	LIB3175-058-P1-K1-F4
Method	BLASTX
NCBI GI	g2501102
BLAST score	554
E value	5.0e-57
Match length	113
% identity	100
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf__2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	151432
Seq. ID	LIB3175-058-P1-K1-F7
Method	BLASTX
NCBI GI	g119143
BLAST score	65
E value	1.0e-52
Match length	108
% identity	90
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1

alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	151433
Seq. ID	LIB3175-058-P1-K1-F8
Method	BLASTX
NCBI GI	g282865
BLAST score	606
E value	4.0e-63
Match length	128
% identity	88
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	151434
Seq. ID	LIB3175-058-P1-K1-F9
Method	BLASTX
NCBI GI	g3024434
BLAST score	367
E value	3.0e-35
Match length	96
% identity	80
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	151435
Seq. ID	LIB3175-058-P1-K1-G10
Method	BLASTN
NCBI GI	g4455262
BLAST score	276
E value	1.0e-154
Match length	339
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	151436
Seq. ID	LIB3175-058-P1-K1-G11
Method	BLASTN
NCBI GI	g4056476
BLAST score	241
E value	1.0e-133
Match length	345
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151437
Seq. ID	LIB3175-058-P1-K1-G12
Method	BLASTX
NCBI GI	g1346485
BLAST score	260
E value	8.0e-23
Match length	62
% identity	77
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_20469_emb_CAA39690_ (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa]

Seq. No.	151438
Seq. ID	LIB3175-058-P1-K1-G2
Method	BLASTX
NCBI GI	g1531762
BLAST score	165
E value	2.0e-11
Match length	35
% identity	89
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	151439
Seq. ID	LIB3175-058-P1-K1-G4
Method	BLASTX
NCBI GI	g2911039
BLAST score	499
E value	1.0e-50
Match length	127
% identity	76
NCBI Description	(AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	151440
Seq. ID	LIB3175-058-P1-K1-G5
Method	BLASTX
NCBI GI	g1002803
BLAST score	756
E value	1.0e-80
Match length	144
% identity	100
NCBI Description	(U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	151441
Seq. ID	LIB3175-058-P1-K1-G6
Method	BLASTX
NCBI GI	g543841
BLAST score	613
E value	6.0e-64
Match length	119
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis

thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	151442
Seq. ID	LIB3175-058-P1-K1-G9
Method	BLASTN
NCBI GI	g3927822
BLAST score	368
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151443
Seq. ID	LIB3175-058-P1-K1-H10
Method	BLASTX
NCBI GI	g132074
BLAST score	788
E value	2.0e-84
Match length	149
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	151444
Seq. ID	LIB3175-058-P1-K1-H11
Method	BLASTN
NCBI GI	g2459406
BLAST score	41
E value	6.0e-14
Match length	207
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151445
Seq. ID	LIB3175-058-P1-K1-H2
Method	BLASTX
NCBI GI	g4583542
BLAST score	413
E value	1.0e-40
Match length	114
% identity	80
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	151446
Seq. ID	LIB3175-058-P1-K1-H3
Method	BLASTX
NCBI GI	g2499327
BLAST score	387
E value	2.0e-37
Match length	126
% identity	63

NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]
Seq. No.	151447
Seq. ID	LIB3175-058-P1-K1-H5
Method	BLASTN
NCBI GI	g2618603
BLAST score	119
E value	3.0e-60
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
Seq. No.	151448
Seq. ID	LIB3175-058-P1-K1-H6
Method	BLASTN
NCBI GI	g4581161
BLAST score	393
E value	0.0e+00
Match length	435
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence
Seq. No.	151449
Seq. ID	LIB3175-058-P1-K1-H7
Method	BLASTX
NCBI GI	g2811226
BLAST score	47
E value	2.0e-56
Match length	120
% identity	52
NCBI Description	(AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
Seq. No.	151450
Seq. ID	LIB3175-058-P1-K1-H8
Method	BLASTN
NCBI GI	g2244829
BLAST score	40
E value	2.0e-13
Match length	68
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	151451
Seq. ID	LIB3175-059-P1-K1-A1
Method	BLASTX
NCBI GI	g1706551
BLAST score	184
E value	8.0e-14
Match length	106

% identity	40
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	151452
Seq. ID	LIB3175-059-P1-K1-A10
Method	BLASTN
NCBI GI	g4558586
BLAST score	314
E value	1.0e-176
Match length	404
% identity	72
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	151453
Seq. ID	LIB3175-059-P1-K1-A11
Method	BLASTX
NCBI GI	g2529229
BLAST score	141
E value	2.0e-33
Match length	100
% identity	80
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	151454
Seq. ID	LIB3175-059-P1-K1-A12
Method	BLASTX
NCBI GI	g1742953
BLAST score	341
E value	3.0e-36
Match length	90
% identity	82
NCBI Description	(Z71445) CLC-a chloride channel protein [Arabidopsis thaliana]

Seq. No.	151455
Seq. ID	LIB3175-059-P1-K1-A4
Method	BLASTX
NCBI GI	g1508783
BLAST score	152
E value	6.0e-33
Match length	100
% identity	83
NCBI Description	(Z54351) SecY [Spinacia oleracea]

Seq. No.	151456
Seq. ID	LIB3175-059-P1-K1-A5
Method	BLASTN
NCBI GI	g3873174
BLAST score	368
E value	0.0e+00
Match length	384
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23,

complete sequence [Arabidopsis thaliana]

Seq. No.	151457
Seq. ID	LIB3175-059-P1-K1-A6
Method	BLASTN
NCBI GI	g2618602
BLAST score	199
E value	1.0e-108
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	151458
Seq. ID	LIB3175-059-P1-K1-A7
Method	BLASTX
NCBI GI	g3885329
BLAST score	611
E value	8.0e-64
Match length	118
% identity	99
NCBI Description	(AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No.	151459
Seq. ID	LIB3175-059-P1-K1-A8
Method	BLASTX
NCBI GI	g2829899
BLAST score	315
E value	4.0e-29
Match length	94
% identity	62
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	151460
Seq. ID	LIB3175-059-P1-K1-A9
Method	BLASTN
NCBI GI	g4589415
BLAST score	169
E value	3.0e-90
Match length	307
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	151461
Seq. ID	LIB3175-059-P1-K1-B1
Method	BLASTX
NCBI GI	g1702986
BLAST score	431
E value	1.0e-42
Match length	87
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	151462
Seq. ID	LIB3175-059-P1-K1-B10
Method	BLASTN
NCBI GI	g3869072
BLAST score	160
E value	1.0e-84
Match length	429
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	151463
Seq. ID	LIB3175-059-P1-K1-B12
Method	BLASTX
NCBI GI	g1169598
BLAST score	175
E value	3.0e-29
Match length	88
% identity	84
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	151464
Seq. ID	LIB3175-059-P1-K1-B2
Method	BLASTN
NCBI GI	g510490
BLAST score	46
E value	7.0e-17
Match length	98
% identity	87
NCBI Description	A.thaliana Apx1b gene

Seq. No.	151465
Seq. ID	LIB3175-059-P1-K1-B3
Method	BLASTX
NCBI GI	g1498053
BLAST score	91
E value	5.0e-52
Match length	114
% identity	81
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	151466
Seq. ID	LIB3175-059-P1-K1-B5
Method	BLASTN
NCBI GI	g4467094
BLAST score	243
E value	1.0e-134
Match length	303
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	151467
Seq. ID	LIB3175-059-P1-K1-B7

Method	BLASTX
NCBI GI	g1769905
BLAST score	596
E value	5.0e-62
Match length	122
% identity	93
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	151468
Seq. ID	LIB3175-059-P1-K1-B8
Method	BLASTX
NCBI GI	g1864017
BLAST score	516
E value	1.0e-52
Match length	103
% identity	96
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	151469
Seq. ID	LIB3175-059-P1-K1-B9
Method	BLASTX
NCBI GI	g2262162
BLAST score	259
E value	2.0e-26
Match length	124
% identity	52
NCBI Description	(AC002329) hypothetical protein similar to A. thaliana protein F19K23.19 [Arabidopsis thaliana]

Seq. No.	151470
Seq. ID	LIB3175-059-P1-K1-C1
Method	BLASTX
NCBI GI	g1351014
BLAST score	567
E value	1.0e-58
Match length	118
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	151471
Seq. ID	LIB3175-059-P1-K1-C10
Method	BLASTX
NCBI GI	g4586255
BLAST score	246
E value	6.0e-21
Match length	46
% identity	100
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	151472
Seq. ID	LIB3175-059-P1-K1-C2
Method	BLASTX
NCBI GI	g1762584
BLAST score	555
E value	3.0e-57

Match length	112
% identity	96
NCBI Description	(U63373) polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]

Seq. No.	151473
Seq. ID	LIB3175-059-P1-K1-C3
Method	BLASTN
NCBI GI	g2584827
BLAST score	165
E value	9.0e-88
Match length	308
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151474
Seq. ID	LIB3175-059-P1-K1-C4
Method	BLASTX
NCBI GI	g2149380
BLAST score	461
E value	3.0e-46
Match length	92
% identity	100
NCBI Description	(U85036) syntaxin homolog [Arabidopsis thaliana]

Seq. No.	151475
Seq. ID	LIB3175-059-P1-K1-C5
Method	BLASTX
NCBI GI	g3892712
BLAST score	430
E value	4.0e-50
Match length	115
% identity	90
NCBI Description	(AL033545) adenine phosphoribosyltransferase (EC 2.4.2.7)-like protein [Arabidopsis thaliana]

Seq. No.	151476
Seq. ID	LIB3175-059-P1-K1-C6
Method	BLASTX
NCBI GI	g114085
BLAST score	503
E value	7.0e-60
Match length	128
% identity	95
NCBI Description	RAS-RELATED PROTEIN ARA-1 >gi_81597_pir__JS0163 Ara protein - Arabidopsis thaliana >gi_538283 (M25471) ras-related protein [Arabidopsis thaliana]

Seq. No.	151477
Seq. ID	LIB3175-059-P1-K1-C7
Method	BLASTX
NCBI GI	g2244750
BLAST score	624
E value	2.0e-65
Match length	121
% identity	98

NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	151478
Seq. ID	LIB3175-059-P1-K1-C8
Method	BLASTX
NCBI GI	g2244977
BLAST score	554
E value	7.0e-57
Match length	129
% identity	89
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	151479
Seq. ID	LIB3175-059-P1-K1-D1
Method	BLASTN
NCBI GI	g2342717
BLAST score	120
E value	8.0e-61
Match length	420
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151480
Seq. ID	LIB3175-059-P1-K1-D12
Method	BLASTX
NCBI GI	g2117612
BLAST score	543
E value	1.0e-55
Match length	136
% identity	70
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	151481
Seq. ID	LIB3175-059-P1-K1-D2
Method	BLASTX
NCBI GI	g4510345
BLAST score	218
E value	1.0e-17
Match length	75
% identity	72
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	151482
Seq. ID	LIB3175-059-P1-K1-D3
Method	BLASTX
NCBI GI	g16374
BLAST score	288
E value	9.0e-26
Match length	84
% identity	71
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	151483

09504600.1600

Seq. ID	LIB3175-059-P1-K1-D4
Method	BLASTN
NCBI GI	g2252848
BLAST score	239
E value	1.0e-132
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	151484
Seq. ID	LIB3175-059-P1-K1-D5
Method	BLASTN
NCBI GI	g3702724
BLAST score	210
E value	1.0e-114
Match length	391
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	151485
Seq. ID	LIB3175-059-P1-K1-D6
Method	BLASTX
NCBI GI	g2462741
BLAST score	562
E value	6.0e-58
Match length	117
% identity	96
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	151486
Seq. ID	LIB3175-059-P1-K1-D9
Method	BLASTX
NCBI GI	g1490606
BLAST score	272
E value	2.0e-30
Match length	69
% identity	100
NCBI Description	(U63734) s-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferase [Arabidopsis thaliana]

Seq. No.	151487
Seq. ID	LIB3175-059-P1-K1-E1
Method	BLASTN
NCBI GI	g4263694
BLAST score	136
E value	1.0e-70
Match length	156
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151488
Seq. ID	LIB3175-059-P1-K1-E10
Method	BLASTX
NCBI GI	g4490302

BLAST score	520
E value	5.0e-53
Match length	140
% identity	75
NCBI Description	(AL035678) Tic22-like protein [Arabidopsis thaliana]

Seq. No.	151489
Seq. ID	LIB3175-059-P1-K1-E11
Method	BLASTX
NCBI GI	g4220445
BLAST score	115
E value	2.0e-05
Match length	121
% identity	4
NCBI Description	(AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673. [Arabidopsis thaliana]

Seq. No.	151490
Seq. ID	LIB3175-059-P1-K1-E12
Method	BLASTX
NCBI GI	g4185505
BLAST score	465
E value	1.0e-46
Match length	112
% identity	79
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	151491
Seq. ID	LIB3175-059-P1-K1-E2
Method	BLASTN
NCBI GI	g1732569
BLAST score	50
E value	2.0e-19
Match length	135
% identity	93
NCBI Description	Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA, complete cds

Seq. No.	151492
Seq. ID	LIB3175-059-P1-K1-E3
Method	BLASTX
NCBI GI	g3286693
BLAST score	420
E value	2.0e-41
Match length	116
% identity	74
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	151493
Seq. ID	LIB3175-059-P1-K1-E4
Method	BLASTX
NCBI GI	g3164222
BLAST score	228
E value	9.0e-19

Match length	74
% identity	54
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205_gb_AAD11593.1_AAD11593 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	151494
Seq. ID	LIB3175-059-P1-K1-E6
Method	BLASTX
NCBI GI	g2262115
BLAST score	125
E value	9.0e-71
Match length	145
% identity	91
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	151495
Seq. ID	LIB3175-059-P1-K1-E7
Method	BLASTX
NCBI GI	g115385
BLAST score	619
E value	5.0e-68
Match length	135
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151496
Seq. ID	LIB3175-059-P1-K1-E8
Method	BLASTX
NCBI GI	g4185505
BLAST score	459
E value	7.0e-46
Match length	112
% identity	79
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	151497
Seq. ID	LIB3175-059-P1-K1-E9
Method	BLASTX
NCBI GI	g3123188
BLAST score	580
E value	5.0e-67
Match length	139
% identity	96
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	151498
Seq. ID	LIB3175-059-P1-K1-F1
Method	BLASTN
NCBI GI	g4263694
BLAST score	128
E value	1.0e-65

Match length	231
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151499
Seq. ID	LIB3175-059-P1-K1-F10
Method	BLASTN
NCBI GI	g3702315
BLAST score	143
E value	2.0e-74
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151500
Seq. ID	LIB3175-059-P1-K1-F11
Method	BLASTX
NCBI GI	g4490719
BLAST score	229
E value	7.0e-19
Match length	83
% identity	54
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	151501
Seq. ID	LIB3175-059-P1-K1-F12
Method	BLASTX
NCBI GI	g3335333
BLAST score	463
E value	2.0e-53
Match length	139
% identity	82
NCBI Description	(AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this gene. [Arabidopsis thaliana]

Seq. No.	151502
Seq. ID	LIB3175-059-P1-K1-F2
Method	BLASTN
NCBI GI	g4263694
BLAST score	116
E value	8.0e-59
Match length	156
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151503
Seq. ID	LIB3175-059-P1-K1-F3
Method	BLASTN
NCBI GI	g4584841
BLAST score	87
E value	3.0e-41
Match length	273

% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	151504
Seq. ID	LIB3175-059-P1-K1-F4
Method	BLASTN
NCBI GI	g4678705
BLAST score	414
E value	0.0e+00
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	151505
Seq. ID	LIB3175-059-P1-K1-F5
Method	BLASTN
NCBI GI	g2398520
BLAST score	337
E value	0.0e+00
Match length	404
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for Hap2a transcription factor

Seq. No.	151506
Seq. ID	LIB3175-059-P1-K1-F6
Method	BLASTX
NCBI GI	g1408471
BLAST score	384
E value	1.0e-44
Match length	110
% identity	87
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	151507
Seq. ID	LIB3175-059-P1-K1-F7
Method	BLASTX
NCBI GI	g4337025
BLAST score	506
E value	2.0e-51
Match length	101
% identity	99
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	151508
Seq. ID	LIB3175-059-P1-K1-F8
Method	BLASTX
NCBI GI	g4218121
BLAST score	356
E value	2.0e-34
Match length	111
% identity	70
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	151509
Seq. ID	LIB3175-059-P1-K1-F9
Method	BLASTX
NCBI GI	g99737
BLAST score	339
E value	2.0e-62
Match length	130
% identity	95
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	151510
Seq. ID	LIB3175-059-P1-K1-G11
Method	BLASTX
NCBI GI	g3158370
BLAST score	378
E value	1.0e-36
Match length	83
% identity	88
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	151511
Seq. ID	LIB3175-059-P1-K1-G12
Method	BLASTX
NCBI GI	g4006890
BLAST score	296
E value	1.0e-26
Match length	66
% identity	91
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	151512
Seq. ID	LIB3175-059-P1-K1-G2
Method	BLASTX
NCBI GI	g2129727
BLAST score	188
E value	3.0e-26
Match length	83
% identity	82
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	151513
Seq. ID	LIB3175-059-P1-K1-G3
Method	BLASTN
NCBI GI	g4691223
BLAST score	258
E value	1.0e-143
Match length	348
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	151514
Seq. ID	LIB3175-059-P1-K1-G4

Method	BLASTN
NCBI GI	g3046854
BLAST score	178
E value	2.0e-95
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	151515
Seq. ID	LIB3175-059-P1-K1-G5
Method	BLASTX
NCBI GI	g2245107
BLAST score	198
E value	3.0e-15
Match length	118
% identity	30
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	151516
Seq. ID	LIB3175-059-P1-K1-G6
Method	BLASTN
NCBI GI	g3859658
BLAST score	384
E value	0.0e+00
Match length	447
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	151517
Seq. ID	LIB3175-059-P1-K1-G7
Method	BLASTX
NCBI GI	g1771162
BLAST score	257
E value	3.0e-22
Match length	105
% identity	49
NCBI Description	(X98930) SBT2 [Lycopersicon esculentum] >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	151518
Seq. ID	LIB3175-059-P1-K1-G8
Method	BLASTX
NCBI GI	g2288887
BLAST score	342
E value	2.0e-32
Match length	70
% identity	94
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	151519

Seq. ID	LIB3175-059-P1-K1-H10
Method	BLASTN
NCBI GI	g4490717
BLAST score	48
E value	5.0e-18
Match length	196
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	151520
Seq. ID	LIB3175-059-P1-K1-H11
Method	BLASTX
NCBI GI	g2245378
BLAST score	458
E value	1.0e-51
Match length	105
% identity	99
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	151521
Seq. ID	LIB3175-059-P1-K1-H12
Method	BLASTX
NCBI GI	g2462754
BLAST score	194
E value	7.0e-15
Match length	54
% identity	69
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	151522
Seq. ID	LIB3175-059-P1-K1-H4
Method	BLASTX
NCBI GI	g112681
BLAST score	548
E value	2.0e-56
Match length	124
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	151523
Seq. ID	LIB3175-059-P1-K1-H5
Method	BLASTX
NCBI GI	g4218963
BLAST score	653
E value	2.0e-73
Match length	147
% identity	96
NCBI Description	(AF093672) xyloglucan endotransglycosylase [Arabidopsis thaliana] >gi_4539300_emb_CAB39603.1_ (AL049480) putative xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis thaliana]

Seq. No.	151524
Seq. ID	LIB3175-059-P1-K1-H6
Method	BLASTX
NCBI GI	g4581146
BLAST score	162
E value	6.0e-21
Match length	65
% identity	86
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	151525
Seq. ID	LIB3175-059-P1-K1-H8
Method	BLASTX
NCBI GI	g4512685
BLAST score	255
E value	6.0e-23
Match length	77
% identity	73
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151526
Seq. ID	LIB3175-059-P1-K1-H9
Method	BLASTX
NCBI GI	g322571
BLAST score	282
E value	4.0e-25
Match length	77
% identity	74
NCBI Description	proteinase inhibitor II - Arabidopsis thaliana >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II [Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	151527
Seq. ID	LIB3175-060-P1-K1-A11
Method	BLASTX
NCBI GI	g231683
BLAST score	526
E value	1.0e-53
Match length	115
% identity	87
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	151528
Seq. ID	LIB3175-060-P1-K1-A12
Method	BLASTX
NCBI GI	g320558
BLAST score	279
E value	9.0e-25
Match length	139
% identity	45

NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	151529
Seq. ID	LIB3175-060-P1-K1-A4
Method	BLASTX
NCBI GI	g3096910
BLAST score	778
E value	3.0e-83
Match length	149
% identity	99
NCBI Description	(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]

Seq. No.	151530
Seq. ID	LIB3175-060-P1-K1-A5
Method	BLASTX
NCBI GI	g4646198
BLAST score	769
E value	3.0e-82
Match length	147
% identity	99
NCBI Description	(AC007230) T23K8.6 [Arabidopsis thaliana]

Seq. No.	151531
Seq. ID	LIB3175-060-P1-K1-A7
Method	BLASTN
NCBI GI	g3449334
BLAST score	33
E value	3.0e-09
Match length	69
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	151532
Seq. ID	LIB3175-060-P1-K1-B11
Method	BLASTX
NCBI GI	g3075394
BLAST score	717
E value	4.0e-76
Match length	146
% identity	96
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	151533
Seq. ID	LIB3175-060-P1-K1-B12
Method	BLASTN
NCBI GI	g2618602
BLAST score	152
E value	6.0e-80
Match length	393
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	151534
Seq. ID	LIB3175-060-P1-K1-B2
Method	BLASTX
NCBI GI	g2723477
BLAST score	217
E value	2.0e-17
Match length	50
% identity	92
NCBI Description	(D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	151535
Seq. ID	LIB3175-060-P1-K1-B3
Method	BLASTX
NCBI GI	g4490323
BLAST score	767
E value	5.0e-82
Match length	147
% identity	98
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	151536
Seq. ID	LIB3175-060-P1-K1-B6
Method	BLASTX
NCBI GI	g2462834
BLAST score	253
E value	1.0e-21
Match length	124
% identity	42
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151537
Seq. ID	LIB3175-060-P1-K1-B7
Method	BLASTX
NCBI GI	g2944446
BLAST score	413
E value	2.0e-40
Match length	141
% identity	55
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No.	151538
Seq. ID	LIB3175-060-P1-K1-B8
Method	BLASTX
NCBI GI	g115783
BLAST score	701
E value	3.0e-74
Match length	140
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	151539
Seq. ID	LIB3175-060-P1-K1-C12

Method	BLASTX
NCBI GI	g2827711
BLAST score	754
E value	2.0e-80
Match length	144
% identity	99
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	151540
Seq. ID	LIB3175-060-P1-K1-C2
Method	BLASTX
NCBI GI	g2924521
BLAST score	62
E value	4.0e-36
Match length	132
% identity	75
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	151541
Seq. ID	LIB3175-060-P1-K1-C3
Method	BLASTN
NCBI GI	g4159707
BLAST score	416
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	151542
Seq. ID	LIB3175-060-P1-K1-C4
Method	BLASTX
NCBI GI	g3386612
BLAST score	237
E value	6.0e-20
Match length	106
% identity	46
NCBI Description	(AC004665) DNA-binding protein, dbp [Arabidopsis thaliana]

Seq. No.	151543
Seq. ID	LIB3175-060-P1-K1-C5
Method	BLASTX
NCBI GI	g4056489
BLAST score	171
E value	4.0e-12
Match length	149
% identity	36
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	151544
Seq. ID	LIB3175-060-P1-K1-C6
Method	BLASTX
NCBI GI	g2791606
BLAST score	236
E value	7.0e-20
Match length	70

% identity	56
NCBI Description	(AL021287) gatB [Mycobacterium tuberculosis]

Seq. No.	151545
Seq. ID	LIB3175-060-P1-K1-D10
Method	BLASTX
NCBI GI	g114654
BLAST score	202
E value	6.0e-16
Match length	80
% identity	60
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - common tobacco chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A ATPase III,H translocating [Nicotiana sp.] >gi_225272_prf__1211235G ATPase III [Nicotiana tabacum]

Seq. No.	151546
Seq. ID	LIB3175-060-P1-K1-D2
Method	BLASTX
NCBI GI	g4097557
BLAST score	627
E value	1.0e-65
Match length	123
% identity	98
NCBI Description	(U64911) ATFP8 [Arabidopsis thaliana]

Seq. No.	151547
Seq. ID	LIB3175-060-P1-K1-D4
Method	BLASTX
NCBI GI	g4204265
BLAST score	369
E value	2.0e-35
Match length	97
% identity	70
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	151548
Seq. ID	LIB3175-060-P1-K1-E10
Method	BLASTX
NCBI GI	g70644
BLAST score	545
E value	6.0e-56
Match length	128
% identity	17
NCBI Description	ubiquitin precursor - common sunflower (fragment)

Seq. No.	151549
Seq. ID	LIB3175-060-P1-K1-E2
Method	BLASTX
NCBI GI	g3915847
BLAST score	263
E value	6.0e-23
Match length	63

% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.	151550
Seq. ID	LIB3175-060-P1-K1-E3
Method	BLASTX
NCBI GI	g1706376
BLAST score	280
E value	7.0e-25
Match length	121
% identity	43
NCBI Description	DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_505560_emb_CAA56160_ (X79723) dfrA [Petunia x hybrida]
Seq. No.	151551
Seq. ID	LIB3175-060-P1-K1-E7
Method	BLASTX
NCBI GI	g4741962
BLAST score	499
E value	1.0e-50
Match length	138
% identity	57
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.	151552
Seq. ID	LIB3175-060-P1-K1-F10
Method	BLASTN
NCBI GI	g2760166
BLAST score	313
E value	1.0e-176
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]
Seq. No.	151553
Seq. ID	LIB3175-060-P1-K1-F2
Method	BLASTX
NCBI GI	g112739
BLAST score	207
E value	2.0e-16
Match length	130
% identity	42
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]
Seq. No.	151554
Seq. ID	LIB3175-060-P1-K1-F3
Method	BLASTN
NCBI GI	g3135250

BLAST score	384
E value	0.0e+00
Match length	451
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151555
Seq. ID	LIB3175-060-P1-K1-F4
Method	BLASTX
NCBI GI	g4454012
BLAST score	561
E value	8.0e-58
Match length	149
% identity	72
NCBI Description	(AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No.	151556
Seq. ID	LIB3175-060-P1-K1-F6
Method	BLASTX
NCBI GI	g2832605
BLAST score	604
E value	7.0e-63
Match length	142
% identity	90
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	151557
Seq. ID	LIB3175-060-P1-K1-F9
Method	BLASTX
NCBI GI	g4455365
BLAST score	382
E value	6.0e-37
Match length	78
% identity	87
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	151558
Seq. ID	LIB3175-060-P1-K1-G11
Method	BLASTX
NCBI GI	g1145697
BLAST score	541
E value	1.0e-55
Match length	115
% identity	49
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	151559
Seq. ID	LIB3175-060-P1-K1-G12
Method	BLASTX
NCBI GI	g3805765
BLAST score	567
E value	1.0e-58
Match length	129
% identity	85

NCBI Description	(AC005693) putative protein kinase [Arabidopsis thaliana]
Seq. No.	151560
Seq. ID	LIB3175-060-P1-K1-G2
Method	BLASTX
NCBI GI	g4753655
BLAST score	407
E value	9.0e-40
Match length	115
% identity	65
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]
Seq. No.	151561
Seq. ID	LIB3175-060-P1-K1-H11
Method	BLASTX
NCBI GI	g4704766
BLAST score	501
E value	9.0e-51
Match length	130
% identity	43
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]
Seq. No.	151562
Seq. ID	LIB3175-060-P1-K1-H2
Method	BLASTX
NCBI GI	g3786021
BLAST score	200
E value	2.0e-15
Match length	68
% identity	59
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.	151563
Seq. ID	LIB3175-060-P1-K1-H3
Method	BLASTX
NCBI GI	g4544399
BLAST score	318
E value	2.0e-29
Match length	123
% identity	46
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	151564
Seq. ID	LIB3175-060-P1-K1-H4
Method	BLASTN
NCBI GI	g3522932
BLAST score	391
E value	0.0e+00
Match length	411
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	151565

Seq. ID	LIB3175-060-P1-K1-H9
Method	BLASTN
NCBI GI	g2342673
BLAST score	34
E value	1.0e-09
Match length	129
% identity	70
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	151566
Seq. ID	LIB3175-061-P1-K1-A11
Method	BLASTX
NCBI GI	g1864017
BLAST score	542
E value	1.0e-55
Match length	106
% identity	97
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]

Seq. No.	151567
Seq. ID	LIB3175-061-P1-K1-A12
Method	BLASTN
NCBI GI	g710625
BLAST score	362
E value	0.0e+00
Match length	366
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	151568
Seq. ID	LIB3175-061-P1-K1-A2
Method	BLASTX
NCBI GI	g2244879
BLAST score	186
E value	3.0e-14
Match length	54
% identity	70
NCBI Description	(Z97338) Nucleotide sequence of a cDNA clone encoding a beta-amylase from Arabidopsis thaliana

Seq. No.	151569
Seq. ID	LIB3175-061-P1-K1-A4
Method	BLASTX
NCBI GI	g4583656
BLAST score	207
E value	2.0e-16
Match length	104
% identity	43
NCBI Description	(AJ010592) ubiquitin-conjugating enzyme [Guillardia theta]

Seq. No.	151570
Seq. ID	LIB3175-061-P1-K1-A6
Method	BLASTN
NCBI GI	g4539378
BLAST score	125
E value	5.0e-64

Match length	202
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	151571
Seq. ID	LIB3175-061-P1-K1-A7
Method	BLASTX
NCBI GI	g2130521
BLAST score	302
E value	7.0e-28
Match length	67
% identity	85
NCBI Description	(U31565) reversibly glycosylatable polypeptide [Pisum sativum]

Seq. No.	151572
Seq. ID	LIB3175-061-P1-K1-A8
Method	BLASTN
NCBI GI	g4757409
BLAST score	230
E value	1.0e-126
Match length	314
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	151573
Seq. ID	LIB3175-061-P1-K1-A9
Method	BLASTN
NCBI GI	g4757409
BLAST score	143
E value	9.0e-75
Match length	265
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	151574
Seq. ID	LIB3175-061-P1-K1-B10
Method	BLASTX
NCBI GI	g3924615
BLAST score	164
E value	3.0e-11
Match length	140
% identity	29
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151575
Seq. ID	LIB3175-061-P1-K1-B11
Method	BLASTX
NCBI GI	g3758833
BLAST score	253
E value	1.0e-23
Match length	104
% identity	58
NCBI Description	(Y18225) MtN6 [Medicago truncatula]

09604076 - 020799

Seq. No.	151576
Seq. ID	LIB3175-061-P1-K1-B12
Method	BLASTN
NCBI GI	g2262135
BLAST score	60
E value	4.0e-25
Match length	280
% identity	88
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	151577
Seq. ID	LIB3175-061-P1-K1-B2
Method	BLASTX
NCBI GI	g4633656
BLAST score	250
E value	2.0e-21
Match length	117
% identity	46
NCBI Description	(AF123263) phenylalanyl tRNA synthetase beta subunit [Mus musculus]

Seq. No.	151578
Seq. ID	LIB3175-061-P1-K1-B3
Method	BLASTX
NCBI GI	g1172872
BLAST score	270
E value	9.0e-24
Match length	88
% identity	66
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	151579
Seq. ID	LIB3175-061-P1-K1-B4
Method	BLASTX
NCBI GI	g2281635
BLAST score	336
E value	2.0e-31
Match length	135
% identity	62
NCBI Description	(AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]

Seq. No.	151580
Seq. ID	LIB3175-061-P1-K1-B5
Method	BLASTN
NCBI GI	g3650026
BLAST score	151
E value	1.0e-79
Match length	219
% identity	92

NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151581
Seq. ID	LIB3175-061-P1-K1-B6
Method	BLASTX
NCBI GI	g3212851
BLAST score	380
E value	1.0e-36
Match length	78
% identity	97
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	151582
Seq. ID	LIB3175-061-P1-K1-B7
Method	BLASTN
NCBI GI	g4646229
BLAST score	293
E value	1.0e-164
Match length	312
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F27A10 genomic sequence, complete sequence

Seq. No.	151583
Seq. ID	LIB3175-061-P1-K1-B8
Method	BLASTX
NCBI GI	g4510430
BLAST score	307
E value	2.0e-28
Match length	62
% identity	94
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	151584
Seq. ID	LIB3175-061-P1-K1-B9
Method	BLASTX
NCBI GI	g543841
BLAST score	575
E value	2.0e-59
Match length	117
% identity	95
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	151585
Seq. ID	LIB3175-061-P1-K1-C1
Method	BLASTX
NCBI GI	g119143
BLAST score	408
E value	4.0e-40
Match length	80

% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]
Seq. No.	151586
Seq. ID	LIB3175-061-P1-K1-C3
Method	BLASTX
NCBI GI	g2623306
BLAST score	424
E value	7.0e-42
Match length	80
% identity	100
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana]
Seq. No.	151587
Seq. ID	LIB3175-061-P1-K1-C6
Method	BLASTN
NCBI GI	g2338711
BLAST score	42
E value	2.0e-14
Match length	224
% identity	88
NCBI Description	Arabidopsis thaliana metallothionein-like protein (MT3) gene, complete cds
Seq. No.	151588
Seq. ID	LIB3175-061-P1-K1-C7
Method	BLASTN
NCBI GI	g3805839
BLAST score	184
E value	5.0e-99
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)
Seq. No.	151589
Seq. ID	LIB3175-061-P1-K1-D1
Method	BLASTN
NCBI GI	g3746914
BLAST score	46
E value	3.0e-17
Match length	58
% identity	95
NCBI Description	Arabidopsis thaliana E2 ubiquitin-conjugating-like enzyme (Ahus5) gene, complete cds
Seq. No.	151590
Seq. ID	LIB3175-061-P1-K1-D10

Method	BLASTX
NCBI GI	g3834309
BLAST score	185
E value	8.0e-14
Match length	129
% identity	42
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	151591
Seq. ID	LIB3175-061-P1-K1-D12
Method	BLASTN
NCBI GI	g3212846
BLAST score	218
E value	1.0e-119
Match length	464
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151592
Seq. ID	LIB3175-061-P1-K1-D2
Method	BLASTX
NCBI GI	g1199804
BLAST score	141
E value	3.0e-09
Match length	42
% identity	71
NCBI Description	(X95639) transmembrane channel protein [Brassica oleracea]

Seq. No.	151593
Seq. ID	LIB3175-061-P1-K1-D3
Method	BLASTN
NCBI GI	g3702724
BLAST score	197
E value	1.0e-107
Match length	260
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	151594
Seq. ID	LIB3175-061-P1-K1-D5
Method	BLASTX
NCBI GI	g2146733
BLAST score	439
E value	2.0e-43
Match length	75
% identity	99
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	151595
Seq. ID	LIB3175-061-P1-K1-D6
Method	BLASTX
NCBI GI	g1695717

BLAST score	443
E value	6.0e-63
Match length	135
% identity	95
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	151596
Seq. ID	LIB3175-061-P1-K1-D7
Method	BLASTX
NCBI GI	g2623962
BLAST score	347
E value	7.0e-33
Match length	74
% identity	92
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	151597
Seq. ID	LIB3175-061-P1-K1-D8
Method	BLASTX
NCBI GI	g4587685
BLAST score	613
E value	5.0e-64
Match length	131
% identity	98
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	151598
Seq. ID	LIB3175-061-P1-K1-D9
Method	BLASTX
NCBI GI	g3033395
BLAST score	149
E value	1.0e-09
Match length	114
% identity	40
NCBI Description	(AC004238) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	151599
Seq. ID	LIB3175-061-P1-K1-E1
Method	BLASTN
NCBI GI	g3297806
BLAST score	177
E value	5.0e-95
Match length	279
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	151600
Seq. ID	LIB3175-061-P1-K1-E10
Method	BLASTX
NCBI GI	g1731990
BLAST score	280
E value	7.0e-25
Match length	140

% identity	45
NCBI Description	(Y09602) serine carboxypeptidase II, CP-MII [Hordeum vulgare]

Seq. No.	151601
Seq. ID	LIB3175-061-P1-K1-E12
Method	BLASTX
NCBI GI	g2546988
BLAST score	200
E value	1.0e-15
Match length	117
% identity	47
NCBI Description	(Y15113) 2-dehydro-3-deoxyphosphoheptonate aldolase [Morinda citrifolia]

Seq. No.	151602
Seq. ID	LIB3175-061-P1-K1-E2
Method	BLASTN
NCBI GI	g3047100
BLAST score	120
E value	7.0e-61
Match length	201
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	151603
Seq. ID	LIB3175-061-P1-K1-E4
Method	BLASTX
NCBI GI	g322577
BLAST score	775
E value	6.0e-83
Match length	150
% identity	99
NCBI Description	Raf protein kinase homolog CTR1 - Arabidopsis thaliana

Seq. No.	151604
Seq. ID	LIB3175-061-P1-K1-E5
Method	BLASTX
NCBI GI	g3123188
BLAST score	516
E value	1.0e-52
Match length	110
% identity	89
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	151605
Seq. ID	LIB3175-061-P1-K1-E6
Method	BLASTX
NCBI GI	g4455226
BLAST score	765
E value	1.0e-81
Match length	149
% identity	98
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	151606
Seq. ID	LIB3175-061-P1-K1-F10
Method	BLASTX
NCBI GI	g4006934
BLAST score	313
E value	5.0e-29
Match length	76
% identity	74
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	151607
Seq. ID	LIB3175-061-P1-K1-F2
Method	BLASTN
NCBI GI	g3702735
BLAST score	185
E value	1.0e-99
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	151608
Seq. ID	LIB3175-061-P1-K1-F3
Method	BLASTX
NCBI GI	g585012
BLAST score	461
E value	4.0e-46
Match length	95
% identity	97
NCBI Description	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) >gi_289205 (L16237) phytoene desaturase [Arabidopsis thaliana] >gi_2244777_emb_CAB10200_ (Z97335) unnamed protein product [Arabidopsis thaliana]

Seq. No.	151609
Seq. ID	LIB3175-061-P1-K1-F4
Method	BLASTX
NCBI GI	g3913035
BLAST score	222
E value	6.0e-36
Match length	125
% identity	57
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_2935474 (AF049098) beta-amylase [Trifolium repens]

Seq. No.	151610
Seq. ID	LIB3175-061-P1-K1-F5
Method	BLASTX
NCBI GI	g4510358
BLAST score	66
E value	9.2e+00
Match length	68
% identity	16
NCBI Description	(AC006921) putative touch-induced calmodulin [Arabidopsis thaliana]

Seq. No. 151611

Seq. ID	LIB3175-061-P1-K1-F7
Method	BLASTX
NCBI GI	g3249096
BLAST score	428
E value	2.0e-42
Match length	104
% identity	86
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	151612
Seq. ID	LIB3175-061-P1-K1-F8
Method	BLASTX
NCBI GI	g3367576
BLAST score	227
E value	1.0e-18
Match length	55
% identity	73
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	151613
Seq. ID	LIB3175-061-P1-K1-F9
Method	BLASTX
NCBI GI	g3482977
BLAST score	546
E value	4.0e-56
Match length	144
% identity	78
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	151614
Seq. ID	LIB3175-061-P1-K1-G12
Method	BLASTX
NCBI GI	g1684855
BLAST score	416
E value	5.0e-41
Match length	92
% identity	19
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	151615
Seq. ID	LIB3175-061-P1-K1-G2
Method	BLASTN
NCBI GI	g4519183
BLAST score	266
E value	1.0e-148
Match length	382
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	151616
Seq. ID	LIB3175-061-P1-K1-G3
Method	BLASTX
NCBI GI	g2832660

BLAST score	326
E value	3.0e-30
Match length	64
% identity	94
NCBI Description	(AL021710) lipase-like protein [Arabidopsis thaliana]

Seq. No.	151617
Seq. ID	LIB3175-061-P1-K1-G5
Method	BLASTN
NCBI GI	g4220643
BLAST score	149
E value	4.0e-78
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	151618
Seq. ID	LIB3175-061-P1-K1-G6
Method	BLASTN
NCBI GI	g4733952
BLAST score	198
E value	1.0e-107
Match length	206
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	151619
Seq. ID	LIB3175-061-P1-K1-G7
Method	BLASTX
NCBI GI	g1362103
BLAST score	432
E value	9.0e-43
Match length	102
% identity	75
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	151620
Seq. ID	LIB3175-061-P1-K1-G8
Method	BLASTX
NCBI GI	g115385
BLAST score	664
E value	6.0e-70
Match length	129
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151621
Seq. ID	LIB3175-061-P1-K1-G9
Method	BLASTN
NCBI GI	g2618602
BLAST score	199

E value	1.0e-108
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	151622
Seq. ID	LIB3175-061-P1-K1-H10
Method	BLASTX
NCBI GI	g2160185
BLAST score	350
E value	5.0e-33
Match length	104
% identity	62
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	151623
Seq. ID	LIB3175-061-P1-K1-H11
Method	BLASTX
NCBI GI	g3063472
BLAST score	534
E value	1.0e-54
Match length	99
% identity	98
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	151624
Seq. ID	LIB3175-061-P1-K1-H12
Method	BLASTN
NCBI GI	g4691223
BLAST score	214
E value	1.0e-117
Match length	262
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	151625
Seq. ID	LIB3175-061-P1-K1-H3
Method	BLASTN
NCBI GI	g3849811
BLAST score	348
E value	0.0e+00
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151626
Seq. ID	LIB3175-061-P1-K1-H4
Method	BLASTX
NCBI GI	g3747111
BLAST score	316
E value	2.0e-29
Match length	68
% identity	90

NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]
Seq. No.	151627
Seq. ID	LIB3175-061-P1-K1-H5
Method	BLASTX
NCBI GI	g2507421
BLAST score	403
E value	1.0e-39
Match length	81
% identity	96
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]
Seq. No.	151628
Seq. ID	LIB3175-061-P1-K1-H7
Method	BLASTX
NCBI GI	g2829913
BLAST score	587
E value	5.0e-61
Match length	125
% identity	90
NCBI Description	(AC002291) putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]
Seq. No.	151629
Seq. ID	LIB3175-062-P1-K1-A1
Method	BLASTX
NCBI GI	g3868857
BLAST score	198
E value	3.0e-15
Match length	74
% identity	62
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]
Seq. No.	151630
Seq. ID	LIB3175-062-P1-K1-A11
Method	BLASTX
NCBI GI	g3882183
BLAST score	326
E value	3.0e-30
Match length	135
% identity	48
NCBI Description	(AB018274) KIAA0731 protein [Homo sapiens]
Seq. No.	151631
Seq. ID	LIB3175-062-P1-K1-A2
Method	BLASTX
NCBI GI	g3402722
BLAST score	608
E value	2.0e-63
Match length	139
% identity	86
NCBI Description	(AC004261) CPDK-related protein [Arabidopsis thaliana]
Seq. No.	151632

Seq. ID	LIB3175-062-P1-K1-A4
Method	BLASTX
NCBI GI	g421836
BLAST score	502
E value	7.0e-51
Match length	101
% identity	100
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No.	151633
Seq. ID	LIB3175-062-P1-K1-A5
Method	BLASTX
NCBI GI	g2398533
BLAST score	360
E value	3.0e-34
Match length	70
% identity	100
NCBI Description	(Y13725) Transcription factor [Arabidopsis thaliana]

Seq. No.	151634
Seq. ID	LIB3175-062-P1-K1-A6
Method	BLASTX
NCBI GI	g115783
BLAST score	576
E value	3.0e-69
Match length	134
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	151635
Seq. ID	LIB3175-062-P1-K1-A7
Method	BLASTX
NCBI GI	g2129769
BLAST score	749
E value	8.0e-80
Match length	143
% identity	99
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	151636
Seq. ID	LIB3175-062-P1-K1-A8
Method	BLASTN
NCBI GI	g3335356
BLAST score	96
E value	9.0e-47
Match length	192
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 151637

Seq. ID	LIB3175-062-P1-K1-B1
Method	BLASTX
NCBI GI	g2245133
BLAST score	569
E value	1.0e-58
Match length	151
% identity	75
NCBI Description	(Z97344) PSII D1 protein processing enzyme [Arabidopsis thaliana]

Seq. No.	151638
Seq. ID	LIB3175-062-P1-K1-B10
Method	BLASTX
NCBI GI	g2244759
BLAST score	418
E value	2.0e-55
Match length	136
% identity	82
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	151639
Seq. ID	LIB3175-062-P1-K1-B11
Method	BLASTX
NCBI GI	g2244759
BLAST score	706
E value	8.0e-75
Match length	147
% identity	90
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	151640
Seq. ID	LIB3175-062-P1-K1-B12
Method	BLASTX
NCBI GI	g1076708
BLAST score	657
E value	5.0e-69
Match length	134
% identity	28
NCBI Description	seed tetraubiquitin - common sunflower >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max] >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092) Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044) putative polyubiquitin [Arabidopsis thaliana] >gi_1096513_prf__2111434A tetraubiquitin [Helianthus annuus]

Seq. No.	151641
Seq. ID	LIB3175-062-P1-K1-B4
Method	BLASTN
NCBI GI	g4589410
BLAST score	302
E value	1.0e-169
Match length	466
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F2O15, complete sequence

Seq. No.	151642
Seq. ID	LIB3175-062-P1-K1-B5
Method	BLASTN
NCBI GI	g1469225
BLAST score	51
E value	8.0e-20
Match length	103
% identity	87
NCBI Description	B.oleracea mRNA for putative major latex protein

Seq. No.	151643
Seq. ID	LIB3175-062-P1-K1-B6
Method	BLASTN
NCBI GI	g4587641
BLAST score	254
E value	1.0e-141
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	151644
Seq. ID	LIB3175-062-P1-K1-B7
Method	BLASTX
NCBI GI	g1169278
BLAST score	283
E value	3.0e-25
Match length	71
% identity	83
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	151645
Seq. ID	LIB3175-062-P1-K1-B9
Method	BLASTX
NCBI GI	g4262154
BLAST score	700
E value	4.0e-74
Match length	155
% identity	95
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	151646
Seq. ID	LIB3175-062-P1-K1-C1
Method	BLASTN
NCBI GI	g2702261
BLAST score	130
E value	3.0e-67
Match length	182
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 151647

Seq. ID	LIB3175-062-P1-K1-C10
Method	BLASTX
NCBI GI	g1550740
BLAST score	55
E value	9.0e-13
Match length	93
% identity	60
NCBI Description	(Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No.	151648
Seq. ID	LIB3175-062-P1-K1-C11
Method	BLASTX
NCBI GI	g2244759
BLAST score	370
E value	1.0e-35
Match length	113
% identity	65
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	151649
Seq. ID	LIB3175-062-P1-K1-C2
Method	BLASTX
NCBI GI	g2160133
BLAST score	431
E value	1.0e-42
Match length	142
% identity	66
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	151650
Seq. ID	LIB3175-062-P1-K1-C3
Method	BLASTX
NCBI GI	g121907
BLAST score	227
E value	8.0e-19
Match length	44
% identity	100
NCBI Description	HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 - Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459) Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215) histone H1-2C [Arabidopsis thaliana]

Seq. No.	151651
Seq. ID	LIB3175-062-P1-K1-C6
Method	BLASTX
NCBI GI	g2262167
BLAST score	617
E value	2.0e-64
Match length	127
% identity	95
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	151652

Seq. ID	LIB3175-062-P1-K1-C7
Method	BLASTX
NCBI GI	g4734009
BLAST score	234
E value	2.0e-19
Match length	100
% identity	48
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151653
Seq. ID	LIB3175-062-P1-K1-C9
Method	BLASTX
NCBI GI	g2244759
BLAST score	389
E value	9.0e-38
Match length	128
% identity	65
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	151654
Seq. ID	LIB3175-062-P1-K1-D1
Method	BLASTX
NCBI GI	g4512675
BLAST score	402
E value	2.0e-39
Match length	94
% identity	80
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	151655
Seq. ID	LIB3175-062-P1-K1-D10
Method	BLASTX
NCBI GI	g2244759
BLAST score	213
E value	4.0e-17
Match length	110
% identity	45
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	151656
Seq. ID	LIB3175-062-P1-K1-D11
Method	BLASTX
NCBI GI	g3273751
BLAST score	106
E value	6.0e-17
Match length	49
% identity	92
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	151657
Seq. ID	LIB3175-062-P1-K1-D3
Method	BLASTN
NCBI GI	g2337888
BLAST score	336
E value	0.0e+00
Match length	403

% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	151658
Seq. ID	LIB3175-062-P1-K1-D4
Method	BLASTN
NCBI GI	g3449326
BLAST score	288
E value	1.0e-161
Match length	300
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	151659
Seq. ID	LIB3175-062-P1-K1-D5
Method	BLASTX
NCBI GI	g1488521
BLAST score	611
E value	1.0e-63
Match length	134
% identity	92
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	151660
Seq. ID	LIB3175-062-P1-K1-D6
Method	BLASTX
NCBI GI	g4586109
BLAST score	381
E value	9.0e-37
Match length	72
% identity	99
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	151661
Seq. ID	LIB3175-062-P1-K1-D7
Method	BLASTX
NCBI GI	g1432083
BLAST score	313
E value	4.0e-29
Match length	63
% identity	98
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	151662
Seq. ID	LIB3175-062-P1-K1-E10
Method	BLASTX
NCBI GI	g4249410
BLAST score	213
E value	3.0e-17
Match length	92
% identity	68
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	151663
Seq. ID	LIB3175-062-P1-K1-E11
Method	BLASTN
NCBI GI	g4249393
BLAST score	38
E value	4.0e-12
Match length	122
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151664
Seq. ID	LIB3175-062-P1-K1-E12
Method	BLASTX
NCBI GI	g2224931
BLAST score	774
E value	8.0e-83
Match length	143
% identity	99
NCBI Description	(AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No.	151665
Seq. ID	LIB3175-062-P1-K1-E2
Method	BLASTX
NCBI GI	g4063568
BLAST score	760
E value	4.0e-81
Match length	153
% identity	99
NCBI Description	(AF035916) ATP synthase beta subunit [Triplochlamys multiflora]

Seq. No.	151666
Seq. ID	LIB3175-062-P1-K1-E3
Method	BLASTX
NCBI GI	g2274857
BLAST score	456
E value	2.0e-45
Match length	136
% identity	71
NCBI Description	(AJ000469) glutathione peroxidase [Arabidopsis thaliana] >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione peroxidase precursor [Arabidopsis thaliana]

Seq. No.	151667
Seq. ID	LIB3175-062-P1-K1-E4
Method	BLASTN
NCBI GI	g2645198
BLAST score	45
E value	5.0e-16
Match length	162
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151668
Seq. ID	LIB3175-062-P1-K1-E5
Method	BLASTX
NCBI GI	g2062421
BLAST score	492
E value	1.0e-49
Match length	117
% identity	75
NCBI Description	(U82123) expansin [Lycopersicon esculentum]

Seq. No.	151669
Seq. ID	LIB3175-062-P1-K1-E6
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	7.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	151670
Seq. ID	LIB3175-062-P1-K1-E7
Method	BLASTX
NCBI GI	g3123188
BLAST score	683
E value	4.0e-72
Match length	134
% identity	98
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	151671
Seq. ID	LIB3175-062-P1-K1-E9
Method	BLASTN
NCBI GI	g4249393
BLAST score	126
E value	2.0e-64
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151672
Seq. ID	LIB3175-062-P1-K1-F1
Method	BLASTX
NCBI GI	g2497753
BLAST score	259
E value	2.0e-22
Match length	105
% identity	45
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	151673

Seq. ID	LIB3175-062-P1-K1-F10
Method	BLASTN
NCBI GI	g3241926
BLAST score	201
E value	1.0e-109
Match length	432
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	151674
Seq. ID	LIB3175-062-P1-K1-F11
Method	BLASTX
NCBI GI	g4567246
BLAST score	565
E value	3.0e-58
Match length	143
% identity	81
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	151675
Seq. ID	LIB3175-062-P1-K1-F3
Method	BLASTX
NCBI GI	g3236240
BLAST score	453
E value	3.0e-45
Match length	135
% identity	68
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	151676
Seq. ID	LIB3175-062-P1-K1-F4
Method	BLASTX
NCBI GI	g3820614
BLAST score	379
E value	2.0e-36
Match length	137
% identity	55
NCBI Description	(AF094516) E1-like protein [Homo sapiens]

Seq. No.	151677
Seq. ID	LIB3175-062-P1-K1-F5
Method	BLASTX
NCBI GI	g1518540
BLAST score	512
E value	4.0e-52
Match length	111
% identity	90
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	151678
Seq. ID	LIB3175-062-P1-K1-F6
Method	BLASTX
NCBI GI	g2062421
BLAST score	508
E value	1.0e-51
Match length	117

% identity	78
NCBI Description	(U82123) expansin [Lycopersicon esculentum]

Seq. No.	151679
Seq. ID	LIB3175-062-P1-K1-F7
Method	BLASTN
NCBI GI	g4220635
BLAST score	93
E value	8.0e-45
Match length	359
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	151680
Seq. ID	LIB3175-062-P1-K1-G1
Method	BLASTX
NCBI GI	g4249388
BLAST score	414
E value	1.0e-40
Match length	84
% identity	100
NCBI Description	(AC005966) Similar to gb_AF025438 Opa-interacting protein (OIP2) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	151681
Seq. ID	LIB3175-062-P1-K1-G11
Method	BLASTN
NCBI GI	g2264318
BLAST score	227
E value	1.0e-124
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	151682
Seq. ID	LIB3175-062-P1-K1-G12
Method	BLASTX
NCBI GI	g3334124
BLAST score	656
E value	5.0e-69
Match length	137
% identity	98
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	151683
Seq. ID	LIB3175-062-P1-K1-G2
Method	BLASTX
NCBI GI	g4580392
BLAST score	735
E value	3.0e-78
Match length	150
% identity	98

NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151684
Seq. ID	LIB3175-062-P1-K1-G3
Method	BLASTX
NCBI GI	g3292814
BLAST score	498
E value	1.0e-50
Match length	121
% identity	85
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	151685
Seq. ID	LIB3175-062-P1-K1-G4
Method	BLASTX
NCBI GI	g3258413
BLAST score	171
E value	5.0e-12
Match length	121
% identity	31
NCBI Description	(AP000007) 404aa long hypothetical alanyl-tRNA synthetase [Pyrococcus horikoshii]

Seq. No.	151686
Seq. ID	LIB3175-062-P1-K1-G5
Method	BLASTX
NCBI GI	g464707
BLAST score	699
E value	5.0e-74
Match length	136
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	151687
Seq. ID	LIB3175-062-P1-K1-G6
Method	BLASTX
NCBI GI	g4100433
BLAST score	218
E value	1.0e-17
Match length	62
% identity	65
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	151688
Seq. ID	LIB3175-062-P1-K1-G7
Method	BLASTX
NCBI GI	g4539316
BLAST score	528
E value	4.0e-54
Match length	110
% identity	99
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	151689
Seq. ID	LIB3175-062-P1-K1-G9
Method	BLASTX
NCBI GI	g4063739
BLAST score	628
E value	1.0e-65
Match length	136
% identity	86
NCBI Description	(AC005851) putative copper/zinc superoxide dismutase [Arabidopsis thaliana]

Seq. No.	151690
Seq. ID	LIB3175-062-P1-K1-H1
Method	BLASTX
NCBI GI	g2244749
BLAST score	659
E value	2.0e-69
Match length	128
% identity	97
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	151691
Seq. ID	LIB3175-062-P1-K1-H10
Method	BLASTX
NCBI GI	g1169476
BLAST score	633
E value	2.0e-66
Match length	121
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	151692
Seq. ID	LIB3175-062-P1-K1-H11
Method	BLASTX
NCBI GI	g3047116
BLAST score	318
E value	2.0e-29
Match length	86
% identity	78
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	151693
Seq. ID	LIB3175-062-P1-K1-H12
Method	BLASTN

NCBI GI	g4757417
BLAST score	190
E value	1.0e-102
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	151694
Seq. ID	LIB3175-062-P1-K1-H3
Method	BLASTX
NCBI GI	g3927825
BLAST score	726
E value	4.0e-77
Match length	154
% identity	90
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	151695
Seq. ID	LIB3175-062-P1-K1-H4
Method	BLASTX
NCBI GI	g3023216
BLAST score	622
E value	5.0e-65
Match length	127
% identity	99
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	151696
Seq. ID	LIB3175-062-P1-K1-H5
Method	BLASTN
NCBI GI	g3449324
BLAST score	234
E value	1.0e-129
Match length	445
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12G2, complete sequence

Seq. No.	151697
Seq. ID	LIB3175-062-P1-K1-H6
Method	BLASTN
NCBI GI	g2980787
BLAST score	166
E value	3.0e-88
Match length	390
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	151698
Seq. ID	LIB3175-062-P1-K1-H9
Method	BLASTX
NCBI GI	g3738316
BLAST score	359

E value	3.0e-34
Match length	82
% identity	82
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	151699
Seq. ID	LIB3175-063-P1-K1-A1
Method	BLASTX
NCBI GI	g3719443
BLAST score	183
E value	8.0e-14
Match length	60
% identity	50
NCBI Description	(AF093751) lipid transfer protein [Brassica oleracea]

Seq. No.	151700
Seq. ID	LIB3175-063-P1-K1-A10
Method	BLASTN
NCBI GI	g3873174
BLAST score	35
E value	4.0e-10
Match length	114
% identity	89
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	151701
Seq. ID	LIB3175-063-P1-K1-A11
Method	BLASTX
NCBI GI	g575457
BLAST score	173
E value	2.0e-12
Match length	134
% identity	30
NCBI Description	(U17018) Cdc40p [Saccharomyces cerevisiae]

Seq. No.	151702
Seq. ID	LIB3175-063-P1-K1-A3
Method	BLASTN
NCBI GI	g2529657
BLAST score	278
E value	1.0e-155
Match length	400
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151703
Seq. ID	LIB3175-063-P1-K1-A4
Method	BLASTX
NCBI GI	g544184
BLAST score	85
E value	2.0e-51
Match length	120
% identity	79
NCBI Description	4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE) (DISPROPORTIONATING ENZYME) (D-ENZYME)

	>gi_322785_pir__A45049 4-alpha-glucanotransferase (EC 2.4.1.25) - potato >gi_296692_emb_CAA48630_ (X68664) 4-alpha-glucanotransferase [Solanum tuberosum]
Seq. No.	151704
Seq. ID	LIB3175-063-P1-K1-A5
Method	BLASTX
NCBI GI	g4454032
BLAST score	456
E value	1.0e-45
Match length	140
% identity	65
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]
Seq. No.	151705
Seq. ID	LIB3175-063-P1-K1-A6
Method	BLASTX
NCBI GI	g4758946
BLAST score	164
E value	2.0e-11
Match length	57
% identity	54
NCBI Description	POP2 (yeast homolog) >gi_4106061_gb_AAD02685_ (AF053318) CCR4-associated factor 1 [Homo sapiens]
Seq. No.	151706
Seq. ID	LIB3175-063-P1-K1-A7
Method	BLASTX
NCBI GI	g3617770
BLAST score	81
E value	1.2e-01
Match length	125
% identity	90
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	151707
Seq. ID	LIB3175-063-P1-K1-A9
Method	BLASTX
NCBI GI	g99696
BLAST score	646
E value	8.0e-68
Match length	138
% identity	88
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]
Seq. No.	151708
Seq. ID	LIB3175-063-P1-K1-B1
Method	BLASTX
NCBI GI	g2258469
BLAST score	289
E value	5.0e-26
Match length	111

% identity	59
NCBI Description	(AF009179) replication protein A1 [Oryza sativa]

Seq. No.	151709
Seq. ID	LIB3175-063-P1-K1-B10
Method	BLASTN
NCBI GI	g3451055
BLAST score	202
E value	1.0e-110
Match length	421
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	151710
Seq. ID	LIB3175-063-P1-K1-B11
Method	BLASTX
NCBI GI	g166835
BLAST score	666
E value	3.0e-70
Match length	134
% identity	99
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	151711
Seq. ID	LIB3175-063-P1-K1-B12
Method	BLASTX
NCBI GI	g4678226
BLAST score	568
E value	1.0e-58
Match length	123
% identity	93
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	151712
Seq. ID	LIB3175-063-P1-K1-B3
Method	BLASTN
NCBI GI	g2584827
BLAST score	49
E value	1.0e-18
Match length	61
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151713
Seq. ID	LIB3175-063-P1-K1-B4
Method	BLASTN
NCBI GI	g4185128
BLAST score	44
E value	2.0e-15
Match length	104
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151714
Seq. ID	LIB3175-063-P1-K1-B5
Method	BLASTX
NCBI GI	g2677828
BLAST score	372
E value	1.0e-35
Match length	98
% identity	71
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	151715
Seq. ID	LIB3175-063-P1-K1-B6
Method	BLASTX
NCBI GI	g1363489
BLAST score	641
E value	3.0e-67
Match length	119
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	151716
Seq. ID	LIB3175-063-P1-K1-B7
Method	BLASTX
NCBI GI	g2688824
BLAST score	256
E value	4.0e-22
Match length	121
% identity	50
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	151717
Seq. ID	LIB3175-063-P1-K1-B8
Method	BLASTX
NCBI GI	g2702268
BLAST score	400
E value	5.0e-39
Match length	76
% identity	100
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	151718
Seq. ID	LIB3175-063-P1-K1-B9
Method	BLASTX
NCBI GI	g2642159
BLAST score	669
E value	1.0e-70
Match length	133
% identity	97
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	151719
Seq. ID	LIB3175-063-P1-K1-C1
Method	BLASTX
NCBI GI	g3482918
BLAST score	627
E value	1.0e-65
Match length	125
% identity	100
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	151720
Seq. ID	LIB3175-063-P1-K1-C10
Method	BLASTX
NCBI GI	g1362103
BLAST score	451
E value	6.0e-45
Match length	105
% identity	77
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]

Seq. No.	151721
Seq. ID	LIB3175-063-P1-K1-C11
Method	BLASTX
NCBI GI	g3831445
BLAST score	701
E value	3.0e-74
Match length	133
% identity	99
NCBI Description	(AC005819) unknown protein [Arabidopsis thaliana]

Seq. No.	151722
Seq. ID	LIB3175-063-P1-K1-C12
Method	BLASTX
NCBI GI	g132074
BLAST score	631
E value	4.0e-66
Match length	114
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	151723
Seq. ID	LIB3175-063-P1-K1-C2
Method	BLASTX
NCBI GI	g3461838
BLAST score	461
E value	4.0e-46
Match length	140
% identity	59
NCBI Description	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	151724
Seq. ID	LIB3175-063-P1-K1-C3
Method	BLASTX
NCBI GI	g4206206
BLAST score	309
E value	2.0e-28
Match length	75
% identity	85
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	151725
Seq. ID	LIB3175-063-P1-K1-C4
Method	BLASTX
NCBI GI	g267083
BLAST score	621
E value	2.0e-67
Match length	128
% identity	98
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	151726
Seq. ID	LIB3175-063-P1-K1-C5
Method	BLASTX
NCBI GI	g3763932
BLAST score	265
E value	4.0e-23
Match length	78
% identity	64
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	151727
Seq. ID	LIB3175-063-P1-K1-C7
Method	BLASTX
NCBI GI	g4580460
BLAST score	484
E value	7.0e-49
Match length	126
% identity	80
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	151728
Seq. ID	LIB3175-063-P1-K1-C8
Method	BLASTN
NCBI GI	g2815404
BLAST score	43
E value	6.0e-15
Match length	178
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	151729
Seq. ID	LIB3175-063-P1-K1-C9
Method	BLASTN
NCBI GI	g3513725
BLAST score	93
E value	7.0e-45
Match length	194
% identity	93
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	151730
Seq. ID	LIB3175-063-P1-K1-D10
Method	BLASTN
NCBI GI	g3241926
BLAST score	107
E value	4.0e-53
Match length	338
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	151731
Seq. ID	LIB3175-063-P1-K1-D11
Method	BLASTX
NCBI GI	g2795809
BLAST score	527
E value	7.0e-54
Match length	96
% identity	100
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	151732
Seq. ID	LIB3175-063-P1-K1-D3
Method	BLASTX
NCBI GI	g3047077
BLAST score	527
E value	7.0e-54
Match length	107
% identity	99
NCBI Description	(AF058914) contains similarity to the conserved C-terminal domain of helicases (Pfam: helicase_C.hmm, score: 90.11), similar to DEAD-box helicases [Arabidopsis thaliana]

Seq. No.	151733
Seq. ID	LIB3175-063-P1-K1-D4
Method	BLASTX
NCBI GI	g3695061
BLAST score	207
E value	2.0e-16
Match length	70
% identity	56
NCBI Description	(AF064788) rac GTPase activating protein 2 [Lotus japonicus]

Seq. No.	151734
Seq. ID	LIB3175-063-P1-K1-D5
Method	BLASTX

NCBI GI	g2129579
BLAST score	642
E value	2.0e-67
Match length	122
% identity	99
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	151735
Seq. ID	LIB3175-063-P1-K1-D6
Method	BLASTN
NCBI GI	g2564049
BLAST score	136
E value	2.0e-70
Match length	305
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	151736
Seq. ID	LIB3175-063-P1-K1-D7
Method	BLASTX
NCBI GI	g3738301
BLAST score	507
E value	1.0e-51
Match length	95
% identity	96
NCBI Description	(AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No.	151737
Seq. ID	LIB3175-063-P1-K1-D8
Method	BLASTX
NCBI GI	g1175013
BLAST score	504
E value	3.0e-51
Match length	113
% identity	87
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	151738
Seq. ID	LIB3175-063-P1-K1-D9
Method	BLASTX
NCBI GI	g2244904
BLAST score	473
E value	1.0e-47
Match length	109
% identity	94
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	151739
Seq. ID	LIB3175-063-P1-K1-E1

Method	BLASTN
NCBI GI	g4006885
BLAST score	305
E value	1.0e-171
Match length	423
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	151740
Seq. ID	LIB3175-063-P1-K1-E10
Method	BLASTX
NCBI GI	g2739375
BLAST score	605
E value	5.0e-63
Match length	125
% identity	98
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	151741
Seq. ID	LIB3175-063-P1-K1-E11
Method	BLASTX
NCBI GI	g2494896
BLAST score	611
E value	8.0e-64
Match length	113
% identity	56
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	151742
Seq. ID	LIB3175-063-P1-K1-E12
Method	BLASTX
NCBI GI	g3668175
BLAST score	651
E value	2.0e-68
Match length	137
% identity	92
NCBI Description	(AB006778) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	151743
Seq. ID	LIB3175-063-P1-K1-E2
Method	BLASTN
NCBI GI	g3449313
BLAST score	394
E value	0.0e+00
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	151744

Seq. ID	LIB3175-063-P1-K1-E3
Method	BLASTX
NCBI GI	g2852640
BLAST score	171
E value	4.0e-12
Match length	129
% identity	33
NCBI Description	(AF007157) unknown [Homo sapiens]

Seq. No.	151745
Seq. ID	LIB3175-063-P1-K1-E4
Method	BLASTN
NCBI GI	g3046851
BLAST score	174
E value	3.0e-93
Match length	265
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	151746
Seq. ID	LIB3175-063-P1-K1-E5
Method	BLASTN
NCBI GI	g3985952
BLAST score	82
E value	4.0e-38
Match length	217
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	151747
Seq. ID	LIB3175-063-P1-K1-E6
Method	BLASTX
NCBI GI	g4490721
BLAST score	292
E value	3.0e-26
Match length	66
% identity	83
NCBI Description	(AL035709) squalene epoxidase-like protein [Arabidopsis thaliana]

Seq. No.	151748
Seq. ID	LIB3175-063-P1-K1-E7
Method	BLASTX
NCBI GI	g1848225
BLAST score	202
E value	9.0e-16
Match length	74
% identity	47
NCBI Description	(U88090) nonspecific lipid transfer protein [Hordeum vulgare]

Seq. No.	151749
Seq. ID	LIB3175-063-P1-K1-E9
Method	BLASTX
NCBI GI	g4803729

BLAST score	65
E value	2.0e-35
Match length	137
% identity	58
NCBI Description	(AJ238880) putative preprolegumain [Nicotiana tabacum]

Seq. No.	151750
Seq. ID	LIB3175-063-P1-K1-F1
Method	BLASTX
NCBI GI	g543565
BLAST score	199
E value	2.0e-15
Match length	64
% identity	52
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	151751
Seq. ID	LIB3175-063-P1-K1-F10
Method	BLASTN
NCBI GI	g2832611
BLAST score	181
E value	2.0e-97
Match length	193
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	151752
Seq. ID	LIB3175-063-P1-K1-F11
Method	BLASTX
NCBI GI	g4539307
BLAST score	266
E value	3.0e-23
Match length	114
% identity	52
NCBI Description	(AL049480) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	151753
Seq. ID	LIB3175-063-P1-K1-F12
Method	BLASTX
NCBI GI	g899608
BLAST score	576
E value	1.0e-59
Match length	120
% identity	21
NCBI Description	(U29158) polyubiquitin [Zea mays]

Seq. No.	151754
Seq. ID	LIB3175-063-P1-K1-F2
Method	BLASTX
NCBI GI	g3036793
BLAST score	154
E value	4.0e-10

Match length	119
% identity	36
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana] >gi_3805855_emb_CAA21475_ (AL031986) putative protein [Arabidopsis thaliana]

Seq. No.	151755
Seq. ID	LIB3175-063-P1-K1-F3
Method	BLASTX
NCBI GI	g2341034
BLAST score	531
E value	2.0e-54
Match length	106
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	151756
Seq. ID	LIB3175-063-P1-K1-F5
Method	BLASTX
NCBI GI	g4154281
BLAST score	400
E value	5.0e-39
Match length	94
% identity	78
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	151757
Seq. ID	LIB3175-063-P1-K1-F6
Method	BLASTX
NCBI GI	g1173187
BLAST score	578
E value	7.0e-60
Match length	117
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	151758
Seq. ID	LIB3175-063-P1-K1-F7
Method	BLASTX
NCBI GI	g4510363
BLAST score	345
E value	1.0e-32
Match length	81
% identity	77
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	151759
Seq. ID	LIB3175-063-P1-K1-F9
Method	BLASTX
NCBI GI	g4741940
BLAST score	423
E value	8.0e-42
Match length	86

% identity	91
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	151760
Seq. ID	LIB3175-063-P1-K1-G1
Method	BLASTX
NCBI GI	g4193388
BLAST score	254
E value	4.0e-22
Match length	76
% identity	72
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	151761
Seq. ID	LIB3175-063-P1-K1-G10
Method	BLASTX
NCBI GI	g2129734
BLAST score	468
E value	5.0e-47
Match length	95
% identity	99
NCBI Description	serine/threonine protein phosphatase type 2A regulatory chain A - Arabidopsis thaliana >gi_1254996 (U27299) serine/threonine protein phosphatase type 2A regulatory subunit A [Arabidopsis thaliana]

Seq. No.	151762
Seq. ID	LIB3175-063-P1-K1-G11
Method	BLASTX
NCBI GI	g2795805
BLAST score	283
E value	3.0e-25
Match length	95
% identity	62
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	151763
Seq. ID	LIB3175-063-P1-K1-G2
Method	BLASTX
NCBI GI	g1363488
BLAST score	520
E value	4.0e-53
Match length	101
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	151764
Seq. ID	LIB3175-063-P1-K1-G3
Method	BLASTX
NCBI GI	g4128133
BLAST score	190

E value	2.0e-14
Match length	63
% identity	52
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	151765
Seq. ID	LIB3175-063-P1-K1-G4
Method	BLASTX
NCBI GI	g82284
BLAST score	157
E value	1.0e-10
Match length	32
% identity	100
NCBI Description	ubiquitin - potato (fragment) >gi_21604_emb_CAA77737_ (Z11671) ubiquitin [Solanum tuberosum]

Seq. No.	151766
Seq. ID	LIB3175-063-P1-K1-G6
Method	BLASTX
NCBI GI	g119143
BLAST score	676
E value	2.0e-71
Match length	133
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	151767
Seq. ID	LIB3175-063-P1-K1-G7
Method	BLASTX
NCBI GI	g1169278
BLAST score	305
E value	6.0e-28
Match length	75
% identity	84
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	151768
Seq. ID	LIB3175-063-P1-K1-G8
Method	BLASTX
NCBI GI	g4006941
BLAST score	501
E value	7.0e-51
Match length	110
% identity	89
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	151769
Seq. ID	LIB3175-063-P1-K1-H1
Method	BLASTX
NCBI GI	g2494275
BLAST score	198
E value	3.0e-15
Match length	56
% identity	62
NCBI Description	ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No.	151770
Seq. ID	LIB3175-063-P1-K1-H10
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	151771
Seq. ID	LIB3175-063-P1-K1-H11
Method	BLASTN
NCBI GI	g2196463
BLAST score	348
E value	0.0e+00
Match length	360
% identity	99
NCBI Description	Arabidopsis thaliana chloroplast trnC, rpoB & rpoC1 genes

Seq. No.	151772
Seq. ID	LIB3175-063-P1-K1-H12
Method	BLASTX
NCBI GI	g2501188
BLAST score	509
E value	8.0e-52
Match length	123
% identity	84
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	151773
Seq. ID	LIB3175-063-P1-K1-H3
Method	BLASTX
NCBI GI	g134976
BLAST score	464
E value	1.0e-46
Match length	89
% identity	99
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	151774
Seq. ID	LIB3175-063-P1-K1-H4
Method	BLASTX
NCBI GI	g2129608
BLAST score	431
E value	1.0e-42
Match length	90
% identity	97
NCBI Description	GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	151775
Seq. ID	LIB3175-063-P1-K1-H5
Method	BLASTN
NCBI GI	g2656029
BLAST score	183
E value	2.0e-98
Match length	355
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	151776
Seq. ID	LIB3175-063-P1-K1-H6
Method	BLASTX
NCBI GI	g1773330
BLAST score	474
E value	1.0e-47
Match length	110
% identity	83
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	151777
Seq. ID	LIB3175-063-P1-K1-H9
Method	BLASTN
NCBI GI	g3702732
BLAST score	228
E value	1.0e-125
Match length	321
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	151778
Seq. ID	LIB3175-064-P1-K1-A10
Method	BLASTX
NCBI GI	g2062161
BLAST score	624
E value	3.0e-65
Match length	124
% identity	49
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	151779
Seq. ID	LIB3175-064-P1-K1-A11
Method	BLASTX

NCBI GI	g3608142
BLAST score	229
E value	6.0e-19
Match length	122
% identity	41
NCBI Description	(AC005314) putative hin1 [Arabidopsis thaliana]

Seq. No.	151780
Seq. ID	LIB3175-064-P1-K1-A12
Method	BLASTX
NCBI GI	g3738261
BLAST score	345
E value	1.0e-32
Match length	121
% identity	67
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	151781
Seq. ID	LIB3175-064-P1-K1-A2
Method	BLASTN
NCBI GI	g2281081
BLAST score	70
E value	3.0e-31
Match length	215
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151782
Seq. ID	LIB3175-064-P1-K1-A7
Method	BLASTN
NCBI GI	g2281081
BLAST score	236
E value	1.0e-130
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151783
Seq. ID	LIB3175-064-P1-K1-A8
Method	BLASTX
NCBI GI	g1695717
BLAST score	184
E value	6.0e-14
Match length	64
% identity	67
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	151784
Seq. ID	LIB3175-064-P1-K1-A9
Method	BLASTX
NCBI GI	g1651459
BLAST score	146
E value	3.0e-09
Match length	124

% identity	31
NCBI Description	(D90732) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	151785
Seq. ID	LIB3175-064-P1-K1-B11
Method	BLASTN
NCBI GI	g4510338
BLAST score	314
E value	1.0e-176
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	151786
Seq. ID	LIB3175-064-P1-K1-B12
Method	BLASTX
NCBI GI	g500837
BLAST score	274
E value	3.0e-24
Match length	126
% identity	40
NCBI Description	(U10556) Ire1p: Probable protein kinase [Saccharomyces cerevisiae]

Seq. No.	151787
Seq. ID	LIB3175-064-P1-K1-B2
Method	BLASTX
NCBI GI	g1175013
BLAST score	439
E value	1.0e-43
Match length	112
% identity	80
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	151788
Seq. ID	LIB3175-064-P1-K1-B4
Method	BLASTX
NCBI GI	g4522012
BLAST score	347
E value	8.0e-33
Match length	121
% identity	56
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151789
Seq. ID	LIB3175-064-P1-K1-B7
Method	BLASTX
NCBI GI	g4006887
BLAST score	329
E value	1.0e-30
Match length	126
% identity	59

NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	151790
Seq. ID	LIB3175-064-P1-K1-B8
Method	BLASTX
NCBI GI	g2275216
BLAST score	274
E value	3.0e-24
Match length	64
% identity	83
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]
Seq. No.	151791
Seq. ID	LIB3175-064-P1-K1-B9
Method	BLASTX
NCBI GI	g1628583
BLAST score	321
E value	7.0e-30
Match length	67
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	151792
Seq. ID	LIB3175-064-P1-K1-C10
Method	BLASTX
NCBI GI	g2924773
BLAST score	673
E value	5.0e-71
Match length	137
% identity	99
NCBI Description	(AC002334) putative mitochondrial chaperonin HSP60 precursor [Arabidopsis thaliana]
Seq. No.	151793
Seq. ID	LIB3175-064-P1-K1-C11
Method	BLASTN
NCBI GI	g4519193
BLAST score	291
E value	1.0e-163
Match length	416
% identity	49
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence
Seq. No.	151794
Seq. ID	LIB3175-064-P1-K1-C3
Method	BLASTX
NCBI GI	g2673917
BLAST score	173
E value	2.0e-12
Match length	71
% identity	43
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	151795
Seq. ID	LIB3175-064-P1-K1-C4
Method	BLASTN
NCBI GI	g4049332
BLAST score	60
E value	4.0e-25
Match length	186
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	151796
Seq. ID	LIB3175-064-P1-K1-C5
Method	BLASTN
NCBI GI	g2827644
BLAST score	291
E value	1.0e-163
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	151797
Seq. ID	LIB3175-064-P1-K1-C8
Method	BLASTN
NCBI GI	g4510360
BLAST score	289
E value	1.0e-161
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	151798
Seq. ID	LIB3175-064-P1-K1-D10
Method	BLASTX
NCBI GI	g1351837
BLAST score	381
E value	5.0e-39
Match length	128
% identity	69
NCBI Description	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA >gi_2144155_pir__S66564 acetyl CoA carboxylase type II beta-carboxyltransferase chain - rape chloroplast >gi_1069998_emb_CAA90747_ (Z50868) acetyl CoA carboxylase carboxyltransferase (beta subunit) [Brassica napus] >gi_1589046_prf__2210244G Ac-CoA carboxylase:SUBUNIT=beta [Brassica napus]

Seq. No.	151799
Seq. ID	LIB3175-064-P1-K1-D11
Method	BLASTN
NCBI GI	g1707006
BLAST score	376
E value	0.0e+00
Match length	392

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151800
Seq. ID	LIB3175-064-P1-K1-D12
Method	BLASTX
NCBI GI	g3377797
BLAST score	551
E value	1.0e-56
Match length	132
% identity	81
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	151801
Seq. ID	LIB3175-064-P1-K1-D3
Method	BLASTX
NCBI GI	g170111
BLAST score	296
E value	9.0e-27
Match length	122
% identity	51
NCBI Description	(M86349) ferredoxin-NADP oxidoreductase [Spinacia oleracea]

Seq. No.	151802
Seq. ID	LIB3175-064-P1-K1-D5
Method	BLASTN
NCBI GI	g3046854
BLAST score	213
E value	1.0e-116
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	151803
Seq. ID	LIB3175-064-P1-K1-D6
Method	BLASTN
NCBI GI	g3420043
BLAST score	349
E value	0.0e+00
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151804
Seq. ID	LIB3175-064-P1-K1-D7
Method	BLASTX
NCBI GI	g2244952
BLAST score	351
E value	2.0e-33
Match length	96

% identity	76
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	151805
Seq. ID	LIB3175-064-P1-K1-D8
Method	BLASTX
NCBI GI	g1076282
BLAST score	670
E value	1.0e-70
Match length	133
% identity	98
NCBI Description	aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase [Arabidopsis thaliana]

Seq. No.	151806
Seq. ID	LIB3175-064-P1-K1-D9
Method	BLASTX
NCBI GI	g1362007
BLAST score	754
E value	2.0e-80
Match length	139
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	151807
Seq. ID	LIB3175-064-P1-K1-E1
Method	BLASTX
NCBI GI	g3786017
BLAST score	386
E value	2.0e-37
Match length	76
% identity	99
NCBI Description	(AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No.	151808
Seq. ID	LIB3175-064-P1-K1-E10
Method	BLASTX
NCBI GI	g2827621
BLAST score	296
E value	8.0e-27
Match length	121
% identity	46
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	151809
Seq. ID	LIB3175-064-P1-K1-E11
Method	BLASTX
NCBI GI	g4455169
BLAST score	155
E value	3.0e-10
Match length	66
% identity	48

DOCKET NO. 5050-4005-2

NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	151810
Seq. ID	LIB3175-064-P1-K1-E5
Method	BLASTX
NCBI GI	g1850546
BLAST score	442
E value	6.0e-44
Match length	89
% identity	99
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	151811
Seq. ID	LIB3175-064-P1-K1-F10
Method	BLASTX
NCBI GI	g1703108
BLAST score	574
E value	2.0e-59
Match length	107
% identity	99
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	151812
Seq. ID	LIB3175-064-P1-K1-F11
Method	BLASTN
NCBI GI	g3080430
BLAST score	199
E value	1.0e-108
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	151813
Seq. ID	LIB3175-064-P1-K1-F12
Method	BLASTX
NCBI GI	g127045
BLAST score	353
E value	1.0e-49
Match length	101
% identity	96
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	151814
Seq. ID	LIB3175-064-P1-K1-F5

Method	BLASTN
NCBI GI	g3413696
BLAST score	144
E value	2.0e-75
Match length	254
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151815
Seq. ID	LIB3175-064-P1-K1-F7
Method	BLASTX
NCBI GI	g82734
BLAST score	588
E value	5.0e-61
Match length	118
% identity	30
NCBI Description	ubiquitin precursor - maize (fragment) >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No.	151816
Seq. ID	LIB3175-064-P1-K1-F8
Method	BLASTX
NCBI GI	g4587587
BLAST score	371
E value	1.0e-35
Match length	72
% identity	100
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	151817
Seq. ID	LIB3175-064-P1-K1-F9
Method	BLASTX
NCBI GI	g3860247
BLAST score	723
E value	7.0e-77
Match length	139
% identity	96
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	151818
Seq. ID	LIB3175-064-P1-K1-G11
Method	BLASTX
NCBI GI	g2055273
BLAST score	660
E value	2.0e-69
Match length	129
% identity	99
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	151819
Seq. ID	LIB3175-064-P1-K1-G12
Method	BLASTX
NCBI GI	g2635765
BLAST score	249
E value	3.0e-21
Match length	81

% identity	60
NCBI Description	(Z99120) similar to NifS protein homolog [Bacillus subtilis]

Seq. No.	151820
Seq. ID	LIB3175-064-P1-K1-G4
Method	BLASTX
NCBI GI	g4581109
BLAST score	503
E value	4.0e-51
Match length	121
% identity	83
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	151821
Seq. ID	LIB3175-064-P1-K1-G5
Method	BLASTX
NCBI GI	g228408
BLAST score	231
E value	3.0e-19
Match length	46
% identity	52
NCBI Description	calmodulin 1 [Arabidopsis thaliana]

Seq. No.	151822
Seq. ID	LIB3175-064-P1-K1-G7
Method	BLASTN
NCBI GI	g2827538
BLAST score	366
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	151823
Seq. ID	LIB3175-064-P1-K1-G8
Method	BLASTN
NCBI GI	g3702735
BLAST score	192
E value	1.0e-104
Match length	260
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	151824
Seq. ID	LIB3175-064-P1-K1-H10
Method	BLASTN
NCBI GI	g3650026
BLAST score	232
E value	1.0e-127
Match length	363
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151825
Seq. ID	LIB3175-064-P1-K1-H11
Method	BLASTN
NCBI GI	g2618602
BLAST score	376
E value	0.0e+00
Match length	400
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	151826
Seq. ID	LIB3175-064-P1-K1-H12
Method	BLASTX
NCBI GI	g166708
BLAST score	637
E value	9.0e-67
Match length	127
% identity	99
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	151827
Seq. ID	LIB3175-064-P1-K1-H2
Method	BLASTX
NCBI GI	g4753652
BLAST score	246
E value	5.0e-21
Match length	75
% identity	56
NCBI Description	(AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	151828
Seq. ID	LIB3175-064-P1-K1-H3
Method	BLASTN
NCBI GI	g3559808
BLAST score	33
E value	3.0e-09
Match length	143
% identity	86
NCBI Description	Arabidopsis thaliana fdh gene

Seq. No.	151829
Seq. ID	LIB3175-064-P1-K1-H5
Method	BLASTX
NCBI GI	g3482918
BLAST score	553
E value	6.0e-57
Match length	110
% identity	100
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	151830
Seq. ID	LIB3175-064-P1-K1-H6
Method	BLASTX

NCBI GI	g1352347
BLAST score	409
E value	5.0e-40
Match length	102
% identity	81
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	151831
Seq. ID	LIB3175-064-P1-K1-H7
Method	BLASTN
NCBI GI	g2245073
BLAST score	291
E value	1.0e-163
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	151832
Seq. ID	LIB3175-064-P1-K1-H8
Method	BLASTX
NCBI GI	g3075394
BLAST score	630
E value	6.0e-66
Match length	122
% identity	100
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	151833
Seq. ID	LIB3175-064-P1-K1-H9
Method	BLASTX
NCBI GI	g4502781
BLAST score	217
E value	2.0e-17
Match length	128
% identity	40
NCBI Description	centromere protein E >gi_399227_sp_Q02224_CENE_HUMAN CENTROMERIC PROTEIN E (CENP-E PROTEIN) >gi_284038_pir__S28261 centromere protein E - human >gi_29865_emb_CAA78727_ (Z15005) CENP-E [Homo sapiens]

Seq. No.	151834
Seq. ID	LIB3175-065-P1-K1-A1
Method	BLASTN
NCBI GI	g4539402
BLAST score	345
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	151835
Seq. ID	LIB3175-065-P1-K1-A10
Method	BLASTX
NCBI GI	g1703227
BLAST score	309
E value	3.0e-28
Match length	85
% identity	71
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine aminotransferase [Hordeum vulgare]

Seq. No.	151836
Seq. ID	LIB3175-065-P1-K1-A11
Method	BLASTX
NCBI GI	g4263772
BLAST score	491
E value	1.0e-49
Match length	94
% identity	100
NCBI Description	(AC006218) hypothetical protein [Arabidopsis thaliana] >gi_4726120_gb_AAD28320.1_AC006436_11 (AC006436) putative aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	151837
Seq. ID	LIB3175-065-P1-K1-A12
Method	BLASTN
NCBI GI	g2760168
BLAST score	332
E value	0.0e+00
Match length	402
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	151838
Seq. ID	LIB3175-065-P1-K1-A2
Method	BLASTX
NCBI GI	g122007
BLAST score	327
E value	2.0e-30
Match length	117
% identity	57
NCBI Description	HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No.	151839
Seq. ID	LIB3175-065-P1-K1-A3
Method	BLASTX
NCBI GI	g2506443
BLAST score	499
E value	1.0e-50
Match length	136

% identity	76
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	151840
Seq. ID	LIB3175-065-P1-K1-A4
Method	BLASTX
NCBI GI	g1076393
BLAST score	543
E value	9.0e-56
Match length	110
% identity	100
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	151841
Seq. ID	LIB3175-065-P1-K1-A5
Method	BLASTN
NCBI GI	g2264318
BLAST score	387
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	151842
Seq. ID	LIB3175-065-P1-K1-A7
Method	BLASTX
NCBI GI	g4586265
BLAST score	529
E value	4.0e-54
Match length	128
% identity	77
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	151843
Seq. ID	LIB3175-065-P1-K1-A8
Method	BLASTX
NCBI GI	g3335365
BLAST score	362
E value	1.0e-34
Match length	90
% identity	80
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	151844
Seq. ID	LIB3175-065-P1-K1-B1

Method	BLASTX
NCBI GI	g2507281
BLAST score	763
E value	1.0e-81
Match length	139
% identity	99
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	151845
Seq. ID	LIB3175-065-P1-K1-B10
Method	BLASTX
NCBI GI	g3786007
BLAST score	490
E value	1.0e-49
Match length	109
% identity	92
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151846
Seq. ID	LIB3175-065-P1-K1-B11
Method	BLASTX
NCBI GI	g3805956
BLAST score	550
E value	1.0e-56
Match length	138
% identity	72
NCBI Description	(Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No.	151847
Seq. ID	LIB3175-065-P1-K1-B12
Method	BLASTN
NCBI GI	g2264302
BLAST score	395
E value	0.0e+00
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	151848
Seq. ID	LIB3175-065-P1-K1-B2
Method	BLASTN
NCBI GI	g414549
BLAST score	86
E value	1.0e-40
Match length	171
% identity	92
NCBI Description	Arabidopsis thaliana Columbia cytosolic triose phosphate isomerase (Atctimc) mRNA, complete cds

Seq. No.	151849
Seq. ID	LIB3175-065-P1-K1-B3
Method	BLASTN
NCBI GI	g4587641
BLAST score	212
E value	1.0e-116

Match length	302
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	151850
Seq. ID	LIB3175-065-P1-K1-B4
Method	BLASTX
NCBI GI	g1172872
BLAST score	383
E value	4.0e-37
Match length	96
% identity	78
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	151851
Seq. ID	LIB3175-065-P1-K1-B5
Method	BLASTX
NCBI GI	g1168728
BLAST score	715
E value	6.0e-76
Match length	129
% identity	100
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	151852
Seq. ID	LIB3175-065-P1-K1-B6
Method	BLASTX
NCBI GI	g2347188
BLAST score	563
E value	4.0e-58
Match length	138
% identity	76
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	151853
Seq. ID	LIB3175-065-P1-K1-B7
Method	BLASTX
NCBI GI	g2245093
BLAST score	498
E value	2.0e-50
Match length	131
% identity	50
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	151854
Seq. ID	LIB3175-065-P1-K1-B8
Method	BLASTX
NCBI GI	g4544399

BLAST score	469
E value	4.0e-47
Match length	133
% identity	66
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	151855
Seq. ID	LIB3175-065-P1-K1-B9
Method	BLASTN
NCBI GI	g4063737
BLAST score	269
E value	1.0e-150
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151856
Seq. ID	LIB3175-065-P1-K1-C1
Method	BLASTX
NCBI GI	g4567267
BLAST score	427
E value	4.0e-42
Match length	81
% identity	96
NCBI Description	(AC006841) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	151857
Seq. ID	LIB3175-065-P1-K1-C10
Method	BLASTX
NCBI GI	g4544402
BLAST score	362
E value	2.0e-34
Match length	116
% identity	21
NCBI Description	(AC007047) putative leucine rich repeat protein [Arabidopsis thaliana]

Seq. No.	151858
Seq. ID	LIB3175-065-P1-K1-C11
Method	BLASTN
NCBI GI	g3928074
BLAST score	218
E value	1.0e-119
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151859
Seq. ID	LIB3175-065-P1-K1-C12
Method	BLASTX
NCBI GI	g4455180
BLAST score	596
E value	6.0e-62

Match length	137
% identity	88
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	151860
Seq. ID	LIB3175-065-P1-K1-C2
Method	BLASTX
NCBI GI	g459020
BLAST score	274
E value	3.0e-24
Match length	110
% identity	47
NCBI Description	(U03392) light harvesting chlorophyll a/b binding protein of PSII [Euglena gracilis]

Seq. No.	151861
Seq. ID	LIB3175-065-P1-K1-C3
Method	BLASTN
NCBI GI	g4580454
BLAST score	43
E value	7.0e-15
Match length	153
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	151862
Seq. ID	LIB3175-065-P1-K1-C4
Method	BLASTN
NCBI GI	g1246400
BLAST score	207
E value	1.0e-113
Match length	337
% identity	94
NCBI Description	A.thaliana mRNA for ferritin

Seq. No.	151863
Seq. ID	LIB3175-065-P1-K1-C6
Method	BLASTX
NCBI GI	g166834
BLAST score	119
E value	4.0e-23
Match length	76
% identity	72
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	151864
Seq. ID	LIB3175-065-P1-K1-C7
Method	BLASTX
NCBI GI	g112682
BLAST score	141
E value	3.0e-27
Match length	98
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	151865
Seq. ID	LIB3175-065-P1-K1-C8
Method	BLASTN
NCBI GI	g4539378
BLAST score	98
E value	7.0e-48
Match length	274
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	151866
Seq. ID	LIB3175-065-P1-K1-C9
Method	BLASTN
NCBI GI	g4006885
BLAST score	331
E value	0.0e+00
Match length	399
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	151867
Seq. ID	LIB3175-065-P1-K1-D11
Method	BLASTX
NCBI GI	g3242719
BLAST score	652
E value	2.0e-68
Match length	126
% identity	99
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	151868
Seq. ID	LIB3175-065-P1-K1-D12
Method	BLASTX
NCBI GI	g2956690
BLAST score	459
E value	6.0e-46
Match length	118
% identity	60
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	151869
Seq. ID	LIB3175-065-P1-K1-D2
Method	BLASTX
NCBI GI	g1174847
BLAST score	458
E value	9.0e-46
Match length	87
% identity	99

NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 1 (UBIQUITIN-PROTEIN LIGASE 4) (UBIQUITIN CARRIER PROTEIN 4) >gi_431266 (L19354) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	151870
Seq. ID	LIB3175-065-P1-K1-D4
Method	BLASTN
NCBI GI	g4309747
BLAST score	125
E value	6.0e-64
Match length	273
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151871
Seq. ID	LIB3175-065-P1-K1-D5
Method	BLASTX
NCBI GI	g4589980
BLAST score	582
E value	3.0e-60
Match length	124
% identity	90
NCBI Description	(AC007195) cyclophilin, 3' partial [Arabidopsis thaliana]

Seq. No.	151872
Seq. ID	LIB3175-065-P1-K1-D6
Method	BLASTX
NCBI GI	g4544399
BLAST score	352
E value	3.0e-33
Match length	69
% identity	100
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	151873
Seq. ID	LIB3175-065-P1-K1-D7
Method	BLASTX
NCBI GI	g3953473
BLAST score	575
E value	1.0e-59
Match length	126
% identity	95
NCBI Description	(AC002328) F22O2.18 [Arabidopsis thaliana]

Seq. No.	151874
Seq. ID	LIB3175-065-P1-K1-D8
Method	BLASTX
NCBI GI	g1170503
BLAST score	531
E value	2.0e-54
Match length	102
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_

(X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	151875
Seq. ID	LIB3175-065-P1-K1-D9
Method	BLASTX
NCBI GI	g4539009
BLAST score	721
E value	1.0e-76
Match length	137
% identity	99
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	151876
Seq. ID	LIB3175-065-P1-K1-E1
Method	BLASTN
NCBI GI	g4455262
BLAST score	223
E value	1.0e-122
Match length	243
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	151877
Seq. ID	LIB3175-065-P1-K1-E11
Method	BLASTX
NCBI GI	g462579
BLAST score	341
E value	4.0e-32
Match length	89
% identity	79
NCBI Description	MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR (NADP-MDH) >gi_481222_pir__S38346 malate dehydrogenase (NADP+) (EC 1.1.1.82) - garden pea >gi_397475_emb_CAA52614_ (X74507) malate dehydrogenase (NADP+) [Pisum sativum]

Seq. No.	151878
Seq. ID	LIB3175-065-P1-K1-E12
Method	BLASTX
NCBI GI	g4006853
BLAST score	542
E value	1.0e-55
Match length	129
% identity	84
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	151879
Seq. ID	LIB3175-065-P1-K1-E3
Method	BLASTX
NCBI GI	g3335366
BLAST score	309
E value	3.0e-28
Match length	124
% identity	44
NCBI Description	(AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	151880
Seq. ID	LIB3175-065-P1-K1-E5
Method	BLASTN
NCBI GI	g1483217
BLAST score	387
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	A.thaliana gene induced upon wounding stress

Seq. No.	151881
Seq. ID	LIB3175-065-P1-K1-E6
Method	BLASTX
NCBI GI	g2827529
BLAST score	403
E value	2.0e-39
Match length	107
% identity	82
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]

Seq. No.	151882
Seq. ID	LIB3175-065-P1-K1-E7
Method	BLASTN
NCBI GI	g2245073
BLAST score	299
E value	1.0e-167
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	151883
Seq. ID	LIB3175-065-P1-K1-E8
Method	BLASTN
NCBI GI	g4309747
BLAST score	130
E value	7.0e-67
Match length	270
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151884
Seq. ID	LIB3175-065-P1-K1-E9
Method	BLASTN
NCBI GI	g4309747
BLAST score	236
E value	1.0e-130
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151885
Seq. ID	LIB3175-065-P1-K1-F1
Method	BLASTX

NCBI GI	g1669389
BLAST score	495
E value	4.0e-50
Match length	94
% identity	97
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	151886
Seq. ID	LIB3175-065-P1-K1-F10
Method	BLASTX
NCBI GI	g2275217
BLAST score	310
E value	2.0e-28
Match length	109
% identity	66
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	151887
Seq. ID	LIB3175-065-P1-K1-F11
Method	BLASTX
NCBI GI	g4220514
BLAST score	567
E value	1.0e-58
Match length	134
% identity	78
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	151888
Seq. ID	LIB3175-065-P1-K1-F12
Method	BLASTX
NCBI GI	g113024
BLAST score	622
E value	5.0e-65
Match length	125
% identity	100
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	151889
Seq. ID	LIB3175-065-P1-K1-F2
Method	BLASTX
NCBI GI	g2446981
BLAST score	554
E value	5.0e-57
Match length	109
% identity	98
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]

Seq. No.	151890
Seq. ID	LIB3175-065-P1-K1-F5
Method	BLASTX
NCBI GI	g99735
BLAST score	432
E value	9.0e-43

Match length	83
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	151891
Seq. ID	LIB3175-065-P1-K1-F6
Method	BLASTX
NCBI GI	g4467156
BLAST score	546
E value	4.0e-56
Match length	138
% identity	69
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	151892
Seq. ID	LIB3175-065-P1-K1-F7
Method	BLASTX
NCBI GI	g1170503
BLAST score	275
E value	7.0e-29
Match length	77
% identity	90
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	151893
Seq. ID	LIB3175-065-P1-K1-F8
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	151894
Seq. ID	LIB3175-065-P1-K1-F9
Method	BLASTX
NCBI GI	g1652105
BLAST score	185
E value	9.0e-14
Match length	55
% identity	58
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	151895
Seq. ID	LIB3175-065-P1-K1-G10
Method	BLASTX
NCBI GI	g1703108
BLAST score	644
E value	1.0e-67
Match length	122

% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	151896
Seq. ID	LIB3175-065-P1-K1-G11
Method	BLASTX
NCBI GI	g131289
BLAST score	697
E value	8.0e-74
Match length	131
% identity	100
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi_225285_prf__1211235W photosystem II 44kD protein [Nicotiana tabacum]

Seq. No.	151897
Seq. ID	LIB3175-065-P1-K1-G12
Method	BLASTN
NCBI GI	g2828185
BLAST score	312
E value	1.0e-175
Match length	396
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	151898
Seq. ID	LIB3175-065-P1-K1-G2
Method	BLASTX
NCBI GI	g2435515
BLAST score	366
E value	5.0e-35
Match length	70
% identity	97
NCBI Description	(AF024504) No definition line found [Arabidopsis thaliana]

Seq. No.	151899
Seq. ID	LIB3175-065-P1-K1-G3
Method	BLASTX
NCBI GI	g4539428
BLAST score	185
E value	9.0e-14
Match length	60
% identity	67
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	151900
Seq. ID	LIB3175-065-P1-K1-G4
Method	BLASTN
NCBI GI	g3985957
BLAST score	41

E value	3.0e-14
Match length	97
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	151901
Seq. ID	LIB3175-065-P1-K1-G5
Method	BLASTN
NCBI GI	g4510323
BLAST score	365
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	151902
Seq. ID	LIB3175-065-P1-K1-G6
Method	BLASTX
NCBI GI	g2252840
BLAST score	194
E value	6.0e-15
Match length	74
% identity	50
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	151903
Seq. ID	LIB3175-065-P1-K1-G8
Method	BLASTX
NCBI GI	g4262174
BLAST score	328
E value	1.0e-30
Match length	65
% identity	98
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	151904
Seq. ID	LIB3175-065-P1-K1-G9
Method	BLASTX
NCBI GI	g3149952
BLAST score	322
E value	7.0e-30
Match length	62
% identity	95
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	151905
Seq. ID	LIB3175-065-P1-K1-H1
Method	BLASTN
NCBI GI	g3869067
BLAST score	397
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	151906
Seq. ID	LIB3175-065-P1-K1-H10
Method	BLASTX
NCBI GI	g4115918
BLAST score	300
E value	3.0e-27
Match length	74
% identity	76
NCBI Description	(AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No.	151907
Seq. ID	LIB3175-065-P1-K1-H11
Method	BLASTX
NCBI GI	g2129640
BLAST score	701
E value	3.0e-74
Match length	138
% identity	99
NCBI Description	magnesium chelatase chain - Arabidopsis thaliana >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase subunit [Arabidopsis thaliana]

Seq. No.	151908
Seq. ID	LIB3175-065-P1-K1-H12
Method	BLASTX
NCBI GI	g82734
BLAST score	593
E value	1.0e-61
Match length	120
% identity	30
NCBI Description	ubiquitin precursor - maize (fragment) >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]

Seq. No.	151909
Seq. ID	LIB3175-065-P1-K1-H2
Method	BLASTN
NCBI GI	g4558586
BLAST score	97
E value	2.0e-47
Match length	251
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	151910
Seq. ID	LIB3175-065-P1-K1-H5
Method	BLASTN
NCBI GI	g2252823
BLAST score	313
E value	1.0e-176
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	151911
Seq. ID	LIB3175-065-P1-K1-H6
Method	BLASTX
NCBI GI	g4539340
BLAST score	166
E value	1.0e-11
Match length	50
% identity	72
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	151912
Seq. ID	LIB3175-065-P1-K1-H8
Method	BLASTX
NCBI GI	g4581146
BLAST score	566
E value	2.0e-58
Match length	116
% identity	98
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	151913
Seq. ID	LIB3175-065-P1-K1-H9
Method	BLASTX
NCBI GI	g4539408
BLAST score	172
E value	2.0e-12
Match length	72
% identity	53
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	151914
Seq. ID	LIB3175-066-P1-K1-A1
Method	BLASTX
NCBI GI	g1711036
BLAST score	289
E value	1.0e-33
Match length	93
% identity	77
NCBI Description	(U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No.	151915
Seq. ID	LIB3175-066-P1-K1-A10
Method	BLASTX
NCBI GI	g3212879
BLAST score	708
E value	4.0e-75
Match length	141
% identity	95
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	151916
Seq. ID	LIB3175-066-P1-K1-A12
Method	BLASTX
NCBI GI	g2146733

BLAST score	458
E value	8.0e-46
Match length	98
% identity	83
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	151917
Seq. ID	LIB3175-066-P1-K1-A2
Method	BLASTX
NCBI GI	g3851636
BLAST score	166
E value	1.0e-11
Match length	109
% identity	59
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	151918
Seq. ID	LIB3175-066-P1-K1-A3
Method	BLASTX
NCBI GI	g1710401
BLAST score	345
E value	2.0e-32
Match length	116
% identity	67
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]

Seq. No.	151919
Seq. ID	LIB3175-066-P1-K1-A4
Method	BLASTX
NCBI GI	g1346735
BLAST score	95
E value	3.0e-03
Match length	114
% identity	71
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_1076562_pir__S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No.	151920
Seq. ID	LIB3175-066-P1-K1-A5
Method	BLASTX
NCBI GI	g2498726
BLAST score	217
E value	2.0e-17
Match length	80
% identity	49
NCBI Description	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (OST5OP) >gi_1085153_pir__JC4132 oligosaccharyltransferase 50k chain - fruit fly (Drosophila melanogaster)

>gi_1019386_emb_CAA57525_ (X81999)
oligosaccharyltransferase subunit [Drosophila melanogaster]

Seq. No.	151921
Seq. ID	LIB3175-066-P1-K1-A6
Method	BLASTN
NCBI GI	g4580744
BLAST score	45
E value	4.0e-16
Match length	84
% identity	89
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	151922
Seq. ID	LIB3175-066-P1-K1-A7
Method	BLASTX
NCBI GI	g3860277
BLAST score	466
E value	5.0e-47
Match length	95
% identity	100
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	151923
Seq. ID	LIB3175-066-P1-K1-A8
Method	BLASTX
NCBI GI	g82441
BLAST score	363
E value	3.0e-35
Match length	67
% identity	97
NCBI Description	photosystem II chlorophyll a-binding protein psbC precursor - barley chloroplast

Seq. No.	151924
Seq. ID	LIB3175-066-P1-K1-B1
Method	BLASTX
NCBI GI	g3355468
BLAST score	422
E value	1.0e-41
Match length	110
% identity	84
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	151925
Seq. ID	LIB3175-066-P1-K1-B10
Method	BLASTN
NCBI GI	g3402671
BLAST score	386
E value	0.0e+00
Match length	425
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151926
Seq. ID	LIB3175-066-P1-K1-B11
Method	BLASTN
NCBI GI	g2924651
BLAST score	413
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	151927
Seq. ID	LIB3175-066-P1-K1-B12
Method	BLASTX
NCBI GI	g2246621
BLAST score	559
E value	1.0e-57
Match length	122
% identity	89
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	151928
Seq. ID	LIB3175-066-P1-K1-B2
Method	BLASTX
NCBI GI	g2645971
BLAST score	696
E value	1.0e-73
Match length	130
% identity	99
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	151929
Seq. ID	LIB3175-066-P1-K1-B5
Method	BLASTX
NCBI GI	g4589398
BLAST score	519
E value	6.0e-53
Match length	125
% identity	74
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	151930
Seq. ID	LIB3175-066-P1-K1-B6
Method	BLASTN
NCBI GI	g3402745
BLAST score	201
E value	1.0e-109
Match length	325
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No. 151931

Seq. ID	LIB3175-066-P1-K1-B7
Method	BLASTN
NCBI GI	g4756963
BLAST score	287
E value	1.0e-160
Match length	321
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	151932
Seq. ID	LIB3175-066-P1-K1-B9
Method	BLASTX
NCBI GI	g1109600
BLAST score	169
E value	2.0e-12
Match length	62
% identity	52
NCBI Description	(D16628) ATsEH [Arabidopsis thaliana] >gi_2760840 (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]

Seq. No.	151933
Seq. ID	LIB3175-066-P1-K1-C1
Method	BLASTN
NCBI GI	g4063730
BLAST score	390
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151934
Seq. ID	LIB3175-066-P1-K1-C10
Method	BLASTX
NCBI GI	g3183274
BLAST score	257
E value	3.0e-22
Match length	84
% identity	60
NCBI Description	HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I >gi_2239182_emb_CAB10102_ (Z97208) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	151935
Seq. ID	LIB3175-066-P1-K1-C11
Method	BLASTX
NCBI GI	g267069
BLAST score	558
E value	2.0e-57
Match length	103
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	151936
Seq. ID	LIB3175-066-P1-K1-C12
Method	BLASTN
NCBI GI	g4199934
BLAST score	257
E value	1.0e-142
Match length	368
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	151937
Seq. ID	LIB3175-066-P1-K1-C2
Method	BLASTN
NCBI GI	g4263586
BLAST score	183
E value	2.0e-98
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F28K20 sequence, complete sequence

Seq. No.	151938
Seq. ID	LIB3175-066-P1-K1-C3
Method	BLASTX
NCBI GI	g4741960
BLAST score	485
E value	6.0e-49
Match length	111
% identity	84
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	151939
Seq. ID	LIB3175-066-P1-K1-C4
Method	BLASTX
NCBI GI	g1619297
BLAST score	438
E value	2.0e-43
Match length	118
% identity	74
NCBI Description	(Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No.	151940
Seq. ID	LIB3175-066-P1-K1-C7
Method	BLASTN
NCBI GI	g4757395
BLAST score	242
E value	1.0e-133
Match length	414
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	151941
Seq. ID	LIB3175-066-P1-K1-C9
Method	BLASTX

NCBI GI	g4432856
BLAST score	755
E value	1.0e-80
Match length	139
% identity	100
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	151942
Seq. ID	LIB3175-066-P1-K1-D10
Method	BLASTN
NCBI GI	g4092472
BLAST score	205
E value	1.0e-111
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana BAC F1K3 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	151943
Seq. ID	LIB3175-066-P1-K1-D3
Method	BLASTX
NCBI GI	g320558
BLAST score	559
E value	1.0e-57
Match length	127
% identity	90
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	151944
Seq. ID	LIB3175-066-P1-K1-D4
Method	BLASTX
NCBI GI	g3193298
BLAST score	158
E value	1.0e-10
Match length	105
% identity	31
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	151945
Seq. ID	LIB3175-066-P1-K1-D5
Method	BLASTX
NCBI GI	g4539291
BLAST score	597
E value	4.0e-62
Match length	119
% identity	97
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	151946
Seq. ID	LIB3175-066-P1-K1-D6
Method	BLASTX
NCBI GI	g1914683
BLAST score	201
E value	1.0e-15
Match length	68
% identity	66

NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	151947
Seq. ID	LIB3175-066-P1-K1-D9
Method	BLASTX
NCBI GI	g2317731
BLAST score	533
E value	1.0e-54
Match length	120
% identity	81
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	151948
Seq. ID	LIB3175-066-P1-K1-E1
Method	BLASTX
NCBI GI	g4056506
BLAST score	302
E value	2.0e-27
Match length	122
% identity	46
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	151949
Seq. ID	LIB3175-066-P1-K1-E10
Method	BLASTX
NCBI GI	g4584523
BLAST score	676
E value	2.0e-71
Match length	130
% identity	100
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	151950
Seq. ID	LIB3175-066-P1-K1-E11
Method	BLASTN
NCBI GI	g3386593
BLAST score	194
E value	1.0e-105
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151951
Seq. ID	LIB3175-066-P1-K1-E2
Method	BLASTX
NCBI GI	g1173438
BLAST score	228
E value	8.0e-19
Match length	134
% identity	34
NCBI Description	DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA >gi_280609_pir__A36195 developmental protein sina - fruit fly (Drosophila melanogaster) >gi_158467 (M38384) SEVEN IN ABSTENTIA [Drosophila melanogaster]

Seq. No.	151952
Seq. ID	LIB3175-066-P1-K1-E3
Method	BLASTX
NCBI GI	g1170089
BLAST score	487
E value	2.0e-49
Match length	99
% identity	98
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	151953
Seq. ID	LIB3175-066-P1-K1-E4
Method	BLASTX
NCBI GI	g2129789
BLAST score	472
E value	2.0e-47
Match length	119
% identity	80
NCBI Description	biotin carboxyl carrier protein precursor (clone BP4) - rape >gi_1070006_emb_CAA62264_ (X90730) Biotin carboxyl carrier protein [Brassica napus] >gi_1589043_prf__2210244D Ac-CoA carboxylase:ISOTYPE=bp4 [Brassica napus]

Seq. No.	151954
Seq. ID	LIB3175-066-P1-K1-E5
Method	BLASTX
NCBI GI	g3377797
BLAST score	630
E value	6.0e-66
Match length	140
% identity	89
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	151955
Seq. ID	LIB3175-066-P1-K1-E6
Method	BLASTN
NCBI GI	g2914688
BLAST score	98
E value	1.0e-47
Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151956
Seq. ID	LIB3175-066-P1-K1-E9
Method	BLASTX
NCBI GI	g4758520

BLAST score	142
E value	7.0e-09
Match length	118
% identity	2
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	151957
Seq. ID	LIB3175-066-P1-K1-F1
Method	BLASTX
NCBI GI	g1076366
BLAST score	657
E value	4.0e-69
Match length	124
% identity	98
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	151958
Seq. ID	LIB3175-066-P1-K1-F10
Method	BLASTN
NCBI GI	g4572664
BLAST score	428
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	151959
Seq. ID	LIB3175-066-P1-K1-F11
Method	BLASTN
NCBI GI	g4510360
BLAST score	46
E value	1.0e-16
Match length	106
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	151960
Seq. ID	LIB3175-066-P1-K1-F12
Method	BLASTN
NCBI GI	g4371278
BLAST score	342
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151961
Seq. ID	LIB3175-066-P1-K1-F2

Method	BLASTX
NCBI GI	g1710780
BLAST score	505
E value	3.0e-51
Match length	128
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	151962
Seq. ID	LIB3175-066-P1-K1-F3
Method	BLASTX
NCBI GI	g4581109
BLAST score	662
E value	1.0e-69
Match length	139
% identity	91
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	151963
Seq. ID	LIB3175-066-P1-K1-F4
Method	BLASTX
NCBI GI	g3914468
BLAST score	320
E value	1.0e-29
Match length	105
% identity	62
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus carota]

Seq. No.	151964
Seq. ID	LIB3175-066-P1-K1-F5
Method	BLASTX
NCBI GI	g4455338
BLAST score	623
E value	4.0e-65
Match length	144
% identity	85
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	151965
Seq. ID	LIB3175-066-P1-K1-F6
Method	BLASTX
NCBI GI	g4193388
BLAST score	437
E value	3.0e-43
Match length	117
% identity	74
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	151966
Seq. ID	LIB3175-066-P1-K1-G1
Method	BLASTX

NCBI GI	g266731
BLAST score	233
E value	2.0e-19
Match length	79
% identity	59
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	151967
Seq. ID	LIB3175-066-P1-K1-G10
Method	BLASTX
NCBI GI	g1702987
BLAST score	565
E value	3.0e-58
Match length	124
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	151968
Seq. ID	LIB3175-066-P1-K1-G11
Method	BLASTN
NCBI GI	g4406790
BLAST score	71
E value	8.0e-32
Match length	217
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T1016 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151969
Seq. ID	LIB3175-066-P1-K1-G12
Method	BLASTX
NCBI GI	g1399380
BLAST score	647
E value	6.0e-68
Match length	138
% identity	85
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	151970
Seq. ID	LIB3175-066-P1-K1-G2
Method	BLASTN
NCBI GI	g4038029
BLAST score	236
E value	1.0e-130
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151971
Seq. ID	LIB3175-066-P1-K1-G3
Method	BLASTX
NCBI GI	g2497753
BLAST score	201
E value	8.0e-16
Match length	81
% identity	44
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	151972
Seq. ID	LIB3175-066-P1-K1-G5
Method	BLASTN
NCBI GI	g3659491
BLAST score	172
E value	7.0e-92
Match length	382
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	151973
Seq. ID	LIB3175-066-P1-K1-G6
Method	BLASTX
NCBI GI	g2244971
BLAST score	539
E value	3.0e-55
Match length	135
% identity	80
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151974
Seq. ID	LIB3175-066-P1-K1-G7
Method	BLASTN
NCBI GI	g3702739
BLAST score	126
E value	2.0e-64
Match length	177
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	151975
Seq. ID	LIB3175-066-P1-K1-G8
Method	BLASTX
NCBI GI	g4454032
BLAST score	272
E value	5.0e-24
Match length	81
% identity	59
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	151976
Seq. ID	LIB3175-066-P1-K1-G9
Method	BLASTX

NCBI GI	g2342722
BLAST score	579
E value	5.0e-60
Match length	125
% identity	92
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	151977
Seq. ID	LIB3175-066-P1-K1-H10
Method	BLASTN
NCBI GI	g4468103
BLAST score	415
E value	0.0e+00
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	151978
Seq. ID	LIB3175-066-P1-K1-H12
Method	BLASTX
NCBI GI	g2947067
BLAST score	302
E value	2.0e-27
Match length	114
% identity	67
NCBI Description	(AC002521) hypothetical protein [Arabidopsis thaliana]

Seq. No.	151979
Seq. ID	LIB3175-066-P1-K1-H2
Method	BLASTX
NCBI GI	g3928103
BLAST score	604
E value	6.0e-63
Match length	133
% identity	90
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	151980
Seq. ID	LIB3175-066-P1-K1-H3
Method	BLASTX
NCBI GI	g2119846
BLAST score	715
E value	6.0e-76
Match length	133
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	151981
Seq. ID	LIB3175-066-P1-K1-H5

Method	BLASTN
NCBI GI	g2264309
BLAST score	37
E value	3.0e-11
Match length	217
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	151982
Seq. ID	LIB3175-066-P1-K1-H6
Method	BLASTX
NCBI GI	g1710780
BLAST score	514
E value	3.0e-52
Match length	134
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	151983
Seq. ID	LIB3175-066-P1-K1-H8
Method	BLASTN
NCBI GI	g4584841
BLAST score	409
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	151984
Seq. ID	LIB3175-066-P1-K1-H9
Method	BLASTN
NCBI GI	g2828183
BLAST score	260
E value	1.0e-144
Match length	383
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	151985
Seq. ID	LIB3175-068-P1-K1-A2
Method	BLASTN
NCBI GI	g2656029
BLAST score	147
E value	5.0e-77
Match length	311
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	151986
Seq. ID	LIB3175-068-P1-K1-A3
Method	BLASTX

NCBI GI	g1209756
BLAST score	46
E value	9.0e-43
Match length	137
% identity	63
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	151987
Seq. ID	LIB3175-068-P1-K1-A5
Method	BLASTX
NCBI GI	g3337356
BLAST score	584
E value	2.0e-60
Match length	116
% identity	99
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	151988
Seq. ID	LIB3175-068-P1-K1-A6
Method	BLASTX
NCBI GI	g3757524
BLAST score	533
E value	2.0e-54
Match length	143
% identity	78
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	151989
Seq. ID	LIB3175-068-P1-K1-A7
Method	BLASTN
NCBI GI	g3355463
BLAST score	208
E value	1.0e-113
Match length	289
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	151990
Seq. ID	LIB3175-068-P1-K1-A8
Method	BLASTX
NCBI GI	g4455353
BLAST score	609
E value	2.0e-63
Match length	147
% identity	84
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	151991
Seq. ID	LIB3175-068-P1-K1-A9
Method	BLASTX
NCBI GI	g4580394
BLAST score	262
E value	8.0e-23
Match length	107

% identity	44
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	151992
Seq. ID	LIB3175-068-P1-K1-B10
Method	BLASTX
NCBI GI	g4154281
BLAST score	431
E value	1.0e-42
Match length	102
% identity	77
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	151993
Seq. ID	LIB3175-068-P1-K1-B11
Method	BLASTX
NCBI GI	g4154281
BLAST score	432
E value	1.0e-42
Match length	103
% identity	77
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	151994
Seq. ID	LIB3175-068-P1-K1-B12
Method	BLASTX
NCBI GI	g2832629
BLAST score	194
E value	9.0e-15
Match length	152
% identity	35
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	151995
Seq. ID	LIB3175-068-P1-K1-B2
Method	BLASTX
NCBI GI	g267073
BLAST score	67
E value	1.0e-62
Match length	136
% identity	87
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	151996
Seq. ID	LIB3175-068-P1-K1-B3
Method	BLASTX
NCBI GI	g3335340
BLAST score	329
E value	5.0e-31
Match length	80
% identity	80
NCBI Description	(AC004512) Strong similarity to xylglucan

	endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]
Seq. No.	151997
Seq. ID	LIB3175-068-P1-K1-B4
Method	BLASTN
NCBI GI	g3510343
BLAST score	408
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.	151998
Seq. ID	LIB3175-068-P1-K1-B5
Method	BLASTX
NCBI GI	g135467
BLAST score	679
E value	1.0e-71
Match length	130
% identity	95
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]
Seq. No.	151999
Seq. ID	LIB3175-068-P1-K1-B6
Method	BLASTX
NCBI GI	g4220527
BLAST score	152
E value	8.0e-10
Match length	44
% identity	64
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]
Seq. No.	152000
Seq. ID	LIB3175-068-P1-K1-B7
Method	BLASTX
NCBI GI	g1175013
BLAST score	608
E value	3.0e-63
Match length	137
% identity	88
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]
Seq. No.	152001
Seq. ID	LIB3175-068-P1-K1-B8
Method	BLASTX
NCBI GI	g4741952
BLAST score	577
E value	9.0e-60

Match length	113
% identity	72
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	152002
Seq. ID	LIB3175-068-P1-K1-B9
Method	BLASTX
NCBI GI	g135467
BLAST score	268
E value	4.0e-24
Match length	53
% identity	91
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	152003
Seq. ID	LIB3175-068-P1-K1-C11
Method	BLASTX
NCBI GI	g2130028
BLAST score	199
E value	7.0e-29
Match length	87
% identity	74
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	152004
Seq. ID	LIB3175-068-P1-K1-C12
Method	BLASTN
NCBI GI	g3426061
BLAST score	68
E value	7.0e-30
Match length	224
% identity	83
NCBI Description	Arabidopsis thaliana mRNA for monooxygenase

Seq. No.	152005
Seq. ID	LIB3175-068-P1-K1-C2
Method	BLASTX
NCBI GI	g132110
BLAST score	690
E value	6.0e-73
Match length	132
% identity	97
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	152006
Seq. ID	LIB3175-068-P1-K1-C4
Method	BLASTN
NCBI GI	g2264318

BLAST score	259
E value	1.0e-144
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	152007
Seq. ID	LIB3175-068-P1-K1-C5
Method	BLASTX
NCBI GI	g3341697
BLAST score	399
E value	8.0e-39
Match length	104
% identity	71
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152008
Seq. ID	LIB3175-068-P1-K1-C6
Method	BLASTX
NCBI GI	g2288887
BLAST score	512
E value	5.0e-52
Match length	98
% identity	100
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	152009
Seq. ID	LIB3175-068-P1-K1-C9
Method	BLASTX
NCBI GI	g1402904
BLAST score	679
E value	1.0e-71
Match length	140
% identity	95
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	152010
Seq. ID	LIB3175-068-P1-K1-D10
Method	BLASTN
NCBI GI	g2462076
BLAST score	373
E value	0.0e+00
Match length	428
% identity	97
NCBI Description	A.thaliana mRNA for oxa1-like gene

Seq. No.	152011
Seq. ID	LIB3175-068-P1-K1-D11
Method	BLASTX
NCBI GI	g3355471
BLAST score	752
E value	3.0e-80

Match length	150
% identity	95
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	152012
Seq. ID	LIB3175-068-P1-K1-D12
Method	BLASTX
NCBI GI	g4585935
BLAST score	720
E value	2.0e-76
Match length	136
% identity	99
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	152013
Seq. ID	LIB3175-068-P1-K1-D2
Method	BLASTX
NCBI GI	g1652892
BLAST score	195
E value	3.0e-15
Match length	76
% identity	26
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	152014
Seq. ID	LIB3175-068-P1-K1-D3
Method	BLASTX
NCBI GI	g132074
BLAST score	569
E value	7.0e-59
Match length	105
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	152015
Seq. ID	LIB3175-068-P1-K1-D4
Method	BLASTX
NCBI GI	g2288887
BLAST score	502
E value	7.0e-51
Match length	96
% identity	100
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	152016
Seq. ID	LIB3175-068-P1-K1-D6
Method	BLASTX

NCBI GI	g2739373
BLAST score	245
E value	9.0e-21
Match length	131
% identity	38
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	152017
Seq. ID	LIB3175-068-P1-K1-D7
Method	BLASTX
NCBI GI	g2462834
BLAST score	186
E value	7.0e-14
Match length	99
% identity	40
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152018
Seq. ID	LIB3175-068-P1-K1-D8
Method	BLASTX
NCBI GI	g4185505
BLAST score	448
E value	1.0e-44
Match length	112
% identity	77
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	152019
Seq. ID	LIB3175-068-P1-K1-D9
Method	BLASTN
NCBI GI	g2760316
BLAST score	219
E value	1.0e-120
Match length	291
% identity	94
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152020
Seq. ID	LIB3175-068-P1-K1-E1
Method	BLASTX
NCBI GI	g1402904
BLAST score	524
E value	1.0e-53
Match length	110
% identity	93
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	152021
Seq. ID	LIB3175-068-P1-K1-E10
Method	BLASTX
NCBI GI	g1082798
BLAST score	200
E value	1.0e-15
Match length	98

% identity	42
NCBI Description	spliceosome-associated protein SAP 61 - human >gi_508723 (U08815) SAP 61 [Homo sapiens]

Seq. No.	152022
Seq. ID	LIB3175-068-P1-K1-E12
Method	BLASTX
NCBI GI	g2459445
BLAST score	202
E value	1.0e-15
Match length	57
% identity	32
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	152023
Seq. ID	LIB3175-068-P1-K1-E2
Method	BLASTX
NCBI GI	g2702376
BLAST score	259
E value	2.0e-22
Match length	100
% identity	48
NCBI Description	(AF038605) Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis elegans]

Seq. No.	152024
Seq. ID	LIB3175-068-P1-K1-E3
Method	BLASTX
NCBI GI	g3461848
BLAST score	642
E value	2.0e-67
Match length	143
% identity	90
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	152025
Seq. ID	LIB3175-068-P1-K1-E4
Method	BLASTX
NCBI GI	g3915826
BLAST score	579
E value	6.0e-60
Match length	134
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	152026
Seq. ID	LIB3175-068-P1-K1-E5
Method	BLASTX
NCBI GI	g2827556
BLAST score	613
E value	7.0e-64

Match length	123
% identity	100
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	152027
Seq. ID	LIB3175-068-P1-K1-E6
Method	BLASTN
NCBI GI	g4544435
BLAST score	402
E value	0.0e+00
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	152028
Seq. ID	LIB3175-068-P1-K1-E7
Method	BLASTX
NCBI GI	g2702376
BLAST score	262
E value	9.0e-23
Match length	100
% identity	49
NCBI Description	(AF038605) Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis elegans]

Seq. No.	152029
Seq. ID	LIB3175-068-P1-K1-E8
Method	BLASTX
NCBI GI	g1304227
BLAST score	447
E value	2.0e-44
Match length	138
% identity	57
NCBI Description	(D63781) Epoxide hydrolase [Glycine max] >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase [Glycine max]

Seq. No.	152030
Seq. ID	LIB3175-068-P1-K1-E9
Method	BLASTN
NCBI GI	g4589419
BLAST score	296
E value	1.0e-166
Match length	355
% identity	58
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	152031
Seq. ID	LIB3175-068-P1-K1-F1
Method	BLASTX

NCBI GI	g4567256
BLAST score	220
E value	7.0e-18
Match length	40
% identity	97
NCBI Description	(AC007070) putative 60S ribosomal protein L39 [Arabidopsis thaliana]

Seq. No.	152032
Seq. ID	LIB3175-068-P1-K1-F10
Method	BLASTN
NCBI GI	g3540210
BLAST score	133
E value	9.0e-69
Match length	235
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152033
Seq. ID	LIB3175-068-P1-K1-F12
Method	BLASTX
NCBI GI	g2244760
BLAST score	433
E value	7.0e-43
Match length	124
% identity	67
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	152034
Seq. ID	LIB3175-068-P1-K1-F3
Method	BLASTX
NCBI GI	g2605769
BLAST score	199
E value	1.0e-18
Match length	98
% identity	63
NCBI Description	(AF027288) NADH dehydrogenase [Olea europaea]

Seq. No.	152035
Seq. ID	LIB3175-068-P1-K1-F4
Method	BLASTX
NCBI GI	g4589398
BLAST score	343
E value	2.0e-32
Match length	75
% identity	81
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	152036
Seq. ID	LIB3175-068-P1-K1-F5
Method	BLASTX
NCBI GI	g4115377
BLAST score	289
E value	3.0e-27
Match length	101
% identity	69

NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	152037
Seq. ID	LIB3175-068-P1-K1-F7
Method	BLASTX
NCBI GI	g3641837
BLAST score	512
E value	4.0e-52
Match length	106
% identity	96
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	152038
Seq. ID	LIB3175-068-P1-K1-F8
Method	BLASTX
NCBI GI	g2160158
BLAST score	330
E value	6.0e-31
Match length	115
% identity	65
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	152039
Seq. ID	LIB3175-068-P1-K1-F9
Method	BLASTX
NCBI GI	g2982303
BLAST score	617
E value	2.0e-64
Match length	137
% identity	81
NCBI Description	(AF051236) hypothetical protein [Picea mariana]

Seq. No.	152040
Seq. ID	LIB3175-068-P1-K1-G10
Method	BLASTN
NCBI GI	g4490734
BLAST score	117
E value	2.0e-59
Match length	153
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	152041
Seq. ID	LIB3175-068-P1-K1-G11
Method	BLASTX
NCBI GI	g4454051
BLAST score	661
E value	1.0e-69
Match length	130
% identity	98
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	152042
Seq. ID	LIB3175-068-P1-K1-G12
Method	BLASTX
NCBI GI	g4725950
BLAST score	282
E value	5.0e-25
Match length	129
% identity	50
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana] >gi_4725951_emb_CAB41722.1_ (AL049730) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	152043
Seq. ID	LIB3175-068-P1-K1-G4
Method	BLASTX
NCBI GI	g3150414
BLAST score	515
E value	2.0e-52
Match length	127
% identity	81
NCBI Description	(AC004165) AtRanBP1b protein [Arabidopsis thaliana]

Seq. No.	152044
Seq. ID	LIB3175-068-P1-K1-G5
Method	BLASTN
NCBI GI	g3250673
BLAST score	211
E value	1.0e-115
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	152045
Seq. ID	LIB3175-068-P1-K1-G6
Method	BLASTX
NCBI GI	g4559396
BLAST score	156
E value	2.0e-10
Match length	42
% identity	71
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	152046
Seq. ID	LIB3175-068-P1-K1-G7
Method	BLASTX
NCBI GI	g120667
BLAST score	463
E value	2.0e-46
Match length	109
% identity	84
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Seq. No.	152047
Seq. ID	LIB3175-068-P1-K1-G8
Method	BLASTX
NCBI GI	g2760606
BLAST score	286
E value	1.0e-25
Match length	57
% identity	100
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	152048
Seq. ID	LIB3175-068-P1-K1-G9
Method	BLASTX
NCBI GI	g1370176
BLAST score	337
E value	1.0e-31
Match length	67
% identity	100
NCBI Description	(Z73937) RAB2A [Lotus japonicus]

Seq. No.	152049
Seq. ID	LIB3175-068-P1-K1-H10
Method	BLASTX
NCBI GI	g4455206
BLAST score	316
E value	3.0e-29
Match length	88
% identity	68
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	152050
Seq. ID	LIB3175-068-P1-K1-H11
Method	BLASTX
NCBI GI	g4689386
BLAST score	289
E value	5.0e-26
Match length	78
% identity	72
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	152051
Seq. ID	LIB3175-068-P1-K1-H12
Method	BLASTX
NCBI GI	g2499327
BLAST score	410
E value	3.0e-40
Match length	111
% identity	76

NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	152052
Seq. ID	LIB3175-068-P1-K1-H2
Method	BLASTX
NCBI GI	g974294
BLAST score	238
E value	6.0e-20
Match length	92
% identity	54
NCBI Description	(U31309) LP6 [Pinus taeda]

Seq. No.	152053
Seq. ID	LIB3175-068-P1-K1-H3
Method	BLASTX
NCBI GI	g1170660
BLAST score	674
E value	4.0e-71
Match length	138
% identity	99
NCBI Description	MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]

Seq. No.	152054
Seq. ID	LIB3175-068-P1-K1-H4
Method	BLASTX
NCBI GI	g2446981
BLAST score	636
E value	1.0e-66
Match length	127
% identity	95
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]

Seq. No.	152055
Seq. ID	LIB3175-068-P1-K1-H6
Method	BLASTX
NCBI GI	g2088654
BLAST score	268
E value	4.0e-35
Match length	111
% identity	77
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	152056
Seq. ID	LIB3175-070-P1-K-A1
Method	BLASTX
NCBI GI	g1585128
BLAST score	288

E value	6.0e-26
Match length	122
% identity	36
NCBI Description	isopeptidase T [Homo sapiens]

Seq. No.	152057
Seq. ID	LIB3175-070-P1-K-A10
Method	BLASTX
NCBI GI	g3941289
BLAST score	248
E value	3.0e-21
Match length	105
% identity	51
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	152058
Seq. ID	LIB3175-070-P1-K-A11
Method	BLASTX
NCBI GI	g3342556
BLAST score	569
E value	8.0e-59
Match length	131
% identity	42
NCBI Description	(AF077528) importin alpha [Arabidopsis thaliana]

Seq. No.	152059
Seq. ID	LIB3175-070-P1-K-A2
Method	BLASTX
NCBI GI	g3421123
BLAST score	521
E value	3.0e-53
Match length	102
% identity	99
NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	152060
Seq. ID	LIB3175-070-P1-K-A3
Method	BLASTN
NCBI GI	g4519193
BLAST score	107
E value	3.0e-53
Match length	319
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	152061
Seq. ID	LIB3175-070-P1-K-A4
Method	BLASTX
NCBI GI	g99681
BLAST score	597
E value	4.0e-62
Match length	135
% identity	89
NCBI Description	cold-regulated protein cor47 - Arabidopsis thaliana (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA

regulated gene [Arabidopsis thaliana]

Seq. No.	152062
Seq. ID	LIB3175-070-P1-K-A5
Method	BLASTX
NCBI GI	g3128192
BLAST score	514
E value	2.0e-52
Match length	140
% identity	69
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	152063
Seq. ID	LIB3175-070-P1-K-A6
Method	BLASTX
NCBI GI	g115783
BLAST score	489
E value	3.0e-49
Match length	123
% identity	85
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152064
Seq. ID	LIB3175-070-P1-K-B1
Method	BLASTX
NCBI GI	g115385
BLAST score	623
E value	4.0e-65
Match length	121
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	152065
Seq. ID	LIB3175-070-P1-K-B10
Method	BLASTN
NCBI GI	g2828182
BLAST score	148
E value	2.0e-77
Match length	421
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	152066
Seq. ID	LIB3175-070-P1-K-B11
Method	BLASTX
NCBI GI	g3024434
BLAST score	508
E value	1.0e-51
Match length	122
% identity	85
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_
(D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	152067
Seq. ID	LIB3175-070-P1-K-B5
Method	BLASTX
NCBI GI	g3953471
BLAST score	687
E value	1.0e-72
Match length	139
% identity	91
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	152068
Seq. ID	LIB3175-070-P1-K-B6
Method	BLASTX
NCBI GI	g4586265
BLAST score	475
E value	9.0e-48
Match length	113
% identity	78
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152069
Seq. ID	LIB3175-070-P1-K-B8
Method	BLASTX
NCBI GI	g4585935
BLAST score	173
E value	9.0e-13
Match length	58
% identity	69
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	152070
Seq. ID	LIB3175-070-P1-K-B9
Method	BLASTX
NCBI GI	g112682
BLAST score	371
E value	7.0e-36
Match length	87
% identity	86
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	152071
Seq. ID	LIB3175-070-P1-K-C1
Method	BLASTX
NCBI GI	g3329463
BLAST score	231
E value	3.0e-31
Match length	110
% identity	65

NCBI Description	(AF061515) ferroxin-dependent glutamate synthase precursor [Spinacia oleracea]

Seq. No.	152072
Seq. ID	LIB3175-070-P1-K-C10
Method	BLASTN
NCBI GI	g3449330
BLAST score	145
E value	8.0e-76
Match length	312
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	152073
Seq. ID	LIB3175-070-P1-K-C11
Method	BLASTX
NCBI GI	g2335099
BLAST score	450
E value	7.0e-45
Match length	133
% identity	32
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	152074
Seq. ID	LIB3175-070-P1-K-C12
Method	BLASTN
NCBI GI	g4415928
BLAST score	62
E value	3.0e-26
Match length	162
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152075
Seq. ID	LIB3175-070-P1-K-C4
Method	BLASTX
NCBI GI	g4454464
BLAST score	513
E value	3.0e-52
Match length	118
% identity	84
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	152076
Seq. ID	LIB3175-070-P1-K-C6
Method	BLASTN
NCBI GI	g2244991
BLAST score	265
E value	1.0e-147
Match length	417
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152077

Seq. ID	LIB3175-070-P1-K-C7
Method	BLASTX
NCBI GI	g4581114
BLAST score	491
E value	1.0e-49
Match length	102
% identity	95
NCBI Description	(AC005825) putative HesB-like protein;required for efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	152078
Seq. ID	LIB3175-070-P1-K-D1
Method	BLASTX
NCBI GI	g3024434
BLAST score	503
E value	5.0e-51
Match length	124
% identity	83
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	152079
Seq. ID	LIB3175-070-P1-K-D10
Method	BLASTN
NCBI GI	g4580745
BLAST score	374
E value	0.0e+00
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	152080
Seq. ID	LIB3175-070-P1-K-D11
Method	BLASTN
NCBI GI	g3128142
BLAST score	328
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	152081
Seq. ID	LIB3175-070-P1-K-D12
Method	BLASTX
NCBI GI	g114591
BLAST score	579
E value	5.0e-60
Match length	124
% identity	94
NCBI Description	ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903 H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_ (X12889) Cf1 ATPase epsilon subunit (AA 1 - 132)

[Arabidopsis thaliana]

Seq. No.	152082
Seq. ID	LIB3175-070-P1-K-D2
Method	BLASTX
NCBI GI	g99735
BLAST score	346
E value	1.0e-32
Match length	76
% identity	87
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	152083
Seq. ID	LIB3175-070-P1-K-D3
Method	BLASTX
NCBI GI	g4468979
BLAST score	282
E value	2.0e-44
Match length	101
% identity	86
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	152084
Seq. ID	LIB3175-070-P1-K-D5
Method	BLASTN
NCBI GI	g4757405
BLAST score	284
E value	1.0e-158
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	152085
Seq. ID	LIB3175-070-P1-K-D6
Method	BLASTN
NCBI GI	g2656029
BLAST score	77
E value	4.0e-35
Match length	406
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	152086
Seq. ID	LIB3175-070-P1-K-D7
Method	BLASTX
NCBI GI	g3901294
BLAST score	379
E value	9.0e-37
Match length	100
% identity	84
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	152087
Seq. ID	LIB3175-070-P1-K-E1

Method	BLASTX
NCBI GI	g2130521
BLAST score	675
E value	3.0e-71
Match length	137
% identity	92
NCBI Description	(U31565) reversibly glycosylatable polypeptide [Pisum sativum]

Seq. No.	152088
Seq. ID	LIB3175-070-P1-K-E10
Method	BLASTN
NCBI GI	g4159705
BLAST score	62
E value	2.0e-26
Match length	101
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	152089
Seq. ID	LIB3175-070-P1-K-E11
Method	BLASTN
NCBI GI	g3426033
BLAST score	119
E value	3.0e-60
Match length	413
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152090
Seq. ID	LIB3175-070-P1-K-E12
Method	BLASTX
NCBI GI	g3426039
BLAST score	253
E value	9.0e-22
Match length	76
% identity	66
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	152091
Seq. ID	LIB3175-070-P1-K-E2
Method	BLASTX
NCBI GI	g349379
BLAST score	450
E value	7.0e-45
Match length	129
% identity	75
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	152092
Seq. ID	LIB3175-070-P1-K-E3
Method	BLASTN
NCBI GI	g3763915
BLAST score	302
E value	1.0e-169

Match length	378
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152093
Seq. ID	LIB3175-070-P1-K-E5
Method	BLASTX
NCBI GI	g4567216
BLAST score	270
E value	9.0e-24
Match length	107
% identity	59
NCBI Description	(AC007113) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152094
Seq. ID	LIB3175-070-P1-K-E6
Method	BLASTX
NCBI GI	g115783
BLAST score	561
E value	7.0e-58
Match length	110
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152095
Seq. ID	LIB3175-070-P1-K-E7
Method	BLASTN
NCBI GI	g3241926
BLAST score	139
E value	3.0e-72
Match length	307
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	152096
Seq. ID	LIB3175-070-P1-K-E8
Method	BLASTX
NCBI GI	g2739366
BLAST score	263
E value	6.0e-23
Match length	125
% identity	46
NCBI Description	(AC002505) SF16 like protein [Arabidopsis thaliana]

Seq. No.	152097
Seq. ID	LIB3175-070-P1-K-E9
Method	BLASTN
NCBI GI	g3510343
BLAST score	318
E value	1.0e-179
Match length	366
% identity	97

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	152098
Seq. ID	LIB3175-070-P1-K-F1
Method	BLASTX
NCBI GI	g2462746
BLAST score	553
E value	6.0e-57
Match length	124
% identity	87
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	152099
Seq. ID	LIB3175-070-P1-K-F10
Method	BLASTX
NCBI GI	g3746067
BLAST score	476
E value	5.0e-48
Match length	123
% identity	79
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152100
Seq. ID	LIB3175-070-P1-K-F12
Method	BLASTX
NCBI GI	g445612
BLAST score	476
E value	6.0e-48
Match length	113
% identity	83
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	152101
Seq. ID	LIB3175-070-P1-K-F2
Method	BLASTX
NCBI GI	g3695383
BLAST score	514
E value	2.0e-52
Match length	111
% identity	90
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	152102
Seq. ID	LIB3175-070-P1-K-F3
Method	BLASTX
NCBI GI	g1707657
BLAST score	141
E value	1.0e-08
Match length	76
% identity	49
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	152103

Seq. ID	LIB3175-070-P1-K-F5
Method	BLASTX
NCBI GI	g2583125
BLAST score	265
E value	3.0e-23
Match length	102
% identity	60
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	152104
Seq. ID	LIB3175-070-P1-K-F6
Method	BLASTX
NCBI GI	g4586263
BLAST score	519
E value	5.0e-53
Match length	109
% identity	93
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152105
Seq. ID	LIB3175-070-P1-K-F7
Method	BLASTX
NCBI GI	g65613
BLAST score	312
E value	1.0e-34
Match length	104
% identity	74
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - garden pea chloroplast >gi_552817 (K01516) cytochrome f [Pisum sativum]

Seq. No.	152106
Seq. ID	LIB3175-070-P1-K-F8
Method	BLASTN
NCBI GI	g4589411
BLAST score	233
E value	1.0e-128
Match length	347
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	152107
Seq. ID	LIB3175-070-P1-K-G1
Method	BLASTX
NCBI GI	g4512651
BLAST score	294
E value	1.0e-26
Match length	129
% identity	46
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	152108
Seq. ID	LIB3175-070-P1-K-G12
Method	BLASTX

NCBI GI	gi362007
BLAST score	720
E value	2.0e-76
Match length	137
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	152109
Seq. ID	LIB3175-070-P1-K-G3
Method	BLASTX
NCBI GI	g70642
BLAST score	104
E value	1.0e-55
Match length	119
% identity	20
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	152110
Seq. ID	LIB3175-070-P1-K-G4
Method	BLASTX
NCBI GI	g464987
BLAST score	641
E value	3.0e-67
Match length	119
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	152111
Seq. ID	LIB3175-070-P1-K-G5
Method	BLASTN
NCBI GI	g4159704
BLAST score	372
E value	0.0e+00
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	152112
Seq. ID	LIB3175-070-P1-K-G6
Method	BLASTN
NCBI GI	g4159703
BLAST score	304
E value	1.0e-170
Match length	324

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	152113
Seq. ID	LIB3175-070-P1-K-G8
Method	BLASTX
NCBI GI	g3894178
BLAST score	247
E value	4.0e-21
Match length	57
% identity	82
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	152114
Seq. ID	LIB3175-070-P1-K-G9
Method	BLASTN
NCBI GI	g4455262
BLAST score	96
E value	9.0e-47
Match length	229
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	152115
Seq. ID	LIB3175-070-P1-K-H10
Method	BLASTN
NCBI GI	g4206764
BLAST score	387
E value	0.0e+00
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	152116
Seq. ID	LIB3175-070-P1-K-H12
Method	BLASTX
NCBI GI	g2499706
BLAST score	191
E value	2.0e-14
Match length	40
% identity	93
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1297302 (U36381) phospholipase D [Arabidopsis thaliana]

Seq. No.	152117
Seq. ID	LIB3175-070-P1-K-H2
Method	BLASTX
NCBI GI	g4490329
BLAST score	379
E value	2.0e-36
Match length	101
% identity	72

NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	152118
Seq. ID	LIB3175-070-P1-K-H4
Method	BLASTX
NCBI GI	g1200256
BLAST score	190
E value	2.0e-14
Match length	122
% identity	35
NCBI Description	(X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No.	152119
Seq. ID	LIB3175-070-P1-K-H5
Method	BLASTX
NCBI GI	g2244806
BLAST score	187
E value	5.0e-14
Match length	105
% identity	43
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152120
Seq. ID	LIB3175-070-P1-K-H7
Method	BLASTN
NCBI GI	g3510347
BLAST score	201
E value	1.0e-109
Match length	395
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	152121
Seq. ID	LIB3175-070-P1-K-H8
Method	BLASTX
NCBI GI	g2829899
BLAST score	268
E value	1.0e-23
Match length	103
% identity	54
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	152122
Seq. ID	LIB3175-070-P1-K-H9
Method	BLASTX
NCBI GI	g113026
BLAST score	90
E value	1.0e-31
Match length	90
% identity	66
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica

napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	152123
Seq. ID	LIB3175-075-P1-K1-A1
Method	BLASTX
NCBI GI	g114330
BLAST score	350
E value	3.0e-33
Match length	98
% identity	73
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35) type 1, plasma membrane - Arabidopsis thaliana >gi_166746 (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]

Seq. No.	152124
Seq. ID	LIB3175-075-P1-K1-A10
Method	BLASTX
NCBI GI	g3386565
BLAST score	202
E value	5.0e-16
Match length	100
% identity	48
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	152125
Seq. ID	LIB3175-075-P1-K1-A11
Method	BLASTN
NCBI GI	g4159705
BLAST score	115
E value	5.0e-58
Match length	284
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	152126
Seq. ID	LIB3175-075-P1-K1-A12
Method	BLASTX
NCBI GI	g112681
BLAST score	352
E value	1.0e-33
Match length	91
% identity	76
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	152127
Seq. ID	LIB3175-075-P1-K1-A3
Method	BLASTX

NCBI GI	g282865
BLAST score	543
E value	8.0e-56
Match length	111
% identity	67
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	152128
Seq. ID	LIB3175-075-P1-K1-A4
Method	BLASTN
NCBI GI	g4567300
BLAST score	164
E value	3.0e-87
Match length	326
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	152129
Seq. ID	LIB3175-075-P1-K1-A6
Method	BLASTX
NCBI GI	g3639089
BLAST score	499
E value	1.0e-50
Match length	105
% identity	90
NCBI Description	(AF090445) phospholipase D1 [Brassica oleracea] >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1 [Brassica oleracea var. capitata]

Seq. No.	152130
Seq. ID	LIB3175-075-P1-K1-A8
Method	BLASTN
NCBI GI	g3281847
BLAST score	214
E value	1.0e-117
Match length	258
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	152131
Seq. ID	LIB3175-075-P1-K1-B1
Method	BLASTX
NCBI GI	g3859606
BLAST score	446
E value	2.0e-44
Match length	108
% identity	83
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	152132
Seq. ID	LIB3175-075-P1-K1-B2
Method	BLASTN
NCBI GI	g4191760
BLAST score	43
E value	7.0e-15
Match length	294
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	152133
Seq. ID	LIB3175-075-P1-K1-B3
Method	BLASTN
NCBI GI	g3492855
BLAST score	51
E value	1.0e-19
Match length	234
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	152134
Seq. ID	LIB3175-075-P1-K1-B5
Method	BLASTX
NCBI GI	g1705677
BLAST score	524
E value	2.0e-53
Match length	106
% identity	98
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	152135
Seq. ID	LIB3175-075-P1-K1-B6
Method	BLASTX
NCBI GI	g2262167
BLAST score	572
E value	3.0e-59
Match length	111
% identity	98
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	152136
Seq. ID	LIB3175-075-P1-K1-B7
Method	BLASTX
NCBI GI	g2213583
BLAST score	338
E value	7.0e-32
Match length	95
% identity	78
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 152137

Seq. ID	LIB3175-075-P1-K1-B8
Method	BLASTX
NCBI GI	g3292833
BLAST score	354
E value	1.0e-33
Match length	101
% identity	60
NCBI Description	(AL031018) putative membrane protein [Arabidopsis thaliana]

Seq. No.	152138
Seq. ID	LIB3175-075-P1-K1-B9
Method	BLASTN
NCBI GI	g3063690
BLAST score	277
E value	1.0e-154
Match length	285
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	152139
Seq. ID	LIB3175-075-P1-K1-C1
Method	BLASTN
NCBI GI	g3128135
BLAST score	161
E value	3.0e-85
Match length	407
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	152140
Seq. ID	LIB3175-075-P1-K1-C10
Method	BLASTX
NCBI GI	g1351221
BLAST score	314
E value	4.0e-29
Match length	58
% identity	100
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945085 (U31096) transcription factor TFIIB [Arabidopsis thaliana] >gi_2618697 (AC002510) transcription factor TFIIB [Arabidopsis thaliana]

Seq. No.	152141
Seq. ID	LIB3175-075-P1-K1-C11
Method	BLASTN
NCBI GI	g2651294
BLAST score	317
E value	1.0e-178
Match length	358
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152142
Seq. ID	LIB3175-075-P1-K1-C12

Method	BLASTX
NCBI GI	g2342727
BLAST score	548
E value	2.0e-56
Match length	103
% identity	97
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152143
Seq. ID	LIB3175-075-P1-K1-C2
Method	BLASTN
NCBI GI	g4538895
BLAST score	147
E value	3.0e-77
Match length	223
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	152144
Seq. ID	LIB3175-075-P1-K1-C3
Method	BLASTX
NCBI GI	g1354272
BLAST score	539
E value	2.0e-55
Match length	106
% identity	100
NCBI Description	(U51036) aspartic proteinase [Arabidopsis thaliana]

Seq. No.	152145
Seq. ID	LIB3175-075-P1-K1-C4
Method	BLASTN
NCBI GI	g2828278
BLAST score	153
E value	1.0e-80
Match length	303
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	152146
Seq. ID	LIB3175-075-P1-K1-C6
Method	BLASTX
NCBI GI	g4741952
BLAST score	568
E value	9.0e-59
Match length	108
% identity	73
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	152147
Seq. ID	LIB3175-075-P1-K1-C7
Method	BLASTX
NCBI GI	g16374
BLAST score	689
E value	7.0e-73
Match length	137

% identity	97
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	152148
Seq. ID	LIB3175-075-P1-K1-C9
Method	BLASTX
NCBI GI	g3023516
BLAST score	330
E value	3.0e-31
Match length	71
% identity	90
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR (DXP SYNTHASE) >gi_1399261 (U27099) DEF [Arabidopsis thaliana]

Seq. No.	152149
Seq. ID	LIB3175-075-P1-K1-D10
Method	BLASTX
NCBI GI	g4204265
BLAST score	382
E value	6.0e-37
Match length	98
% identity	71
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	152150
Seq. ID	LIB3175-075-P1-K1-D11
Method	BLASTN
NCBI GI	g3985955
BLAST score	355
E value	0.0e+00
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	152151
Seq. ID	LIB3175-075-P1-K1-D3
Method	BLASTX
NCBI GI	g4538943
BLAST score	455
E value	2.0e-45
Match length	127
% identity	70
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	152152
Seq. ID	LIB3175-075-P1-K1-D4
Method	BLASTX
NCBI GI	g99697
BLAST score	650
E value	2.0e-68
Match length	124
% identity	97
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone

lambdaAtgsr2) - Arabidopsis thaliana

Seq. No.	152153
Seq. ID	LIB3175-075-P1-K1-D6
Method	BLASTX
NCBI GI	g2335099
BLAST score	445
E value	2.0e-44
Match length	122
% identity	66
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	152154
Seq. ID	LIB3175-075-P1-K1-D7
Method	BLASTN
NCBI GI	g3643588
BLAST score	143
E value	1.0e-74
Match length	376
% identity	75
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152155
Seq. ID	LIB3175-075-P1-K1-D8
Method	BLASTN
NCBI GI	g4220510
BLAST score	309
E value	1.0e-173
Match length	341
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	152156
Seq. ID	LIB3175-075-P1-K1-D9
Method	BLASTX
NCBI GI	g1170503
BLAST score	385
E value	2.0e-37
Match length	75
% identity	97
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	152157
Seq. ID	LIB3175-075-P1-K1-E1
Method	BLASTN
NCBI GI	g3176694
BLAST score	163
E value	7.0e-87
Match length	175
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152158
Seq. ID	LIB3175-075-P1-K1-E10
Method	BLASTN
NCBI GI	g2351062
BLAST score	197
E value	1.0e-107
Match length	332
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	152159
Seq. ID	LIB3175-075-P1-K1-E11
Method	BLASTX
NCBI GI	g4586038
BLAST score	462
E value	2.0e-46
Match length	89
% identity	98
NCBI Description	(AC007109) putative heat shock protein [Arabidopsis thaliana]

Seq. No.	152160
Seq. ID	LIB3175-075-P1-K1-E12
Method	BLASTX
NCBI GI	g2213592
BLAST score	212
E value	2.0e-17
Match length	70
% identity	38
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	152161
Seq. ID	LIB3175-075-P1-K1-E2
Method	BLASTX
NCBI GI	g3158370
BLAST score	410
E value	2.0e-40
Match length	82
% identity	96
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	152162
Seq. ID	LIB3175-075-P1-K1-E3
Method	BLASTX
NCBI GI	g1550738
BLAST score	365
E value	7.0e-35
Match length	104
% identity	73
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 152163

Seq. ID	LIB3175-075-P1-K1-E4
Method	BLASTX
NCBI GI	g1145697
BLAST score	540
E value	2.0e-55
Match length	125
% identity	87
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	152164
Seq. ID	LIB3175-075-P1-K1-E6
Method	BLASTN
NCBI GI	g516248
BLAST score	318
E value	1.0e-179
Match length	365
% identity	100
NCBI Description	A.thaliana gene for porphobilinogen deaminase

Seq. No.	152165
Seq. ID	LIB3175-075-P1-K1-E7
Method	BLASTX
NCBI GI	g2829893
BLAST score	435
E value	3.0e-43
Match length	101
% identity	87
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	152166
Seq. ID	LIB3175-075-P1-K1-E8
Method	BLASTX
NCBI GI	g2494117
BLAST score	158
E value	9.0e-11
Match length	83
% identity	35
NCBI Description	(AC002376) Contains similarity to Papaver S3 self-incompatibility protein (gb_X87100). [Arabidopsis thaliana]

Seq. No.	152167
Seq. ID	LIB3175-075-P1-K1-E9
Method	BLASTN
NCBI GI	g4589428
BLAST score	231
E value	1.0e-127
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	152168
Seq. ID	LIB3175-075-P1-K1-F1
Method	BLASTN
NCBI GI	g3212846

BLAST score	211
E value	1.0e-115
Match length	211
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152169
Seq. ID	LIB3175-075-P1-K1-F10
Method	BLASTN
NCBI GI	g2656024
BLAST score	110
E value	6.0e-55
Match length	317
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	152170
Seq. ID	LIB3175-075-P1-K1-F11
Method	BLASTX
NCBI GI	g4539348
BLAST score	373
E value	6.0e-36
Match length	112
% identity	65
NCBI Description	(AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No.	152171
Seq. ID	LIB3175-075-P1-K1-F2
Method	BLASTX
NCBI GI	g2407800
BLAST score	396
E value	1.0e-38
Match length	81
% identity	99
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	152172
Seq. ID	LIB3175-075-P1-K1-F3
Method	BLASTX
NCBI GI	g166834
BLAST score	757
E value	8.0e-81
Match length	146
% identity	99
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	152173
Seq. ID	LIB3175-075-P1-K1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	445
E value	1.0e-44
Match length	94

% identity	91
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	152174
Seq. ID	LIB3175-075-P1-K1-F6
Method	BLASTX
NCBI GI	g1063415
BLAST score	617
E value	2.0e-64
Match length	118
% identity	99
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	152175
Seq. ID	LIB3175-075-P1-K1-F7
Method	BLASTN
NCBI GI	g4220633
BLAST score	234
E value	1.0e-129
Match length	238
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	152176
Seq. ID	LIB3175-075-P1-K1-F8
Method	BLASTN
NCBI GI	g2114077
BLAST score	67
E value	7.0e-30
Match length	111
% identity	88
NCBI Description	Arabidopsis thaliana DNA for larger subunit of Rubisco, beta subunit of coupling factor one, partial cds

Seq. No.	152177
Seq. ID	LIB3175-075-P1-K1-F9
Method	BLASTN
NCBI GI	g1865682
BLAST score	203
E value	1.0e-110
Match length	349
% identity	95
NCBI Description	A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No.	152178
Seq. ID	LIB3175-075-P1-K1-G1
Method	BLASTX
NCBI GI	g542050
BLAST score	200
E value	1.0e-15
Match length	87
% identity	43
NCBI Description	catechol O-methyltransferase (EC 2.1.1.6) III - common tobacco >gi_429114_emb_CAA50561_ (X71430) catechol

O-methyltransferase [Nicotiana tabacum]

Seq. No.	152179
Seq. ID	LIB3175-075-P1-K1-G11
Method	BLASTN
NCBI GI	g3510340
BLAST score	53
E value	2.0e-21
Match length	104
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	152180
Seq. ID	LIB3175-075-P1-K1-G12
Method	BLASTX
NCBI GI	g3688799
BLAST score	510
E value	6.0e-52
Match length	103
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	152181
Seq. ID	LIB3175-075-P1-K1-G4
Method	BLASTX
NCBI GI	g4154281
BLAST score	327
E value	2.0e-30
Match length	77
% identity	77
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	152182
Seq. ID	LIB3175-075-P1-K1-G7
Method	BLASTN
NCBI GI	g3241923
BLAST score	209
E value	1.0e-114
Match length	291
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	152183
Seq. ID	LIB3175-075-P1-K1-G8
Method	BLASTN
NCBI GI	g4589414
BLAST score	103
E value	9.0e-51
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No. 152184

Seq. ID	LIB3175-075-P1-K1-G9
Method	BLASTX
NCBI GI	g3719443
BLAST score	183
E value	8.0e-14
Match length	60
% identity	50
NCBI Description	(AF093751) lipid transfer protein [Brassica oleracea]

Seq. No.	152185
Seq. ID	LIB3175-075-P1-K1-H1
Method	BLASTX
NCBI GI	g1684855
BLAST score	479
E value	2.0e-48
Match length	97
% identity	23
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	152186
Seq. ID	LIB3175-075-P1-K1-H10
Method	BLASTN
NCBI GI	g1657620
BLAST score	96
E value	9.0e-47
Match length	180
% identity	88
NCBI Description	Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No.	152187
Seq. ID	LIB3175-075-P1-K1-H12
Method	BLASTX
NCBI GI	g4193388
BLAST score	455
E value	2.0e-45
Match length	113
% identity	75
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	152188
Seq. ID	LIB3175-075-P1-K1-H2
Method	BLASTN
NCBI GI	g3335331
BLAST score	358
E value	0.0e+00
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152189
Seq. ID	LIB3175-075-P1-K1-H3
Method	BLASTX
NCBI GI	g99735
BLAST score	534

E value	6.0e-55
Match length	101
% identity	99
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	152190
Seq. ID	LIB3175-075-P1-K1-H4
Method	BLASTX
NCBI GI	g1628583
BLAST score	639
E value	4.0e-67
Match length	124
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	152191
Seq. ID	LIB3175-075-P1-K1-H5
Method	BLASTX
NCBI GI	g2924784
BLAST score	349
E value	4.0e-33
Match length	106
% identity	17
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	152192
Seq. ID	LIB3175-075-P1-K1-H6
Method	BLASTN
NCBI GI	g4263762
BLAST score	126
E value	2.0e-64
Match length	262
% identity	76
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152193
Seq. ID	LIB3175-075-P1-K1-H8
Method	BLASTN
NCBI GI	g2281081
BLAST score	280
E value	1.0e-156
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152194
Seq. ID	LIB3175-075-P1-K1-H9
Method	BLASTN
NCBI GI	g4455321
BLAST score	103
E value	4.0e-51

Match length	178
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	152195
Seq. ID	LIB3175-076-P1-K1-A1
Method	BLASTX
NCBI GI	g2129772
BLAST score	510
E value	6.0e-52
Match length	115
% identity	86
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	152196
Seq. ID	LIB3175-076-P1-K1-A10
Method	BLASTX
NCBI GI	g2829927
BLAST score	171
E value	4.0e-12
Match length	117
% identity	36
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	152197
Seq. ID	LIB3175-076-P1-K1-A12
Method	BLASTN
NCBI GI	g4220643
BLAST score	185
E value	1.0e-100
Match length	244
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	152198
Seq. ID	LIB3175-076-P1-K1-A3
Method	BLASTX
NCBI GI	g4512658
BLAST score	225
E value	2.0e-18
Match length	75
% identity	49
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152199
Seq. ID	LIB3175-076-P1-K1-A4
Method	BLASTN
NCBI GI	g468525
BLAST score	78
E value	8.0e-36
Match length	125
% identity	90
NCBI Description	A.thaliana mRNA for NADPH thioredoxin reductase

Seq. No.	152200
Seq. ID	LIB3175-076-P1-K1-A5
Method	BLASTX
NCBI GI	g3834326
BLAST score	460
E value	5.0e-46
Match length	95
% identity	95
NCBI Description	(AC005679) Similar to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_T46595 and gb_AI09918 come from this gene. [Arabidopsis thaliana]

Seq. No.	152201
Seq. ID	LIB3175-076-P1-K1-A7
Method	BLASTX
NCBI GI	g399900
BLAST score	590
E value	2.0e-61
Match length	118
% identity	96
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	152202
Seq. ID	LIB3175-076-P1-K1-A8
Method	BLASTX
NCBI GI	g2982453
BLAST score	684
E value	3.0e-72
Match length	138
% identity	97
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	152203
Seq. ID	LIB3175-076-P1-K1-A9
Method	BLASTN
NCBI GI	g3292807
BLAST score	177
E value	8.0e-95
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	152204
Seq. ID	LIB3175-076-P1-K1-B1
Method	BLASTX
NCBI GI	g2464855
BLAST score	674
E value	4.0e-71
Match length	148
% identity	87

NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.	152205
Seq. ID	LIB3175-076-P1-K1-B10
Method	BLASTX
NCBI GI	g4200165
BLAST score	659
E value	2.0e-69
Match length	142
% identity	79
NCBI Description	(Y16262) neutral invertase [Daucus carota]
Seq. No.	152206
Seq. ID	LIB3175-076-P1-K1-B11
Method	BLASTN
NCBI GI	g2760164
BLAST score	37
E value	3.0e-11
Match length	283
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.	152207
Seq. ID	LIB3175-076-P1-K1-B12
Method	BLASTX
NCBI GI	g4504961
BLAST score	167
E value	1.0e-11
Match length	105
% identity	39
NCBI Description	lamin B receptor >gi_2494369_sp_Q14739_LBR_HUMAN LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) >gi_627510_pir__A53616 lamin B receptor - human >gi_438639 (L25931) lamin B receptor [Homo sapiens]
Seq. No.	152208
Seq. ID	LIB3175-076-P1-K1-B2
Method	BLASTX
NCBI GI	g1279640
BLAST score	174
E value	2.0e-12
Match length	49
% identity	67
NCBI Description	(X92204) NAM [Petunia x hybrida]
Seq. No.	152209
Seq. ID	LIB3175-076-P1-K1-B3
Method	BLASTX
NCBI GI	g4704766
BLAST score	362
E value	1.0e-34
Match length	115
% identity	44
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	152210
Seq. ID	LIB3175-076-P1-K1-B4
Method	BLASTX
NCBI GI	g3850585
BLAST score	130
E value	5.0e-42
Match length	147
% identity	70
NCBI Description	(AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and gb_T20569 come from this gene. [Arabidopsis thaliana]

Seq. No.	152211
Seq. ID	LIB3175-076-P1-K1-B5
Method	BLASTX
NCBI GI	g2244752
BLAST score	268
E value	1.0e-23
Match length	73
% identity	73
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152212
Seq. ID	LIB3175-076-P1-K1-B6
Method	BLASTX
NCBI GI	g2244752
BLAST score	201
E value	3.0e-16
Match length	59
% identity	69
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152213
Seq. ID	LIB3175-076-P1-K1-B7
Method	BLASTN
NCBI GI	g1033194
BLAST score	194
E value	1.0e-105
Match length	283
% identity	92
NCBI Description	Arabidopsis thaliana AT103 mRNA, complete cds

Seq. No.	152214
Seq. ID	LIB3175-076-P1-K1-B8
Method	BLASTN
NCBI GI	g4539378
BLAST score	293
E value	1.0e-164
Match length	316
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	152215
Seq. ID	LIB3175-076-P1-K1-B9
Method	BLASTX
NCBI GI	g113026
BLAST score	540

E value	2.0e-55
Match length	120
% identity	87
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	152216
Seq. ID	LIB3175-076-P1-K1-C1
Method	BLASTX
NCBI GI	g1931647
BLAST score	571
E value	4.0e-59
Match length	127
% identity	85
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	152217
Seq. ID	LIB3175-076-P1-K1-C10
Method	BLASTX
NCBI GI	g2104455
BLAST score	159
E value	1.0e-10
Match length	87
% identity	40
NCBI Description	(Z95397) unknown [Schizosaccharomyces pombe]

Seq. No.	152218
Seq. ID	LIB3175-076-P1-K1-C11
Method	BLASTN
NCBI GI	g4006815
BLAST score	162
E value	6.0e-86
Match length	389
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152219
Seq. ID	LIB3175-076-P1-K1-C12
Method	BLASTX
NCBI GI	g3193316
BLAST score	644
E value	1.0e-67
Match length	144
% identity	85
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	152220
Seq. ID	LIB3175-076-P1-K1-C2
Method	BLASTN

NCBI GI	g4455348
BLAST score	233
E value	1.0e-128
Match length	393
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	152221
Seq. ID	LIB3175-076-P1-K1-C3
Method	BLASTN
NCBI GI	g12219
BLAST score	156
E value	3.0e-82
Match length	252
% identity	97
NCBI Description	Mustard chloroplast trnk gene for tRNA-Lys(UUU)

Seq. No.	152222
Seq. ID	LIB3175-076-P1-K1-C5
Method	BLASTX
NCBI GI	g4508078
BLAST score	495
E value	3.0e-50
Match length	89
% identity	98
NCBI Description	(AC005882) 64134 [Arabidopsis thaliana]

Seq. No.	152223
Seq. ID	LIB3175-076-P1-K1-C7
Method	BLASTN
NCBI GI	g2245073
BLAST score	276
E value	1.0e-154
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152224
Seq. ID	LIB3175-076-P1-K1-C8
Method	BLASTN
NCBI GI	g3046853
BLAST score	153
E value	9.0e-81
Match length	165
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	152225
Seq. ID	LIB3175-076-P1-K1-C9
Method	BLASTX
NCBI GI	g1172872
BLAST score	643
E value	2.0e-67
Match length	140

% identity	89
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.	152226
Seq. ID	LIB3175-076-P1-K1-D1
Method	BLASTX
NCBI GI	g2119846
BLAST score	56
E value	6.0e-59
Match length	117
% identity	93
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	152227
Seq. ID	LIB3175-076-P1-K1-D10
Method	BLASTX
NCBI GI	g1071913
BLAST score	434
E value	6.0e-43
Match length	119
% identity	70
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]
Seq. No.	152228
Seq. ID	LIB3175-076-P1-K1-D11
Method	BLASTX
NCBI GI	g419789
BLAST score	313
E value	9.0e-29
Match length	91
% identity	65
NCBI Description	hypothetical protein - potato
Seq. No.	152229
Seq. ID	LIB3175-076-P1-K1-D12
Method	BLASTX
NCBI GI	g3193292
BLAST score	706
E value	7.0e-75
Match length	143
% identity	99
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	152230
Seq. ID	LIB3175-076-P1-K1-D3
Method	BLASTX
NCBI GI	g4262239
BLAST score	427
E value	3.0e-42
Match length	106
% identity	85
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	152231
Seq. ID	LIB3175-076-P1-K1-D7
Method	BLASTX
NCBI GI	g115783
BLAST score	624
E value	3.0e-65
Match length	117
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152232
Seq. ID	LIB3175-076-P1-K1-D8
Method	BLASTX
NCBI GI	g3894197
BLAST score	224
E value	2.0e-18
Match length	98
% identity	41
NCBI Description	(AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152233
Seq. ID	LIB3175-076-P1-K1-D9
Method	BLASTX
NCBI GI	g4455193
BLAST score	465
E value	1.0e-46
Match length	93
% identity	100
NCBI Description	(AL035440) fimbrin-like protein (ATFIM1) [Arabidopsis thaliana]

Seq. No.	152234
Seq. ID	LIB3175-076-P1-K1-E1
Method	BLASTN
NCBI GI	g2827038
BLAST score	52
E value	1.0e-20
Match length	60
% identity	97
NCBI Description	Arabidopsis thaliana chloroplast processing enzyme (CPE) gene, complete cds

Seq. No.	152235
Seq. ID	LIB3175-076-P1-K1-E11
Method	BLASTX
NCBI GI	g1709534
BLAST score	331
E value	6.0e-31
Match length	111
% identity	65
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir__S66637 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis thaliana >gi_829100_emb_CAA60740_ (X87330) pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] >gi_870866_emb_CAA60446_ (X86777) pyrroline-5-carboxylate synthetase A [Arabidopsis thaliana] >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate synthase [Arabidopsis thaliana] >gi_2642162 (AC003000) delta-1-pyrroline 5-carboxylase synthetase, P5C1 [Arabidopsis thaliana]

Seq. No.	152236
Seq. ID	LIB3175-076-P1-K1-E12
Method	BLASTN
NCBI GI	g3395421
BLAST score	263
E value	1.0e-146
Match length	287
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152237
Seq. ID	LIB3175-076-P1-K1-E2
Method	BLASTX
NCBI GI	g2921323
BLAST score	209
E value	1.0e-16
Match length	60
% identity	67
NCBI Description	(AF034112) beta-1,3-glucanase 7 [Glycine max]

Seq. No.	152238
Seq. ID	LIB3175-076-P1-K1-E4
Method	BLASTN
NCBI GI	g14342
BLAST score	260
E value	1.0e-144
Match length	304
% identity	97
NCBI Description	A.thaliana mRNA for carbonic anhydrase

Seq. No.	152239
Seq. ID	LIB3175-076-P1-K1-E5
Method	BLASTX

NCBI GI	g132102
BLAST score	450
E value	7.0e-45
Match length	121
% identity	68
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	152240
Seq. ID	LIB3175-076-P1-K1-E8
Method	BLASTX
NCBI GI	g3860260
BLAST score	292
E value	2.0e-26
Match length	62
% identity	100
NCBI Description	(AC005824) putative acidic ribosomal protein [Arabidopsis thaliana]

Seq. No.	152241
Seq. ID	LIB3175-076-P1-K1-E9
Method	BLASTN
NCBI GI	g4512656
BLAST score	190
E value	1.0e-103
Match length	209
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	152242
Seq. ID	LIB3175-076-P1-K1-F1
Method	BLASTN
NCBI GI	g16300
BLAST score	187
E value	1.0e-101
Match length	253
% identity	93
NCBI Description	A.thaliana mRNA for glycine rich protein >gi_166836_gb_L00648_ATHRBPA Arabidopsis thaliana RNA-binding protein mRNA, complete cds

Seq. No.	152243
Seq. ID	LIB3175-076-P1-K1-F10
Method	BLASTX
NCBI GI	g2501188
BLAST score	516
E value	1.0e-52
Match length	118
% identity	88
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	152244
Seq. ID	LIB3175-076-P1-K1-F11
Method	BLASTX
NCBI GI	g3980378
BLAST score	548
E value	3.0e-56
Match length	119
% identity	90
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	152245
Seq. ID	LIB3175-076-P1-K1-F12
Method	BLASTX
NCBI GI	g3122572
BLAST score	518
E value	8.0e-53
Match length	141
% identity	71
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	152246
Seq. ID	LIB3175-076-P1-K1-F3
Method	BLASTX
NCBI GI	g267527
BLAST score	250
E value	1.0e-21
Match length	54
% identity	91
NCBI Description	RAS-RELATED PROTEIN YPT3 >gi_282952_pir__S23523 GTP-binding protein Np-ypt3 - curled-leaved tobacco >gi_19715_emb_CAA45351_ (X63874) Np-ypt3 [Nicotiana plumbaginifolia]

Seq. No.	152247
Seq. ID	LIB3175-076-P1-K1-F4
Method	BLASTX
NCBI GI	g3355480
BLAST score	203
E value	6.0e-16
Match length	81
% identity	51
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	152248
Seq. ID	LIB3175-076-P1-K1-F5
Method	BLASTX
NCBI GI	g112681
BLAST score	603
E value	9.0e-63

Match length	138
% identity	85
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	152249
Seq. ID	LIB3175-076-P1-K1-F7
Method	BLASTX
NCBI GI	g3355311
BLAST score	478
E value	4.0e-48
Match length	107
% identity	87
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]

Seq. No.	152250
Seq. ID	LIB3175-076-P1-K1-F8
Method	BLASTX
NCBI GI	g127045
BLAST score	616
E value	3.0e-64
Match length	119
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	152251
Seq. ID	LIB3175-076-P1-K1-G10
Method	BLASTX
NCBI GI	g421826
BLAST score	432
E value	8.0e-43
Match length	110
% identity	75
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	152252
Seq. ID	LIB3175-076-P1-K1-G11
Method	BLASTX
NCBI GI	g2252857
BLAST score	279
E value	7.0e-25
Match length	98
% identity	63
NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	152253
Seq. ID	LIB3175-076-P1-K1-G12
Method	BLASTX
NCBI GI	g2119846
BLAST score	709
E value	3.0e-75
Match length	134
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	152254
Seq. ID	LIB3175-076-P1-K1-G3
Method	BLASTX
NCBI GI	g2160190
BLAST score	439
E value	8.0e-44
Match length	93
% identity	88
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	152255
Seq. ID	LIB3175-076-P1-K1-G4
Method	BLASTX
NCBI GI	g4204296
BLAST score	521
E value	3.0e-53
Match length	99
% identity	99
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	152256
Seq. ID	LIB3175-076-P1-K1-G5
Method	BLASTX
NCBI GI	g1657617
BLAST score	118
E value	4.0e-64
Match length	129
% identity	94
NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	152257
Seq. ID	LIB3175-076-P1-K1-G9
Method	BLASTX
NCBI GI	g3043529
BLAST score	142
E value	9.0e-09
Match length	73

% identity	36
NCBI Description	(AJ002204) polyamine oxidase [Zea mays]

Seq. No.	152258
Seq. ID	LIB3175-076-P1-K1-H1
Method	BLASTN
NCBI GI	g3241926
BLAST score	133
E value	7.0e-69
Match length	189
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	152259
Seq. ID	LIB3175-076-P1-K1-H10
Method	BLASTX
NCBI GI	g2982301
BLAST score	285
E value	1.0e-25
Match length	112
% identity	55
NCBI Description	(AF051235) YGL010w-like protein [Picea mariana]

Seq. No.	152260
Seq. ID	LIB3175-076-P1-K1-H12
Method	BLASTX
NCBI GI	g4753651
BLAST score	452
E value	3.0e-45
Match length	96
% identity	92
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	152261
Seq. ID	LIB3175-076-P1-K1-H3
Method	BLASTN
NCBI GI	g3047100
BLAST score	84
E value	2.0e-39
Match length	196
% identity	86
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	152262
Seq. ID	LIB3175-076-P1-K1-H4
Method	BLASTX
NCBI GI	g3152581
BLAST score	430
E value	1.0e-42
Match length	101
% identity	85
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	152263
Seq. ID	LIB3175-076-P1-K1-H5
Method	BLASTX
NCBI GI	g282865
BLAST score	642
E value	3.0e-67
Match length	130
% identity	70
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	152264
Seq. ID	LIB3175-076-P1-K1-H7
Method	BLASTX
NCBI GI	g4557016
BLAST score	138
E value	1.0e-08
Match length	73
% identity	42
NCBI Description	cell division cycle 27 >gi_231708_sp_P30260_CC27_HUMAN PROTEIN CDC27HS (CELL DIVISION CYCLE PROTEIN 27 HOMOLOG) >gi_2134884_pir__A48792 CDC27 - human >gi_405833 (U00001) Human homologue of S. pombe nuc2+ and A. nidulans bimA [Homo sapiens]

Seq. No.	152265
Seq. ID	LIB3175-076-P1-K1-H8
Method	BLASTX
NCBI GI	g1628622
BLAST score	742
E value	4.0e-79
Match length	143
% identity	99
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	152266
Seq. ID	LIB3175-076-P1-K1-H9
Method	BLASTN
NCBI GI	g870791
BLAST score	79
E value	2.0e-36
Match length	184
% identity	41
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete cds

Seq. No.	152267
Seq. ID	LIB3175-077-P1-K1-A1
Method	BLASTX

NCBI GI	g481914
BLAST score	548
E value	2.0e-56
Match length	109
% identity	94
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica napus]

Seq. No.	152268
Seq. ID	LIB3175-077-P1-K1-A10
Method	BLASTX
NCBI GI	g1703108
BLAST score	590
E value	3.0e-61
Match length	109
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	152269
Seq. ID	LIB3175-077-P1-K1-A11
Method	BLASTN
NCBI GI	g2618730
BLAST score	143
E value	7.0e-75
Match length	147
% identity	99
NCBI Description	Arabidopsis thaliana early auxin-induced (IAA21) mRNA, partial cds

Seq. No.	152270
Seq. ID	LIB3175-077-P1-K1-A12
Method	BLASTX
NCBI GI	g3522929
BLAST score	556
E value	3.0e-57
Match length	107
% identity	100
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	152271
Seq. ID	LIB3175-077-P1-K1-A2
Method	BLASTN
NCBI GI	g3776002
BLAST score	376
E value	0.0e+00
Match length	407
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH13

Seq. No. 152272

Seq. ID	LIB3175-077-P1-K1-A3
Method	BLASTN
NCBI GI	g3776002
BLAST score	285
E value	1.0e-159
Match length	321
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH13

Seq. No.	152273
Seq. ID	LIB3175-077-P1-K1-A4
Method	BLASTX
NCBI GI	g4185505
BLAST score	453
E value	3.0e-45
Match length	115
% identity	76
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	152274
Seq. ID	LIB3175-077-P1-K1-A5
Method	BLASTX
NCBI GI	g4580455
BLAST score	473
E value	2.0e-47
Match length	100
% identity	96
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	152275
Seq. ID	LIB3175-077-P1-K1-A6
Method	BLASTN
NCBI GI	g2529657
BLAST score	45
E value	1.0e-16
Match length	129
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152276
Seq. ID	LIB3175-077-P1-K1-A8
Method	BLASTX
NCBI GI	g267069
BLAST score	575
E value	2.0e-59
Match length	133
% identity	89
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	152277
Seq. ID	LIB3175-077-P1-K1-A9
Method	BLASTX

NCBI GI	g4741960
BLAST score	572
E value	4.0e-59
Match length	127
% identity	86
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	152278
Seq. ID	LIB3175-077-P1-K1-B1
Method	BLASTN
NCBI GI	g2264315
BLAST score	212
E value	1.0e-116
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	152279
Seq. ID	LIB3175-077-P1-K1-B10
Method	BLASTX
NCBI GI	g2494113
BLAST score	605
E value	5.0e-63
Match length	108
% identity	100
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	152280
Seq. ID	LIB3175-077-P1-K1-B11
Method	BLASTX
NCBI GI	g4585879
BLAST score	647
E value	6.0e-68
Match length	138
% identity	84
NCBI Description	(AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

Seq. No.	152281
Seq. ID	LIB3175-077-P1-K1-B2
Method	BLASTX
NCBI GI	g1168529
BLAST score	400
E value	6.0e-39
Match length	86
% identity	91
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	152282
Seq. ID	LIB3175-077-P1-K1-B3

Method	BLASTN
NCBI GI	g2191126
BLAST score	206
E value	1.0e-112
Match length	329
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	152283
Seq. ID	LIB3175-077-P1-K1-B4
Method	BLASTN
NCBI GI	g4757414
BLAST score	363
E value	0.0e+00
Match length	367
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	152284
Seq. ID	LIB3175-077-P1-K1-B5
Method	BLASTX
NCBI GI	g1170939
BLAST score	506
E value	2.0e-51
Match length	102
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	152285
Seq. ID	LIB3175-077-P1-K1-B6
Method	BLASTN
NCBI GI	g2760165
BLAST score	376
E value	0.0e+00
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	152286
Seq. ID	LIB3175-077-P1-K1-B8
Method	BLASTX
NCBI GI	g1076316
BLAST score	569
E value	9.0e-59
Match length	109
% identity	99
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	152287
Seq. ID	LIB3175-077-P1-K1-C1
Method	BLASTX
NCBI GI	g2244952
BLAST score	645
E value	1.0e-67
Match length	138
% identity	93
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	152288
Seq. ID	LIB3175-077-P1-K1-C10
Method	BLASTX
NCBI GI	g1429211
BLAST score	460
E value	5.0e-46
Match length	124
% identity	74
NCBI Description	(X99116) HMG-I/Y protein [Arabidopsis thaliana] >gi_2809402 (AF041253) high mobility group protein a [Arabidopsis thaliana]

Seq. No.	152289
Seq. ID	LIB3175-077-P1-K1-C11
Method	BLASTX
NCBI GI	g1360088
BLAST score	316
E value	4.0e-29
Match length	62
% identity	89
NCBI Description	(X97947) Zn finger protein [Nicotiana tabacum]

Seq. No.	152290
Seq. ID	LIB3175-077-P1-K1-C12
Method	BLASTN
NCBI GI	g4757388
BLAST score	77
E value	2.0e-35
Match length	209
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	152291
Seq. ID	LIB3175-077-P1-K1-C2
Method	BLASTX
NCBI GI	g2829891
BLAST score	292
E value	3.0e-26
Match length	136
% identity	72
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	152292
Seq. ID	LIB3175-077-P1-K1-C3
Method	BLASTX

NCBI GI	g3914394
BLAST score	313
E value	6.0e-29
Match length	103
% identity	70
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No.	152293
Seq. ID	LIB3175-077-P1-K1-C4
Method	BLASTX
NCBI GI	g166835
BLAST score	776
E value	5.0e-83
Match length	148
% identity	100
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642170 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	152294
Seq. ID	LIB3175-077-P1-K1-C5
Method	BLASTX
NCBI GI	g2506277
BLAST score	609
E value	1.0e-63
Match length	128
% identity	95
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	152295
Seq. ID	LIB3175-077-P1-K1-C6
Method	BLASTX
NCBI GI	g4741960
BLAST score	541
E value	2.0e-55
Match length	123
% identity	85
NCBI Description	(AF134130) Lhcb6 protein [Arabidopsis thaliana]

Seq. No.	152296
Seq. ID	LIB3175-077-P1-K1-C7
Method	BLASTX
NCBI GI	g4263712
BLAST score	449
E value	1.0e-44
Match length	124
% identity	73
NCBI Description	(AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 152297

Seq. ID	LIB3175-077-P1-K1-C8
Method	BLASTX
NCBI GI	g2829275
BLAST score	382
E value	6.0e-37
Match length	72
% identity	100
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	152298
Seq. ID	LIB3175-077-P1-K1-C9
Method	BLASTX
NCBI GI	g113024
BLAST score	42
E value	3.0e-63
Match length	146
% identity	91
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	152299
Seq. ID	LIB3175-077-P1-K1-D1
Method	BLASTX
NCBI GI	g119975
BLAST score	476
E value	1.0e-50
Match length	121
% identity	87
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	152300
Seq. ID	LIB3175-077-P1-K1-D10
Method	BLASTN
NCBI GI	g4512656
BLAST score	323
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	152301
Seq. ID	LIB3175-077-P1-K1-D11
Method	BLASTX
NCBI GI	g3096945
BLAST score	563
E value	4.0e-58
Match length	107

% identity	100
NCBI Description	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]

Seq. No.	152302
Seq. ID	LIB3175-077-P1-K1-D12
Method	BLASTX
NCBI GI	g3461817
BLAST score	513
E value	3.0e-52
Match length	139
% identity	64
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	152303
Seq. ID	LIB3175-077-P1-K1-D2
Method	BLASTX
NCBI GI	g119975
BLAST score	177
E value	2.0e-13
Match length	61
% identity	66
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	152304
Seq. ID	LIB3175-077-P1-K1-D3
Method	BLASTN
NCBI GI	g972928
BLAST score	203
E value	1.0e-110
Match length	223
% identity	98
NCBI Description	Arabidopsis thaliana IAA13 (IAA13) gene, complete cds

Seq. No.	152305
Seq. ID	LIB3175-077-P1-K1-D4
Method	BLASTX
NCBI GI	g3482924
BLAST score	321
E value	9.0e-30
Match length	112
% identity	57
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	152306
Seq. ID	LIB3175-077-P1-K1-D5
Method	BLASTX
NCBI GI	g2827711
BLAST score	597
E value	5.0e-62
Match length	116
% identity	99

NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	152307
Seq. ID	LIB3175-077-P1-K1-D6
Method	BLASTN
NCBI GI	g3869064
BLAST score	57
E value	3.0e-23
Match length	154
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1013, complete sequence [Arabidopsis thaliana]

Seq. No.	152308
Seq. ID	LIB3175-077-P1-K1-D7
Method	BLASTX
NCBI GI	g4583542
BLAST score	338
E value	1.0e-31
Match length	136
% identity	58
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	152309
Seq. ID	LIB3175-077-P1-K1-D8
Method	BLASTX
NCBI GI	g1769905
BLAST score	223
E value	9.0e-19
Match length	76
% identity	66
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	152310
Seq. ID	LIB3175-077-P1-K1-D9
Method	BLASTX
NCBI GI	g1170089
BLAST score	606
E value	3.0e-63
Match length	122
% identity	98
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	152311
Seq. ID	LIB3175-077-P1-K1-E1
Method	BLASTN
NCBI GI	g4713943
BLAST score	319
E value	1.0e-179

Match length	375
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	152312
Seq. ID	LIB3175-077-P1-K1-E11
Method	BLASTX
NCBI GI	g282865
BLAST score	563
E value	4.0e-58
Match length	130
% identity	83
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	152313
Seq. ID	LIB3175-077-P1-K1-E2
Method	BLASTX
NCBI GI	g4581109
BLAST score	560
E value	9.0e-58
Match length	131
% identity	83
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	152314
Seq. ID	LIB3175-077-P1-K1-E3
Method	BLASTX
NCBI GI	g2760345
BLAST score	290
E value	3.0e-26
Match length	90
% identity	18
NCBI Description	(U84967) ubiquitin [Arabidopsis thaliana]

Seq. No.	152315
Seq. ID	LIB3175-077-P1-K1-E4
Method	BLASTN
NCBI GI	g3650026
BLAST score	330
E value	0.0e+00
Match length	401
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152316
Seq. ID	LIB3175-077-P1-K1-E5
Method	BLASTN
NCBI GI	g4558521
BLAST score	60
E value	4.0e-25

Match length	196
% identity	85
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	152317
Seq. ID	LIB3175-077-P1-K1-E6
Method	BLASTX
NCBI GI	g115767
BLAST score	594
E value	9.0e-62
Match length	115
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	152318
Seq. ID	LIB3175-077-P1-K1-E7
Method	BLASTN
NCBI GI	g3402745
BLAST score	223
E value	1.0e-122
Match length	446
% identity	56
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	152319
Seq. ID	LIB3175-077-P1-K1-E9
Method	BLASTN
NCBI GI	g1113782
BLAST score	98
E value	5.0e-48
Match length	170
% identity	89
NCBI Description	Arabidopsis thaliana Thi1 protein mRNA, complete cds

Seq. No.	152320
Seq. ID	LIB3175-077-P1-K1-F10
Method	BLASTX
NCBI GI	g3193316
BLAST score	490
E value	2.0e-49
Match length	106
% identity	87
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	152321
Seq. ID	LIB3175-077-P1-K1-F11
Method	BLASTN
NCBI GI	g3461834

BLAST score	267
E value	1.0e-148
Match length	438
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152322
Seq. ID	LIB3175-077-P1-K1-F12
Method	BLASTX
NCBI GI	g1914685
BLAST score	330
E value	8.0e-31
Match length	74
% identity	82
NCBI Description	(Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No.	152323
Seq. ID	LIB3175-077-P1-K1-F4
Method	BLASTX
NCBI GI	g3334223
BLAST score	644
E value	1.0e-67
Match length	124
% identity	98
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD) >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_2392518 (U89267) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_3098559_gb_AAC15697.1_ (AF047834) 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	152324
Seq. ID	LIB3175-077-P1-K1-F5
Method	BLASTX
NCBI GI	g2499327
BLAST score	469
E value	5.0e-47
Match length	138
% identity	70
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	152325
Seq. ID	LIB3175-077-P1-K1-F6
Method	BLASTX
NCBI GI	g4006834
BLAST score	682
E value	5.0e-72
Match length	134
% identity	99
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	152326
Seq. ID	LIB3175-077-P1-K1-F7
Method	BLASTX
NCBI GI	g2275217
BLAST score	531
E value	3.0e-54
Match length	124
% identity	84
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	152327
Seq. ID	LIB3175-077-P1-K1-F8
Method	BLASTX
NCBI GI	g544134
BLAST score	389
E value	1.0e-37
Match length	147
% identity	24
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	152328
Seq. ID	LIB3175-077-P1-K1-F9
Method	BLASTX
NCBI GI	g2281631
BLAST score	283
E value	3.0e-25
Match length	53
% identity	100
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	152329
Seq. ID	LIB3175-077-P1-K1-G10
Method	BLASTN
NCBI GI	g2062153
BLAST score	181
E value	3.0e-97
Match length	181
% identity	100
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152330
Seq. ID	LIB3175-077-P1-K1-G11
Method	BLASTX
NCBI GI	g4680661
BLAST score	147
E value	3.0e-09
Match length	100
% identity	25
NCBI Description	(AF132945) CGI-11 protein [Homo sapiens]

Seq. No.	152331

Seq. ID	LIB3175-077-P1-K1-G12
Method	BLASTX
NCBI GI	g2146727
BLAST score	552
E value	8.0e-57
Match length	111
% identity	100
NCBI Description	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 - Arabidopsis thaliana (fragment) >gi_598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	152332
Seq. ID	LIB3175-077-P1-K1-G2
Method	BLASTX
NCBI GI	g3334244
BLAST score	381
E value	1.0e-50
Match length	123
% identity	84
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica juncea]

Seq. No.	152333
Seq. ID	LIB3175-077-P1-K1-G5
Method	BLASTX
NCBI GI	g4741948
BLAST score	705
E value	1.0e-74
Match length	132
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	152334
Seq. ID	LIB3175-077-P1-K1-G6
Method	BLASTX
NCBI GI	g4454036
BLAST score	343
E value	3.0e-32
Match length	62
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	152335
Seq. ID	LIB3175-077-P1-K1-G7
Method	BLASTN
NCBI GI	g2959729
BLAST score	403
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No. 152336

Seq. ID	LIB3175-077-P1-K1-G8
Method	BLASTX
NCBI GI	g1706772
BLAST score	760
E value	4.0e-81
Match length	144
% identity	100
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	152337
Seq. ID	LIB3175-077-P1-K1-G9
Method	BLASTX
NCBI GI	g4508073
BLAST score	638
E value	7.0e-67
Match length	140
% identity	91
NCBI Description	(AC005882) 43220 [Arabidopsis thaliana]

Seq. No.	152338
Seq. ID	LIB3175-077-P1-K1-H1
Method	BLASTX
NCBI GI	g1216504
BLAST score	67
E value	4.7e+00
Match length	115
% identity	12
NCBI Description	(U49245) geranylgeranyl transferase type II beta-subunit [Homo sapiens]

Seq. No.	152339
Seq. ID	LIB3175-077-P1-K1-H10
Method	BLASTN
NCBI GI	g4580745
BLAST score	443
E value	0.0e+00
Match length	443
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	152340
Seq. ID	LIB3175-077-P1-K1-H11
Method	BLASTX
NCBI GI	g1402906
BLAST score	627

E value	1.0e-65
Match length	140
% identity	89
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	152341
Seq. ID	LIB3175-077-P1-K1-H12
Method	BLASTX
NCBI GI	g4585980
BLAST score	438
E value	2.0e-43
Match length	132
% identity	70
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	152342
Seq. ID	LIB3175-077-P1-K1-H2
Method	BLASTX
NCBI GI	g1350965
BLAST score	423
E value	3.0e-47
Match length	96
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12)

Seq. No.	152343
Seq. ID	LIB3175-077-P1-K1-H5
Method	BLASTX
NCBI GI	g1170409
BLAST score	469
E value	5.0e-47
Match length	117
% identity	79
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana] >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

Seq. No.	152344
Seq. ID	LIB3175-077-P1-K1-H6
Method	BLASTX
NCBI GI	g4585980
BLAST score	616
E value	3.0e-64
Match length	136
% identity	87
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	152345
Seq. ID	LIB3175-077-P1-K1-H7
Method	BLASTX
NCBI GI	g1086263

BLAST score	237
E value	1.0e-27
Match length	135
% identity	54
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	152346
Seq. ID	LIB3175-077-P1-K1-H8
Method	BLASTX
NCBI GI	g2335096
BLAST score	183
E value	2.0e-13
Match length	101
% identity	34
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152347
Seq. ID	LIB3175-077-P1-K1-H9
Method	BLASTN
NCBI GI	g4468103
BLAST score	429
E value	0.0e+00
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	152348
Seq. ID	LIB3175-078-P1-K1-A1
Method	BLASTN
NCBI GI	g3702730
BLAST score	180
E value	1.0e-96
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence [Arabidopsis thaliana]

Seq. No.	152349
Seq. ID	LIB3175-078-P1-K1-A11
Method	BLASTX
NCBI GI	g2894563
BLAST score	497
E value	2.0e-50
Match length	96
% identity	97
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	152350
Seq. ID	LIB3175-078-P1-K1-A12
Method	BLASTN
NCBI GI	g2264318
BLAST score	384
E value	0.0e+00
Match length	415
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	152351
Seq. ID	LIB3175-078-P1-K1-A2
Method	BLASTX
NCBI GI	g2281094
BLAST score	515
E value	2.0e-52
Match length	101
% identity	100
NCBI Description	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_ (AJ133519) molybdopterin synthase large subunit [Arabidopsis thaliana]

Seq. No.	152352
Seq. ID	LIB3175-078-P1-K1-A3
Method	BLASTX
NCBI GI	g2842477
BLAST score	504
E value	3.0e-51
Match length	112
% identity	83
NCBI Description	(AL021749) copper-binding protein-like [Arabidopsis thaliana]

Seq. No.	152353
Seq. ID	LIB3175-078-P1-K1-A4
Method	BLASTX
NCBI GI	g3212869
BLAST score	665
E value	5.0e-70
Match length	135
% identity	95
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	152354
Seq. ID	LIB3175-078-P1-K1-A5
Method	BLASTX
NCBI GI	g3360289
BLAST score	545
E value	5.0e-56
Match length	138
% identity	70
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	152355
Seq. ID	LIB3175-078-P1-K1-A6
Method	BLASTX
NCBI GI	g2623298
BLAST score	650
E value	3.0e-68
Match length	136
% identity	89
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis

thaliana]

Seq. No.	152356
Seq. ID	LIB3175-078-P1-K1-A7
Method	BLASTX
NCBI GI	g4680212
BLAST score	195
E value	4.0e-15
Match length	99
% identity	45
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	152357
Seq. ID	LIB3175-078-P1-K1-A8
Method	BLASTX
NCBI GI	g2688824
BLAST score	215
E value	2.0e-17
Match length	69
% identity	67
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]

Seq. No.	152358
Seq. ID	LIB3175-078-P1-K1-A9
Method	BLASTX
NCBI GI	g127041
BLAST score	505
E value	3.0e-51
Match length	98
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	152359
Seq. ID	LIB3175-078-P1-K1-B1
Method	BLASTX
NCBI GI	g4056497
BLAST score	417
E value	6.0e-41
Match length	94
% identity	90
NCBI Description	(AC005896) putative histone H2B [Arabidopsis thaliana]

Seq. No.	152360
Seq. ID	LIB3175-078-P1-K1-B10
Method	BLASTX
NCBI GI	g2244979
BLAST score	647
E value	6.0e-68
Match length	135
% identity	97
NCBI Description	(Z97340) similarity to enoyl-CoA hydratase [Arabidopsis thaliana]

Seq. No.	152361
Seq. ID	LIB3175-078-P1-K1-B11
Method	BLASTX
NCBI GI	g2462081
BLAST score	507
E value	2.0e-51
Match length	126
% identity	79
NCBI Description	(Y09427) squamosa-promoter binding protein like 3 [Arabidopsis thaliana]

Seq. No.	152362
Seq. ID	LIB3175-078-P1-K1-B12
Method	BLASTN
NCBI GI	g4757678
BLAST score	47
E value	3.0e-17
Match length	269
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	152363
Seq. ID	LIB3175-078-P1-K1-B2
Method	BLASTX
NCBI GI	g2119846
BLAST score	639
E value	5.0e-67
Match length	123
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	152364
Seq. ID	LIB3175-078-P1-K1-B3
Method	BLASTX
NCBI GI	g1709970
BLAST score	61
E value	3.0e-45
Match length	124
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	152365
Seq. ID	LIB3175-078-P1-K1-B4
Method	BLASTX
NCBI GI	g1050918
BLAST score	254
E value	7.0e-22
Match length	94
% identity	50

NCBI Description	(X92648) lipid transfer protein [Helianthus annuus]

Seq. No.	152366
Seq. ID	LIB3175-078-P1-K1-B5
Method	BLASTX
NCBI GI	g1350720
BLAST score	502
E value	6.0e-51
Match length	111
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	152367
Seq. ID	LIB3175-078-P1-K1-B6
Method	BLASTX
NCBI GI	g2829891
BLAST score	615
E value	3.0e-64
Match length	134
% identity	90
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	152368
Seq. ID	LIB3175-078-P1-K1-B9
Method	BLASTX
NCBI GI	g416681
BLAST score	153
E value	4.0e-10
Match length	121
% identity	35
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_280404_pir__S26198 H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP synthase (delta subunit) [Nicotiana tabacum]

Seq. No.	152369
Seq. ID	LIB3175-078-P1-K1-C1
Method	BLASTX
NCBI GI	g2435406
BLAST score	425
E value	6.0e-42
Match length	139
% identity	62
NCBI Description	(U83490) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	152370
Seq. ID	LIB3175-078-P1-K1-C10
Method	BLASTN
NCBI GI	g3047074
BLAST score	33
E value	5.0e-09
Match length	78
% identity	94
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	152371

Seq. ID	LIB3175-078-P1-K1-C11
Method	BLASTX
NCBI GI	g4510363
BLAST score	369
E value	2.0e-35
Match length	86
% identity	77
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	152372
Seq. ID	LIB3175-078-P1-K1-C12
Method	BLASTX
NCBI GI	g1518540
BLAST score	539
E value	2.0e-55
Match length	114
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	152373
Seq. ID	LIB3175-078-P1-K1-C3
Method	BLASTX
NCBI GI	g4585879
BLAST score	627
E value	1.0e-65
Match length	137
% identity	82
NCBI Description	(AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

Seq. No.	152374
Seq. ID	LIB3175-078-P1-K1-C4
Method	BLASTX
NCBI GI	g2129639
BLAST score	574
E value	2.0e-59
Match length	115
% identity	97
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	152375
Seq. ID	LIB3175-078-P1-K1-C5
Method	BLASTN
NCBI GI	g2653884
BLAST score	150
E value	7.0e-79
Match length	287
% identity	82
NCBI Description	Arabidopsis thaliana phospholipase D-gamma mRNA, complete cds

Seq. No.	152376
Seq. ID	LIB3175-078-P1-K1-C7
Method	BLASTX

NCBI GI	g4580457
BLAST score	141
E value	1.0e-08
Match length	91
% identity	37
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152377
Seq. ID	LIB3175-078-P1-K1-C9
Method	BLASTN
NCBI GI	g1532162
BLAST score	120
E value	7.0e-61
Match length	343
% identity	89
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	152378
Seq. ID	LIB3175-078-P1-K1-D1
Method	BLASTX
NCBI GI	g3915023
BLAST score	525
E value	1.0e-53
Match length	135
% identity	71
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	152379
Seq. ID	LIB3175-078-P1-K1-D10
Method	BLASTX
NCBI GI	g4581109
BLAST score	610
E value	1.0e-63
Match length	133
% identity	90
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	152380
Seq. ID	LIB3175-078-P1-K1-D11
Method	BLASTN
NCBI GI	g4220637
BLAST score	209
E value	1.0e-114
Match length	221
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	152381
Seq. ID	LIB3175-078-P1-K1-D2
Method	BLASTX

NCBI GI	g481914
BLAST score	601
E value	1.0e-62
Match length	120
% identity	92
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica napus]

Seq. No.	152382
Seq. ID	LIB3175-078-P1-K1-D4
Method	BLASTX
NCBI GI	g4539408
BLAST score	230
E value	5.0e-19
Match length	52
% identity	85
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	152383
Seq. ID	LIB3175-078-P1-K1-D5
Method	BLASTN
NCBI GI	g3449334
BLAST score	58
E value	6.0e-24
Match length	249
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	152384
Seq. ID	LIB3175-078-P1-K1-D6
Method	BLASTN
NCBI GI	g4263774
BLAST score	355
E value	0.0e+00
Match length	416
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152385
Seq. ID	LIB3175-078-P1-K1-D7
Method	BLASTX
NCBI GI	g2062167
BLAST score	522
E value	3.0e-53
Match length	98
% identity	100
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	152386
Seq. ID	LIB3175-078-P1-K1-D8
Method	BLASTX
NCBI GI	g4218122
BLAST score	659

E value	2.0e-69
Match length	131
% identity	98
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	152387
Seq. ID	LIB3175-078-P1-K1-E1
Method	BLASTX
NCBI GI	g3157937
BLAST score	51
E value	2.0e-61
Match length	130
% identity	96
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	152388
Seq. ID	LIB3175-078-P1-K1-E10
Method	BLASTN
NCBI GI	g4159709
BLAST score	160
E value	1.0e-84
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	152389
Seq. ID	LIB3175-078-P1-K1-E11
Method	BLASTN
NCBI GI	g4033837
BLAST score	370
E value	0.0e+00
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for sigma-like factor

Seq. No.	152390
Seq. ID	LIB3175-078-P1-K1-E2
Method	BLASTX
NCBI GI	g1352463
BLAST score	554
E value	5.0e-57
Match length	123
% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	152391
Seq. ID	LIB3175-078-P1-K1-E3
Method	BLASTN
NCBI GI	g2760168
BLAST score	259

E value	1.0e-144
Match length	390
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	152392
Seq. ID	LIB3175-078-P1-K1-E5
Method	BLASTN
NCBI GI	g2618602
BLAST score	402
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	152393
Seq. ID	LIB3175-078-P1-K1-E6
Method	BLASTX
NCBI GI	g3080412
BLAST score	243
E value	1.0e-20
Match length	112
% identity	44
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	152394
Seq. ID	LIB3175-078-P1-K1-F10
Method	BLASTN
NCBI GI	g3413696
BLAST score	262
E value	1.0e-145
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152395
Seq. ID	LIB3175-078-P1-K1-F11
Method	BLASTX
NCBI GI	g417381
BLAST score	750
E value	5.0e-80
Match length	138
% identity	100
NCBI Description	NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_16400_emb_CAA45041_ (X63445) nitrilase I [Arabidopsis thaliana]

Seq. No.	152396
Seq. ID	LIB3175-078-P1-K1-F12
Method	BLASTX
NCBI GI	g4538963
BLAST score	296
E value	4.0e-35
Match length	109

% identity	73
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	152397
Seq. ID	LIB3175-078-P1-K1-F3
Method	BLASTX
NCBI GI	g629602
BLAST score	435
E value	4.0e-43
Match length	91
% identity	91
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	152398
Seq. ID	LIB3175-078-P1-K1-F4
Method	BLASTX
NCBI GI	g3377843
BLAST score	531
E value	2.0e-54
Match length	135
% identity	78
NCBI Description	(AF076274) contains similarity to rat p47 protein (GB:AB002086) [Arabidopsis thaliana]

Seq. No.	152399
Seq. ID	LIB3175-078-P1-K1-F5
Method	BLASTX
NCBI GI	g3851636
BLAST score	307
E value	3.0e-28
Match length	84
% identity	67
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	152400
Seq. ID	LIB3175-078-P1-K1-F6
Method	BLASTN
NCBI GI	g3426033
BLAST score	157
E value	4.0e-83
Match length	290
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152401
Seq. ID	LIB3175-078-P1-K1-F7
Method	BLASTX
NCBI GI	g4586263
BLAST score	231
E value	1.0e-19
Match length	70

% identity	64
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152402
Seq. ID	LIB3175-078-P1-K1-F8
Method	BLASTX
NCBI GI	g3738287
BLAST score	635
E value	1.0e-66
Match length	137
% identity	92
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	152403
Seq. ID	LIB3175-078-P1-K1-F9
Method	BLASTN
NCBI GI	g2342673
BLAST score	306
E value	1.0e-172
Match length	345
% identity	98
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152404
Seq. ID	LIB3175-078-P1-K1-G1
Method	BLASTX
NCBI GI	g2369714
BLAST score	563
E value	4.0e-58
Match length	123
% identity	91
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	152405
Seq. ID	LIB3175-078-P1-K1-G10
Method	BLASTX
NCBI GI	g1352463
BLAST score	638
E value	7.0e-67
Match length	137
% identity	92
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	152406
Seq. ID	LIB3175-078-P1-K1-G11
Method	BLASTX
NCBI GI	g477280
BLAST score	256
E value	4.0e-22
Match length	76
% identity	66
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi_410633_bbs_136740 cytochrome

c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]

Seq. No.	152407
Seq. ID	LIB3175-078-P1-K1-G12
Method	BLASTX
NCBI GI	g124224
BLAST score	520
E value	4.0e-53
Match length	113
% identity	86
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	152408
Seq. ID	LIB3175-078-P1-K1-G2
Method	BLASTN
NCBI GI	g2924652
BLAST score	284
E value	1.0e-158
Match length	339
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	152409
Seq. ID	LIB3175-078-P1-K1-G3
Method	BLASTX
NCBI GI	g1169476
BLAST score	650
E value	3.0e-68
Match length	126
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	152410
Seq. ID	LIB3175-078-P1-K1-G4
Method	BLASTX
NCBI GI	g2497753
BLAST score	261
E value	1.0e-22
Match length	110
% identity	46
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	152411
Seq. ID	LIB3175-078-P1-K1-G5
Method	BLASTX
NCBI GI	g1255852
BLAST score	252

E value	1.0e-21
Match length	123
% identity	41
NCBI Description	(U53339) simmilar to enoyl-CoA hydratases [Caenorhabditis elegans]

Seq. No.	152412
Seq. ID	LIB3175-078-P1-K1-G7
Method	BLASTX
NCBI GI	g4455293
BLAST score	432
E value	9.0e-43
Match length	135
% identity	73
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	152413
Seq. ID	LIB3175-078-P1-K1-G9
Method	BLASTN
NCBI GI	g4220636
BLAST score	59
E value	1.0e-24
Match length	165
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	152414
Seq. ID	LIB3175-078-P1-K1-H10
Method	BLASTN
NCBI GI	g4757392
BLAST score	347
E value	0.0e+00
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	152415
Seq. ID	LIB3175-078-P1-K1-H11
Method	BLASTN
NCBI GI	g4199934
BLAST score	62
E value	3.0e-26
Match length	290
% identity	34
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	152416
Seq. ID	LIB3175-078-P1-K1-H12
Method	BLASTN
NCBI GI	g4589409
BLAST score	223
E value	1.0e-122
Match length	270
% identity	96

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	152417
Seq. ID	LIB3175-078-P1-K1-H2
Method	BLASTX
NCBI GI	g1352664
BLAST score	354
E value	1.0e-33
Match length	68
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	152418
Seq. ID	LIB3175-078-P1-K1-H3
Method	BLASTX
NCBI GI	g2154609
BLAST score	587
E value	6.0e-61
Match length	114
% identity	100
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_ (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	152419
Seq. ID	LIB3175-078-P1-K1-H6
Method	BLASTX
NCBI GI	g4753655
BLAST score	336
E value	2.0e-31
Match length	79
% identity	77
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	152420
Seq. ID	LIB3175-078-P1-K1-H8
Method	BLASTN
NCBI GI	g4519188
BLAST score	385
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	152421
Seq. ID	LIB3175-078-P1-K1-H9
Method	BLASTX

NCBI GI	g3927836
BLAST score	666
E value	3.0e-70
Match length	136
% identity	97
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	152422
Seq. ID	LIB3175-079-P1-K1-A1
Method	BLASTX
NCBI GI	g1922246
BLAST score	520
E value	3.0e-53
Match length	100
% identity	99
NCBI Description	(Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No.	152423
Seq. ID	LIB3175-079-P1-K1-A10
Method	BLASTX
NCBI GI	g3367632
BLAST score	363
E value	1.0e-34
Match length	69
% identity	99
NCBI Description	(AJ000539) phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	152424
Seq. ID	LIB3175-079-P1-K1-A11
Method	BLASTX
NCBI GI	g4734007
BLAST score	621
E value	7.0e-65
Match length	128
% identity	97
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152425
Seq. ID	LIB3175-079-P1-K1-A12
Method	BLASTX
NCBI GI	g2274857
BLAST score	554
E value	5.0e-57
Match length	125
% identity	89
NCBI Description	(AJ000469) glutathione peroxidase [Arabidopsis thaliana] >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione peroxidase precursor [Arabidopsis thaliana]

Seq. No.	152426
Seq. ID	LIB3175-079-P1-K1-A2
Method	BLASTX
NCBI GI	g2499811
BLAST score	615
E value	4.0e-64
Match length	118

% identity	98
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	152427
Seq. ID	LIB3175-079-P1-K1-A3
Method	BLASTN
NCBI GI	g1871173
BLAST score	352
E value	0.0e+00
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	152428
Seq. ID	LIB3175-079-P1-K1-A7
Method	BLASTX
NCBI GI	g1363489
BLAST score	622
E value	5.0e-65
Match length	132
% identity	88
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152429
Seq. ID	LIB3175-079-P1-K1-A8
Method	BLASTX
NCBI GI	g3785997
BLAST score	624
E value	3.0e-65
Match length	125
% identity	98
NCBI Description	(AC005499) putative annexin [Arabidopsis thaliana]

Seq. No.	152430
Seq. ID	LIB3175-079-P1-K1-A9
Method	BLASTX
NCBI GI	g3402676
BLAST score	618
E value	1.0e-64
Match length	119
% identity	35
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	152431
Seq. ID	LIB3175-079-P1-K1-B1
Method	BLASTX
NCBI GI	g1237102
BLAST score	236
E value	9.0e-20
Match length	93
% identity	55

NCBI Description	(L40358) calmodulin-binding protein [Arabidopsis thaliana] >gi_1589171_prf__2210340A calmodulin-binding protein [Arabidopsis thaliana]
Seq. No.	152432
Seq. ID	LIB3175-079-P1-K1-B10
Method	BLASTX
NCBI GI	g3249065
BLAST score	641
E value	3.0e-67
Match length	141
% identity	93
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]
Seq. No.	152433
Seq. ID	LIB3175-079-P1-K1-B12
Method	BLASTN
NCBI GI	g4096078
BLAST score	48
E value	7.0e-18
Match length	175
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	152434
Seq. ID	LIB3175-079-P1-K1-B2
Method	BLASTX
NCBI GI	g1923256
BLAST score	451
E value	6.0e-45
Match length	117
% identity	79
NCBI Description	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]
Seq. No.	152435
Seq. ID	LIB3175-079-P1-K1-B3
Method	BLASTX
NCBI GI	g2257743
BLAST score	394
E value	3.0e-38
Match length	103
% identity	81
NCBI Description	(U62020) lysine-sensitive aspartate kinase [Arabidopsis thaliana]
Seq. No.	152436
Seq. ID	LIB3175-079-P1-K1-B4
Method	BLASTN
NCBI GI	g4454587
BLAST score	136
E value	2.0e-70
Match length	432
% identity	99

NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	152437
Seq. ID	LIB3175-079-P1-K1-B5
Method	BLASTX
NCBI GI	g3126967
BLAST score	398
E value	7.0e-50
Match length	118
% identity	15
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No.	152438
Seq. ID	LIB3175-079-P1-K1-B6
Method	BLASTX
NCBI GI	g4583542
BLAST score	324
E value	5.0e-30
Match length	135
% identity	57
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	152439
Seq. ID	LIB3175-079-P1-K1-B7
Method	BLASTN
NCBI GI	g2959729
BLAST score	379
E value	0.0e+00
Match length	387
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	152440
Seq. ID	LIB3175-079-P1-K1-B8
Method	BLASTX
NCBI GI	g2760330
BLAST score	209
E value	8.0e-33
Match length	97
% identity	73
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	152441
Seq. ID	LIB3175-079-P1-K1-B9
Method	BLASTX
NCBI GI	g115783
BLAST score	652
E value	2.0e-68
Match length	127
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152442
Seq. ID	LIB3175-079-P1-K1-C1
Method	BLASTN
NCBI GI	g4512690
BLAST score	285
E value	1.0e-159
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	152443
Seq. ID	LIB3175-079-P1-K1-C10
Method	BLASTX
NCBI GI	g3236238
BLAST score	509
E value	8.0e-52
Match length	106
% identity	90
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	152444
Seq. ID	LIB3175-079-P1-K1-C11
Method	BLASTX
NCBI GI	g115783
BLAST score	634
E value	2.0e-66
Match length	125
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152445
Seq. ID	LIB3175-079-P1-K1-C12
Method	BLASTN
NCBI GI	g3449326
BLAST score	407
E value	0.0e+00
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	152446
Seq. ID	LIB3175-079-P1-K1-C2
Method	BLASTX
NCBI GI	g4580460
BLAST score	710
E value	3.0e-75
Match length	143
% identity	97
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	152447
Seq. ID	LIB3175-079-P1-K1-C3
Method	BLASTX
NCBI GI	g2842480
BLAST score	623
E value	4.0e-65
Match length	126
% identity	97
NCBI Description	(AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]

Seq. No.	152448
Seq. ID	LIB3175-079-P1-K1-C4
Method	BLASTN
NCBI GI	g4063730
BLAST score	54
E value	2.0e-21
Match length	208
% identity	85
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	152449
Seq. ID	LIB3175-079-P1-K1-C5
Method	BLASTX
NCBI GI	g4220446
BLAST score	658
E value	3.0e-69
Match length	141
% identity	94
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	152450
Seq. ID	LIB3175-079-P1-K1-C6
Method	BLASTX
NCBI GI	g1172872
BLAST score	605
E value	5.0e-63
Match length	119
% identity	97
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	152451
Seq. ID	LIB3175-079-P1-K1-C7
Method	BLASTX
NCBI GI	g119975

BLAST score	45
E value	1.0e-39
Match length	120
% identity	78
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	152452
Seq. ID	LIB3175-079-P1-K1-C8
Method	BLASTN
NCBI GI	g4587641
BLAST score	195
E value	1.0e-105
Match length	397
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	152453
Seq. ID	LIB3175-079-P1-K1-C9
Method	BLASTN
NCBI GI	g4467131
BLAST score	188
E value	1.0e-101
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	152454
Seq. ID	LIB3175-079-P1-K1-D1
Method	BLASTN
NCBI GI	g3851669
BLAST score	198
E value	1.0e-107
Match length	206
% identity	99
NCBI Description	Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	152455
Seq. ID	LIB3175-079-P1-K1-D10
Method	BLASTN
NCBI GI	g3449326
BLAST score	366
E value	0.0e+00
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	152456
Seq. ID	LIB3175-079-P1-K1-D11
Method	BLASTX

NCBI GI	g1703108
BLAST score	642
E value	2.0e-67
Match length	121
% identity	98
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	152457
Seq. ID	LIB3175-079-P1-K1-D12
Method	BLASTN
NCBI GI	g3033373
BLAST score	391
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152458
Seq. ID	LIB3175-079-P1-K1-D2
Method	BLASTX
NCBI GI	g4704766
BLAST score	440
E value	1.0e-43
Match length	115
% identity	43
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	152459
Seq. ID	LIB3175-079-P1-K1-D3
Method	BLASTX
NCBI GI	g2894445
BLAST score	303
E value	1.0e-27
Match length	115
% identity	70
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	152460
Seq. ID	LIB3175-079-P1-K1-D4
Method	BLASTX
NCBI GI	g585421
BLAST score	739
E value	1.0e-78
Match length	146
% identity	92
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	152461
Seq. ID	LIB3175-079-P1-K1-D5

Method	BLASTX
NCBI GI	g1707364
BLAST score	218
E value	1.0e-17
Match length	102
% identity	37
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	152462
Seq. ID	LIB3175-079-P1-K1-D6
Method	BLASTX
NCBI GI	g3080371
BLAST score	464
E value	1.0e-46
Match length	97
% identity	93
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	152463
Seq. ID	LIB3175-079-P1-K1-D7
Method	BLASTN
NCBI GI	g4455168
BLAST score	128
E value	2.0e-65
Match length	233
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	152464
Seq. ID	LIB3175-079-P1-K1-D8
Method	BLASTX
NCBI GI	g3236240
BLAST score	244
E value	5.0e-21
Match length	70
% identity	64
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	152465
Seq. ID	LIB3175-079-P1-K1-E1
Method	BLASTN
NCBI GI	g2062153
BLAST score	390
E value	0.0e+00
Match length	430
% identity	98
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152466
Seq. ID	LIB3175-079-P1-K1-E11
Method	BLASTX
NCBI GI	g2160296
BLAST score	397
E value	1.0e-38

Match length	138
% identity	52
NCBI Description	(D61395) gamma-VPE [Arabidopsis thaliana]

Seq. No.	152467
Seq. ID	LIB3175-079-P1-K1-E12
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	152468
Seq. ID	LIB3175-079-P1-K1-E2
Method	BLASTX
NCBI GI	g1705463
BLAST score	534
E value	1.0e-54
Match length	117
% identity	87
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi_1589016_prf__2209438A biotin synthase [Arabidopsis thaliana]

Seq. No.	152469
Seq. ID	LIB3175-079-P1-K1-E3
Method	BLASTX
NCBI GI	g3367516
BLAST score	740
E value	8.0e-79
Match length	141
% identity	100
NCBI Description	(AC004392) Similar to beta-glucosidase BGQ60 precursor gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No.	152470
Seq. ID	LIB3175-079-P1-K1-E4
Method	BLASTX
NCBI GI	g1170939
BLAST score	320
E value	1.0e-29
Match length	66
% identity	89
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	152471
Seq. ID	LIB3175-079-P1-K1-E5
Method	BLASTN
NCBI GI	g4376087
BLAST score	232
E value	1.0e-127
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	152472
Seq. ID	LIB3175-079-P1-K1-E6
Method	BLASTN
NCBI GI	g4510360
BLAST score	294
E value	1.0e-164
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	152473
Seq. ID	LIB3175-079-P1-K1-E7
Method	BLASTX
NCBI GI	g2245055
BLAST score	607
E value	3.0e-63
Match length	141
% identity	87
NCBI Description	(Z97342) resistance gene homolog (fragment) [Arabidopsis thaliana]

Seq. No.	152474
Seq. ID	LIB3175-079-P1-K1-E8
Method	BLASTX
NCBI GI	g4049350
BLAST score	610
E value	1.0e-63
Match length	117
% identity	99
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	152475
Seq. ID	LIB3175-079-P1-K1-F1
Method	BLASTX
NCBI GI	g4371284
BLAST score	699
E value	5.0e-74
Match length	141
% identity	96
NCBI Description	(AC006260) putative plasma membrane intrinsic protein 2B [Arabidopsis thaliana]

Seq. No.	152476
Seq. ID	LIB3175-079-P1-K1-F10

Method	BLASTN
NCBI GI	g4510360
BLAST score	234
E value	1.0e-129
Match length	325
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	152477
Seq. ID	LIB3175-079-P1-K1-F11
Method	BLASTX
NCBI GI	g2317913
BLAST score	520
E value	4.0e-53
Match length	102
% identity	99
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	152478
Seq. ID	LIB3175-079-P1-K1-F12
Method	BLASTX
NCBI GI	g322552
BLAST score	625
E value	2.0e-65
Match length	126
% identity	98
NCBI Description	nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment) >gi_16396_emb_CAA49170_ (X69373) nucleoside diphosphate kinase [Arabidopsis thaliana]

Seq. No.	152479
Seq. ID	LIB3175-079-P1-K1-F3
Method	BLASTX
NCBI GI	g1363489
BLAST score	687
E value	1.0e-72
Match length	127
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152480
Seq. ID	LIB3175-079-P1-K1-F4
Method	BLASTX
NCBI GI	g1363489
BLAST score	736
E value	2.0e-78
Match length	139
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152481

Seq. ID	LIB3175-079-P1-K1-F5
Method	BLASTX
NCBI GI	g1362009
BLAST score	547
E value	3.0e-56
Match length	134
% identity	43
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	152482
Seq. ID	LIB3175-079-P1-K1-F6
Method	BLASTX
NCBI GI	g3367590
BLAST score	599
E value	2.0e-62
Match length	124
% identity	99
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	152483
Seq. ID	LIB3175-079-P1-K1-F7
Method	BLASTX
NCBI GI	g4583542
BLAST score	315
E value	4.0e-29
Match length	117
% identity	63
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	152484
Seq. ID	LIB3175-079-P1-K1-F8
Method	BLASTX
NCBI GI	g1336084
BLAST score	577
E value	1.0e-59
Match length	109
% identity	100
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	152485
Seq. ID	LIB3175-079-P1-K1-F9
Method	BLASTX
NCBI GI	g2317913
BLAST score	541
E value	2.0e-55
Match length	106
% identity	100
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	152486
Seq. ID	LIB3175-079-P1-K1-G1
Method	BLASTN
NCBI GI	g3985933
BLAST score	60

E value	5.0e-25
Match length	429
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9E15, complete sequence [Arabidopsis thaliana]

Seq. No.	152487
Seq. ID	LIB3175-079-P1-K1-G11
Method	BLASTX
NCBI GI	g113026
BLAST score	596
E value	6.0e-62
Match length	128
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	152488
Seq. ID	LIB3175-079-P1-K1-G12
Method	BLASTX
NCBI GI	g2435511
BLAST score	310
E value	2.0e-28
Match length	103
% identity	56
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	152489
Seq. ID	LIB3175-079-P1-K1-G2
Method	BLASTX
NCBI GI	g266693
BLAST score	545
E value	6.0e-56
Match length	135
% identity	82
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	152490
Seq. ID	LIB3175-079-P1-K1-G3
Method	BLASTX
NCBI GI	g2654122
BLAST score	380
E value	1.0e-36
Match length	124
% identity	65
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	152491

Seq. ID	LIB3175-079-P1-K1-G4
Method	BLASTN
NCBI GI	g3241925
BLAST score	103
E value	5.0e-51
Match length	185
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	152492
Seq. ID	LIB3175-079-P1-K1-G5
Method	BLASTN
NCBI GI	g4519194
BLAST score	205
E value	1.0e-111
Match length	276
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	152493
Seq. ID	LIB3175-079-P1-K1-G6
Method	BLASTX
NCBI GI	g1350680
BLAST score	594
E value	1.0e-61
Match length	116
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	152494
Seq. ID	LIB3175-079-P1-K1-G7
Method	BLASTX
NCBI GI	g1363489
BLAST score	46
E value	7.0e-69
Match length	131
% identity	98
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152495
Seq. ID	LIB3175-079-P1-K1-G9
Method	BLASTX
NCBI GI	g3249065
BLAST score	448
E value	8.0e-45
Match length	105
% identity	90
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	152496
Seq. ID	LIB3175-079-P1-K1-H1

Method	BLASTN
NCBI GI	g4757414
BLAST score	370
E value	0.0e+00
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	152497
Seq. ID	LIB3175-079-P1-K1-H11
Method	BLASTN
NCBI GI	g4544405
BLAST score	312
E value	1.0e-175
Match length	404
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	152498
Seq. ID	LIB3175-079-P1-K1-H12
Method	BLASTX
NCBI GI	g1652057
BLAST score	402
E value	4.0e-39
Match length	145
% identity	57
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	152499
Seq. ID	LIB3175-079-P1-K1-H4
Method	BLASTX
NCBI GI	g4741940
BLAST score	561
E value	7.0e-58
Match length	102
% identity	66
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	152500
Seq. ID	LIB3175-079-P1-K1-H5
Method	BLASTX
NCBI GI	g1575752
BLAST score	340
E value	3.0e-32
Match length	77
% identity	84
NCBI Description	(U70672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	152501
Seq. ID	LIB3175-079-P1-K1-H6
Method	BLASTX
NCBI GI	g669138
BLAST score	382
E value	8.0e-37
Match length	88

% identity	83
NCBI Description	(Z37395) rubisco large subunit [Hyssopus officinalis] >gi_1093913_prf__2104490N RuBisCO:SUBUNIT=large [Hyssopus officinalis]

Seq. No.	152502
Seq. ID	LIB3175-079-P1-K1-H7
Method	BLASTX
NCBI GI	g345829
BLAST score	176
E value	9.0e-13
Match length	74
% identity	51
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	152503
Seq. ID	LIB3175-079-P1-K1-H8
Method	BLASTX
NCBI GI	g729470
BLAST score	308
E value	2.0e-28
Match length	74
% identity	78
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	152504
Seq. ID	LIB3175-079-P1-K1-H9
Method	BLASTX
NCBI GI	g1336084
BLAST score	514
E value	2.0e-52
Match length	98
% identity	100
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	152505
Seq. ID	LIB3175-080-P1-K1-A1
Method	BLASTX
NCBI GI	g1402914
BLAST score	362
E value	6.0e-35
Match length	74
% identity	97
NCBI Description	(X98318) peroxidase [Arabidopsis thaliana]

Seq. No.	152506
Seq. ID	LIB3175-080-P1-K1-A10
Method	BLASTN
NCBI GI	g4337186
BLAST score	233
E value	1.0e-128

Match length	342
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152507
Seq. ID	LIB3175-080-P1-K1-A11
Method	BLASTX
NCBI GI	g4678951
BLAST score	98
E value	1.0e-09
Match length	37
% identity	100
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	152508
Seq. ID	LIB3175-080-P1-K1-A12
Method	BLASTX
NCBI GI	g1175012
BLAST score	507
E value	1.0e-51
Match length	110
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	152509
Seq. ID	LIB3175-080-P1-K1-A3
Method	BLASTX
NCBI GI	g2623962
BLAST score	495
E value	4.0e-50
Match length	102
% identity	92
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	152510
Seq. ID	LIB3175-080-P1-K1-A4
Method	BLASTN
NCBI GI	g2342673
BLAST score	258
E value	1.0e-143
Match length	318
% identity	95
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152511
Seq. ID	LIB3175-080-P1-K1-A5
Method	BLASTN
NCBI GI	g2494110
BLAST score	331
E value	0.0e+00
Match length	346
% identity	99

NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152512
Seq. ID	LIB3175-080-P1-K1-A6
Method	BLASTX
NCBI GI	g133872
BLAST score	531
E value	2.0e-54
Match length	116
% identity	92
NCBI Description	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast - spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]

Seq. No.	152513
Seq. ID	LIB3175-080-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	299
E value	2.0e-27
Match length	83
% identity	72
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	152514
Seq. ID	LIB3175-080-P1-K1-A8
Method	BLASTN
NCBI GI	g2924768
BLAST score	92
E value	2.0e-44
Match length	198
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152515
Seq. ID	LIB3175-080-P1-K1-A9
Method	BLASTN
NCBI GI	g2828182
BLAST score	212
E value	1.0e-116
Match length	293
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	152516
Seq. ID	LIB3175-080-P1-K1-B1

Method	BLASTX
NCBI GI	g1174162
BLAST score	386
E value	8.0e-38
Match length	71
% identity	96
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	152517
Seq. ID	LIB3175-080-P1-K1-B12
Method	BLASTX
NCBI GI	g4586265
BLAST score	409
E value	4.0e-40
Match length	115
% identity	72
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152518
Seq. ID	LIB3175-080-P1-K1-B3
Method	BLASTN
NCBI GI	g4538972
BLAST score	201
E value	1.0e-109
Match length	303
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)

Seq. No.	152519
Seq. ID	LIB3175-080-P1-K1-B4
Method	BLASTX
NCBI GI	g1169278
BLAST score	187
E value	3.0e-14
Match length	45
% identity	84
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	152520
Seq. ID	LIB3175-080-P1-K1-B5
Method	BLASTN
NCBI GI	g4512690
BLAST score	145
E value	4.0e-76
Match length	173
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	152521
Seq. ID	LIB3175-080-P1-K1-B6
Method	BLASTN
NCBI GI	g2656024

BLAST score	178
E value	1.0e-95
Match length	309
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	152522
Seq. ID	LIB3175-080-P1-K1-B7
Method	BLASTN
NCBI GI	g3406034
BLAST score	115
E value	2.0e-58
Match length	130
% identity	98
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	152523
Seq. ID	LIB3175-080-P1-K1-B9
Method	BLASTN
NCBI GI	g4589418
BLAST score	272
E value	1.0e-151
Match length	300
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	152524
Seq. ID	LIB3175-080-P1-K1-C1
Method	BLASTX
NCBI GI	g1076440
BLAST score	351
E value	2.0e-33
Match length	83
% identity	82
NCBI Description	acyl-CoA binding protein - rape >gi_1076441_pir__S49102 acyl-CoA binding protein - rape >gi_509265_emb_CAA54390_ (X77134) acyl-CoA binding protein [Brassica napus]

Seq. No.	152525
Seq. ID	LIB3175-080-P1-K1-C10
Method	BLASTX
NCBI GI	g4185505
BLAST score	450
E value	8.0e-45
Match length	115
% identity	76
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	152526
Seq. ID	LIB3175-080-P1-K1-C11
Method	BLASTN
NCBI GI	g1402915
BLAST score	187

E value	1.0e-101
Match length	311
% identity	91
NCBI Description	A.thaliana mRNA for peroxidase, prxr7

Seq. No.	152527
Seq. ID	LIB3175-080-P1-K1-C12
Method	BLASTX
NCBI GI	g4158221
BLAST score	536
E value	6.0e-55
Match length	129
% identity	75
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	152528
Seq. ID	LIB3175-080-P1-K1-C2
Method	BLASTX
NCBI GI	g4586265
BLAST score	257
E value	2.0e-22
Match length	62
% identity	76
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152529
Seq. ID	LIB3175-080-P1-K1-C3
Method	BLASTN
NCBI GI	g4587641
BLAST score	230
E value	1.0e-126
Match length	331
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	152530
Seq. ID	LIB3175-080-P1-K1-C4
Method	BLASTX
NCBI GI	g4586799
BLAST score	420
E value	2.0e-41
Match length	106
% identity	77
NCBI Description	(AB015221) NtRb1 [Nicotiana tabacum]

Seq. No.	152531
Seq. ID	LIB3175-080-P1-K1-C6
Method	BLASTN
NCBI GI	g4512690
BLAST score	262
E value	1.0e-145
Match length	345
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	152532
Seq. ID	LIB3175-080-P1-K1-C7
Method	BLASTX
NCBI GI	g1708313
BLAST score	461
E value	2.0e-47
Match length	106
% identity	98
NCBI Description	HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi_999396_bbs_163637 (S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No.	152533
Seq. ID	LIB3175-080-P1-K1-C8
Method	BLASTX
NCBI GI	g1769905
BLAST score	276
E value	1.0e-24
Match length	95
% identity	59
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	152534
Seq. ID	LIB3175-080-P1-K1-C9
Method	BLASTX
NCBI GI	g2760347
BLAST score	530
E value	3.0e-54
Match length	111
% identity	17
NCBI Description	(U84968) ubiquitin [Arabidopsis thaliana]

Seq. No.	152535
Seq. ID	LIB3175-080-P1-K1-D10
Method	BLASTN
NCBI GI	g533708
BLAST score	341
E value	0.0e+00
Match length	376
% identity	99
NCBI Description	Arabidopsis thaliana Columbia homeotic APETALA2 protein (APETALA2) mRNA, complete cds

Seq. No.	152536
Seq. ID	LIB3175-080-P1-K1-D11
Method	BLASTX
NCBI GI	g421826
BLAST score	541
E value	1.0e-55
Match length	126
% identity	81
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	152537
Seq. ID	LIB3175-080-P1-K1-D12
Method	BLASTX
NCBI GI	g1871185
BLAST score	170
E value	5.0e-12
Match length	46
% identity	76
NCBI Description	(U90439) seven in absentia isolog [Arabidopsis thaliana]

Seq. No.	152538
Seq. ID	LIB3175-080-P1-K1-D3
Method	BLASTX
NCBI GI	g132166
BLAST score	136
E value	1.0e-08
Match length	35
% identity	86
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	152539
Seq. ID	LIB3175-080-P1-K1-D5
Method	BLASTN
NCBI GI	g4757417
BLAST score	203
E value	1.0e-110
Match length	281
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	152540
Seq. ID	LIB3175-080-P1-K1-D6
Method	BLASTX
NCBI GI	g1402904
BLAST score	518
E value	6.0e-53
Match length	107
% identity	93
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	152541
Seq. ID	LIB3175-080-P1-K1-D8
Method	BLASTX
NCBI GI	g4056467
BLAST score	570
E value	6.0e-59
Match length	108
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	152542
Seq. ID	LIB3175-080-P1-K1-D9
Method	BLASTX
NCBI GI	g1169598
BLAST score	328
E value	1.0e-30
Match length	73
% identity	84
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	152543
Seq. ID	LIB3175-080-P1-K1-E10
Method	BLASTX
NCBI GI	g3080437
BLAST score	639
E value	4.0e-67
Match length	126
% identity	97
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	152544
Seq. ID	LIB3175-080-P1-K1-E12
Method	BLASTN
NCBI GI	g1946354
BLAST score	203
E value	1.0e-110
Match length	227
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	152545
Seq. ID	LIB3175-080-P1-K1-E3
Method	BLASTX
NCBI GI	g1169009
BLAST score	164
E value	2.0e-11
Match length	84
% identity	49
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi_437777_emb_CAA52814_ (X74814) 0-Methyltransferase [Eucalyptus gunnii]

Seq. No.	152546
Seq. ID	LIB3175-080-P1-K1-E4
Method	BLASTX
NCBI GI	g1345592
BLAST score	538
E value	3.0e-55
Match length	109
% identity	99

NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	152547
Seq. ID	LIB3175-080-P1-K1-E5
Method	BLASTX
NCBI GI	g4049348
BLAST score	413
E value	1.0e-40
Match length	82
% identity	99
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	152548
Seq. ID	LIB3175-080-P1-K1-E6
Method	BLASTN
NCBI GI	g3420043
BLAST score	293
E value	1.0e-164
Match length	332
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152549
Seq. ID	LIB3175-080-P1-K1-E7
Method	BLASTX
NCBI GI	g2088654
BLAST score	444
E value	3.0e-44
Match length	100
% identity	88
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	152550
Seq. ID	LIB3175-080-P1-K1-E9
Method	BLASTN
NCBI GI	g3738275
BLAST score	251
E value	1.0e-139
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152551
Seq. ID	LIB3175-080-P1-K1-F10
Method	BLASTN
NCBI GI	g2924733
BLAST score	234
E value	1.0e-129
Match length	297
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	152552
Seq. ID	LIB3175-080-P1-K1-F11
Method	BLASTX
NCBI GI	g3372230
BLAST score	536
E value	5.0e-55
Match length	110
% identity	93
NCBI Description	(AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No.	152553
Seq. ID	LIB3175-080-P1-K1-F12
Method	BLASTX
NCBI GI	g4206206
BLAST score	425
E value	5.0e-42
Match length	98
% identity	89
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	152554
Seq. ID	LIB3175-080-P1-K1-F2
Method	BLASTN
NCBI GI	g4512690
BLAST score	106
E value	2.0e-52
Match length	171
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	152555
Seq. ID	LIB3175-080-P1-K1-F3
Method	BLASTX
NCBI GI	g3043415
BLAST score	619
E value	1.0e-64
Match length	123
% identity	98
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	152556
Seq. ID	LIB3175-080-P1-K1-F4
Method	BLASTX
NCBI GI	g4191778
BLAST score	521
E value	3.0e-53
Match length	104
% identity	99
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

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Seq. No.	152557
Seq. ID	LIB3175-080-P1-K1-F5
Method	BLASTX
NCBI GI	g4314378
BLAST score	188
E value	3.0e-14
Match length	100
% identity	43
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	152558
Seq. ID	LIB3175-080-P1-K1-F6
Method	BLASTN
NCBI GI	g12540
BLAST score	64
E value	2.0e-27
Match length	134
% identity	93
NCBI Description	Chloroplast Sinapis alba tRNA-Ser gene and psbI gene for I polypeptide of photosystem II

Seq. No.	152559
Seq. ID	LIB3175-080-P1-K1-F7
Method	BLASTX
NCBI GI	g729102
BLAST score	573
E value	2.0e-59
Match length	113
% identity	100
NCBI Description	CHALCONE--FLAVONONE ISOMERASE >gi_320138_pir__JQ1687 chalcone isomerase (EC 5.5.1.6) - Arabidopsis thaliana >gi_166660_gb_AAA32766.1_ (M86358) chalcone isomerase [Arabidopsis thaliana]

Seq. No.	152560
Seq. ID	LIB3175-080-P1-K1-F9
Method	BLASTN
NCBI GI	g1209241
BLAST score	325
E value	0.0e+00
Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	152561
Seq. ID	LIB3175-080-P1-K1-G11
Method	BLASTN
NCBI GI	g2707927
BLAST score	227
E value	1.0e-125
Match length	254
% identity	97
NCBI Description	A.thaliana mRNA for outward rectifying potassium channel KCO1

Seq. No.	152562
Seq. ID	LIB3175-080-P1-K1-G12

Method	BLASTX
NCBI GI	g1703219
BLAST score	298
E value	3.0e-27
Match length	95
% identity	60
NCBI Description	AIG1 PROTEIN >gi_1127804 (U40856) AIG1 [Arabidopsis thaliana]

Seq. No.	152563
Seq. ID	LIB3175-080-P1-K1-G4
Method	BLASTX
NCBI GI	g1703227
BLAST score	188
E value	2.0e-14
Match length	50
% identity	70
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine aminotransferase [Hordeum vulgare]

Seq. No.	152564
Seq. ID	LIB3175-080-P1-K1-G7
Method	BLASTX
NCBI GI	g267073
BLAST score	538
E value	3.0e-55
Match length	100
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	152565
Seq. ID	LIB3175-080-P1-K1-G8
Method	BLASTX
NCBI GI	g2804280
BLAST score	621
E value	6.0e-65
Match length	121
% identity	98
NCBI Description	(AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase [Arabidopsis thaliana]

Seq. No.	152566
Seq. ID	LIB3175-080-P1-K1-G9
Method	BLASTX
NCBI GI	g2832359
BLAST score	373
E value	7.0e-36
Match length	90
% identity	83
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	152567
Seq. ID	LIB3175-080-P1-K1-H10
Method	BLASTX
NCBI GI	g1076678
BLAST score	297
E value	2.0e-27
Match length	62
% identity	95
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	152568
Seq. ID	LIB3175-080-P1-K1-H12
Method	BLASTX
NCBI GI	g544424
BLAST score	269
E value	9.0e-33
Match length	78
% identity	87
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	152569
Seq. ID	LIB3175-080-P1-K1-H5
Method	BLASTN
NCBI GI	g4678315
BLAST score	123
E value	8.0e-63
Match length	249
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	152570
Seq. ID	LIB3175-080-P1-K1-H6
Method	BLASTX
NCBI GI	g488571
BLAST score	395
E value	1.0e-38
Match length	91
% identity	89
NCBI Description	(U09462) histone H3.2 [Medicago sativa]

Seq. No.	152571
Seq. ID	LIB3175-080-P1-K1-H7
Method	BLASTX
NCBI GI	g2654122
BLAST score	572
E value	4.0e-59
Match length	130
% identity	88
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	152572
Seq. ID	LIB3175-080-P1-K1-H8
Method	BLASTX
NCBI GI	g4220446
BLAST score	417
E value	4.0e-41
Match length	109
% identity	85
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	152573
Seq. ID	LIB3175-080-P1-K1-H9
Method	BLASTX
NCBI GI	g118926
BLAST score	165
E value	1.0e-11
Match length	70
% identity	53
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	152574
Seq. ID	LIB3175-081-P1-K1-A1
Method	BLASTN
NCBI GI	g1865678
BLAST score	245
E value	1.0e-135
Match length	346
% identity	98
NCBI Description	A.thaliana ATB2 gene

Seq. No.	152575
Seq. ID	LIB3175-081-P1-K1-A10
Method	BLASTX
NCBI GI	g3688175
BLAST score	538
E value	4.0e-55
Match length	122
% identity	84
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]

Seq. No.	152576
Seq. ID	LIB3175-081-P1-K1-A11
Method	BLASTN
NCBI GI	g2828183
BLAST score	94
E value	2.0e-45

Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	152577
Seq. ID	LIB3175-081-P1-K1-A12
Method	BLASTX
NCBI GI	g1170621
BLAST score	289
E value	3.0e-26
Match length	64
% identity	88
NCBI Description	KINESIN-LIKE PROTEIN C >gi_1084342_pir__S48020 kinesin-related protein katC - Arabidopsis thaliana >gi_1438844_dbj_BAA04674_ (D21138) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No.	152578
Seq. ID	LIB3175-081-P1-K1-A2
Method	BLASTX
NCBI GI	g625977
BLAST score	601
E value	2.0e-62
Match length	118
% identity	99
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	152579
Seq. ID	LIB3175-081-P1-K1-A3
Method	BLASTN
NCBI GI	g4757410
BLAST score	66
E value	4.0e-29
Match length	118
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	152580
Seq. ID	LIB3175-081-P1-K1-A5
Method	BLASTX
NCBI GI	g3193289
BLAST score	603
E value	9.0e-63
Match length	142
% identity	85
NCBI Description	(AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]

Seq. No.	152581
Seq. ID	LIB3175-081-P1-K1-A6
Method	BLASTX

NCBI GI	g3063449
BLAST score	85
E value	3.0e-56
Match length	119
% identity	88
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	152582
Seq. ID	LIB3175-081-P1-K1-A7
Method	BLASTN
NCBI GI	g2494110
BLAST score	380
E value	0.0e+00
Match length	403
% identity	94
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152583
Seq. ID	LIB3175-081-P1-K1-A8
Method	BLASTN
NCBI GI	g2815404
BLAST score	415
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	152584
Seq. ID	LIB3175-081-P1-K1-A9
Method	BLASTX
NCBI GI	g127045
BLAST score	725
E value	4.0e-77
Match length	138
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	152585
Seq. ID	LIB3175-081-P1-K1-B10
Method	BLASTX
NCBI GI	g4262174
BLAST score	704
E value	1.0e-74
Match length	132
% identity	99
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	152586
Seq. ID	LIB3175-081-P1-K1-B11

Method	BLASTX
NCBI GI	g113782
BLAST score	486
E value	4.0e-49
Match length	109
% identity	89
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	152587
Seq. ID	LIB3175-081-P1-K1-B12
Method	BLASTX
NCBI GI	g2493144
BLAST score	420
E value	2.0e-41
Match length	118
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	152588
Seq. ID	LIB3175-081-P1-K1-B3
Method	BLASTN
NCBI GI	g4733953
BLAST score	101
E value	1.0e-49
Match length	257
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	152589
Seq. ID	LIB3175-081-P1-K1-B4
Method	BLASTX
NCBI GI	g3096908
BLAST score	269
E value	1.0e-23
Match length	133
% identity	48
NCBI Description	(AJ005811) cytidine deaminase [Arabidopsis thaliana] >gi_3818576 (AF080676) cytidine deaminase 2 [Arabidopsis thaliana]

Seq. No.	152590
Seq. ID	LIB3175-081-P1-K1-B5
Method	BLASTN
NCBI GI	g4262221
BLAST score	373
E value	0.0e+00
Match length	405

% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152591
Seq. ID	LIB3175-081-P1-K1-B6
Method	BLASTX
NCBI GI	g4206206
BLAST score	517
E value	1.0e-52
Match length	112
% identity	90
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	152592
Seq. ID	LIB3175-081-P1-K1-B7
Method	BLASTX
NCBI GI	g3738259
BLAST score	460
E value	5.0e-46
Match length	109
% identity	83
NCBI Description	(AB018411) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	152593
Seq. ID	LIB3175-081-P1-K1-B8
Method	BLASTX
NCBI GI	g3819699
BLAST score	560
E value	1.0e-57
Match length	140
% identity	83
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	152594
Seq. ID	LIB3175-081-P1-K1-B9
Method	BLASTX
NCBI GI	g3184283
BLAST score	585
E value	2.0e-60
Match length	132
% identity	92
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	152595
Seq. ID	LIB3175-081-P1-K1-C1
Method	BLASTX
NCBI GI	g902584
BLAST score	46
E value	8.0e-50
Match length	119
% identity	13
NCBI Description	(U29159) polyubiquitin containing 7 ubiquitin monomers [Zea

mays]

Seq. No.	152596
Seq. ID	LIB3175-081-P1-K1-C10
Method	BLASTX
NCBI GI	g2781394
BLAST score	616
E value	3.0e-64
Match length	125
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	152597
Seq. ID	LIB3175-081-P1-K1-C11
Method	BLASTN
NCBI GI	g4006885
BLAST score	335
E value	0.0e+00
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	152598
Seq. ID	LIB3175-081-P1-K1-C12
Method	BLASTX
NCBI GI	g4586265
BLAST score	548
E value	2.0e-56
Match length	140
% identity	76
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152599
Seq. ID	LIB3175-081-P1-K1-C2
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	152600
Seq. ID	LIB3175-081-P1-K1-C3
Method	BLASTX
NCBI GI	g4585935
BLAST score	594
E value	9.0e-62
Match length	111
% identity	99
NCBI Description	(AC007211) putative chlorophyll A/B binding protein [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1 (AF134123) Lhcb2 protein [Arabidopsis thaliana]

Seq. No. 152601

Seq. ID	LIB3175-081-P1-K1-C4
Method	BLASTX
NCBI GI	g1168748
BLAST score	642
E value	2.0e-67
Match length	126
% identity	62
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	152602
Seq. ID	LIB3175-081-P1-K1-C6
Method	BLASTN
NCBI GI	g2914688
BLAST score	90
E value	5.0e-43
Match length	290
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152603
Seq. ID	LIB3175-081-P1-K1-C7
Method	BLASTN
NCBI GI	g3063690
BLAST score	404
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	152604
Seq. ID	LIB3175-081-P1-K1-C8
Method	BLASTX
NCBI GI	g3168840
BLAST score	374
E value	6.0e-36
Match length	119
% identity	66
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	152605
Seq. ID	LIB3175-081-P1-K1-C9
Method	BLASTN
NCBI GI	g2182287
BLAST score	365
E value	0.0e+00
Match length	365
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	152606
Seq. ID	LIB3175-081-P1-K1-D1
Method	BLASTX

NCBI GI	g2497753
BLAST score	263
E value	6.0e-23
Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	152607
Seq. ID	LIB3175-081-P1-K1-D10
Method	BLASTX
NCBI GI	g114085
BLAST score	569
E value	8.0e-59
Match length	114
% identity	99
NCBI Description	RAS-RELATED PROTEIN ARA-1 >gi_81597_pir__JS0163 Ara protein - Arabidopsis thaliana >gi_538283 (M25471) ras-related protein [Arabidopsis thaliana]

Seq. No.	152608
Seq. ID	LIB3175-081-P1-K1-D11
Method	BLASTX
NCBI GI	g2654122
BLAST score	495
E value	4.0e-50
Match length	130
% identity	77
NCBI Description	(AF034694) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	152609
Seq. ID	LIB3175-081-P1-K1-D12
Method	BLASTX
NCBI GI	g4469022
BLAST score	674
E value	4.0e-71
Match length	131
% identity	99
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	152610
Seq. ID	LIB3175-081-P1-K1-D2
Method	BLASTX
NCBI GI	g3785990
BLAST score	395
E value	2.0e-38
Match length	109
% identity	79
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152611
Seq. ID	LIB3175-081-P1-K1-D3
Method	BLASTX

NCBI GI	g2129577
BLAST score	472
E value	2.0e-47
Match length	100
% identity	90
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	152612
Seq. ID	LIB3175-081-P1-K1-D5
Method	BLASTN
NCBI GI	g2098816
BLAST score	247
E value	1.0e-136
Match length	335
% identity	93
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	152613
Seq. ID	LIB3175-081-P1-K1-D6
Method	BLASTN
NCBI GI	g4756963
BLAST score	54
E value	5.0e-22
Match length	120
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	152614
Seq. ID	LIB3175-081-P1-K1-D7
Method	BLASTX
NCBI GI	g4261517
BLAST score	176
E value	7.0e-13
Match length	73
% identity	56
NCBI Description	(AF117334) cysteine proteinase inhibitor [Ipomoea batatas]

Seq. No.	152615
Seq. ID	LIB3175-081-P1-K1-D9
Method	BLASTN
NCBI GI	g4584387
BLAST score	365
E value	0.0e+00
Match length	381
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	152616
Seq. ID	LIB3175-081-P1-K1-E1
Method	BLASTX
NCBI GI	g3540208
BLAST score	725
E value	4.0e-77
Match length	139

% identity	98
NCBI Description	(AC004260) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	152617
Seq. ID	LIB3175-081-P1-K1-E11
Method	BLASTX
NCBI GI	g1617274
BLAST score	641
E value	3.0e-67
Match length	135
% identity	84
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	152618
Seq. ID	LIB3175-081-P1-K1-E12
Method	BLASTX
NCBI GI	g1769895
BLAST score	473
E value	1.0e-47
Match length	89
% identity	100
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	152619
Seq. ID	LIB3175-081-P1-K1-E2
Method	BLASTX
NCBI GI	g112741
BLAST score	683
E value	3.0e-72
Match length	129
% identity	98
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	152620
Seq. ID	LIB3175-081-P1-K1-E3
Method	BLASTX
NCBI GI	g114335
BLAST score	486
E value	5.0e-49
Match length	118
% identity	80
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	152621
Seq. ID	LIB3175-081-P1-K1-E4
Method	BLASTX
NCBI GI	g3915847
BLAST score	546

E value	5.0e-56
Match length	119
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	152622
Seq. ID	LIB3175-081-P1-K1-E5
Method	BLASTX
NCBI GI	g1388084
BLAST score	610
E value	1.0e-63
Match length	118
% identity	100
NCBI Description	(U35829) thioredoxin h [Arabidopsis thaliana]

Seq. No.	152623
Seq. ID	LIB3175-081-P1-K1-E6
Method	BLASTN
NCBI GI	g510490
BLAST score	158
E value	1.0e-83
Match length	170
% identity	98
NCBI Description	A.thaliana Apx1b gene

Seq. No.	152624
Seq. ID	LIB3175-081-P1-K1-E8
Method	BLASTX
NCBI GI	g2829911
BLAST score	188
E value	4.0e-14
Match length	134
% identity	9
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	152625
Seq. ID	LIB3175-081-P1-K1-E9
Method	BLASTX
NCBI GI	g4585882
BLAST score	436
E value	3.0e-43
Match length	83
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	152626
Seq. ID	LIB3175-081-P1-K1-F1
Method	BLASTX
NCBI GI	g100525
BLAST score	496
E value	2.0e-50
Match length	105
% identity	22
NCBI Description	ubiquitin precursor UbB2 - common sunflower (fragment) >gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein

[Helianthus annuus]

Seq. No.	152627
Seq. ID	LIB3175-081-P1-K1-F10
Method	BLASTN
NCBI GI	g3559806
BLAST score	407
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for nuclear protein HCF136

Seq. No.	152628
Seq. ID	LIB3175-081-P1-K1-F12
Method	BLASTX
NCBI GI	g2511574
BLAST score	555
E value	4.0e-57
Match length	112
% identity	100
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	152629
Seq. ID	LIB3175-081-P1-K1-F3
Method	BLASTX
NCBI GI	g4586263
BLAST score	667
E value	3.0e-70
Match length	131
% identity	96
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152630
Seq. ID	LIB3175-081-P1-K1-F4
Method	BLASTX
NCBI GI	g1771160
BLAST score	384
E value	4.0e-37
Match length	136
% identity	54
NCBI Description	(X98929) SBT1 [Lycopersicon esculentum] >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like protease [Lycopersicon esculentum]

Seq. No.	152631
Seq. ID	LIB3175-081-P1-K1-F5
Method	BLASTX
NCBI GI	g2244910
BLAST score	290
E value	4.0e-26
Match length	133
% identity	56
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	152632

Seq. ID	LIB3175-081-P1-K1-F7
Method	BLASTX
NCBI GI	g2495365
BLAST score	212
E value	6.0e-17
Match length	98
% identity	97
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	152633
Seq. ID	LIB3175-081-P1-K1-F8
Method	BLASTX
NCBI GI	g1432083
BLAST score	532
E value	2.0e-54
Match length	120
% identity	88
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	152634
Seq. ID	LIB3175-081-P1-K1-F9
Method	BLASTN
NCBI GI	g1107500
BLAST score	190
E value	1.0e-103
Match length	222
% identity	96
NCBI Description	A.thaliana mRNA for unknown protein (clone YAP037)

Seq. No.	152635
Seq. ID	LIB3175-081-P1-K1-G1
Method	BLASTX
NCBI GI	g3882081
BLAST score	506
E value	2.0e-51
Match length	103
% identity	36
NCBI Description	(AJ012552) polyubiquitin [Vicia faba]

Seq. No.	152636
Seq. ID	LIB3175-081-P1-K1-G11
Method	BLASTX
NCBI GI	g4218120
BLAST score	637
E value	9.0e-67
Match length	126
% identity	99
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	152637
Seq. ID	LIB3175-081-P1-K1-G12
Method	BLASTX

NCBI GI	g3451065
BLAST score	565
E value	2.0e-58
Match length	121
% identity	91
NCBI Description	(AL031326) water channel - like protein [Arabidopsis thaliana]

Seq. No.	152638
Seq. ID	LIB3175-081-P1-K1-G3
Method	BLASTX
NCBI GI	g1486472
BLAST score	614
E value	4.0e-64
Match length	140
% identity	86
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	152639
Seq. ID	LIB3175-081-P1-K1-G4
Method	BLASTX
NCBI GI	g3193297
BLAST score	555
E value	4.0e-57
Match length	130
% identity	80
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	152640
Seq. ID	LIB3175-081-P1-K1-G5
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	152641
Seq. ID	LIB3175-081-P1-K1-G6
Method	BLASTN
NCBI GI	g3046854
BLAST score	128
E value	1.0e-65
Match length	402
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	152642
Seq. ID	LIB3175-081-P1-K1-G7
Method	BLASTX
NCBI GI	g927575
BLAST score	356

E value	8.0e-34
Match length	82
% identity	74
NCBI Description	(U12926) alpha galactosidase [Glycine max]

Seq. No.	152643
Seq. ID	LIB3175-081-P1-K1-G8
Method	BLASTN
NCBI GI	g2564051
BLAST score	300
E value	1.0e-168
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	152644
Seq. ID	LIB3175-081-P1-K1-G9
Method	BLASTX
NCBI GI	g4725950
BLAST score	82
E value	3.0e-20
Match length	100
% identity	64
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana] >gi_4725951_emb_CAB41722.1_ (AL049730) putative proline-rich protein [Arabidopsis thaliana]

Seq. No.	152645
Seq. ID	LIB3175-081-P1-K1-H10
Method	BLASTN
NCBI GI	g4519193
BLAST score	119
E value	2.0e-60
Match length	166
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	152646
Seq. ID	LIB3175-081-P1-K1-H11
Method	BLASTN
NCBI GI	g2244901
BLAST score	36
E value	1.0e-10
Match length	168
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152647
Seq. ID	LIB3175-081-P1-K1-H12
Method	BLASTN
NCBI GI	g2245073
BLAST score	190
E value	1.0e-102
Match length	255

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152648
Seq. ID	LIB3175-081-P1-K1-H2
Method	BLASTX
NCBI GI	g3860277
BLAST score	600
E value	2.0e-62
Match length	142
% identity	85
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	152649
Seq. ID	LIB3175-081-P1-K1-H3
Method	BLASTX
NCBI GI	g2677828
BLAST score	268
E value	2.0e-23
Match length	69
% identity	74
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	152650
Seq. ID	LIB3175-081-P1-K1-H5
Method	BLASTN
NCBI GI	g511598
BLAST score	361
E value	0.0e+00
Match length	412
% identity	27
NCBI Description	Arabidopsis thaliana cell wall protein (APTR-1) gene, complete cds

Seq. No.	152651
Seq. ID	LIB3175-081-P1-K1-H7
Method	BLASTX
NCBI GI	g4704613
BLAST score	547
E value	3.0e-56
Match length	115
% identity	91
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	152652
Seq. ID	LIB3175-081-P1-K1-H8
Method	BLASTN
NCBI GI	g2864607
BLAST score	99
E value	3.0e-48
Match length	175
% identity	33
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	152653
Seq. ID	LIB3175-081-P1-K1-H9
Method	BLASTX
NCBI GI	g267069
BLAST score	558
E value	2.0e-57
Match length	103
% identity	100
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	152654
Seq. ID	LIB3175-082-P1-K1-A1
Method	BLASTX
NCBI GI	g2499236
BLAST score	611
E value	9.0e-64
Match length	134
% identity	89
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis thaliana]

Seq. No.	152655
Seq. ID	LIB3175-082-P1-K1-A10
Method	BLASTX
NCBI GI	g2244750
BLAST score	542
E value	1.0e-55
Match length	118
% identity	88
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	152656
Seq. ID	LIB3175-082-P1-K1-A11
Method	BLASTX
NCBI GI	g99759
BLAST score	574
E value	2.0e-59
Match length	124
% identity	87
NCBI Description	superoxide dismutase (EC 1.15.1.1) (Fe) - Arabidopsis thaliana (fragment)

Seq. No.	152657
Seq. ID	LIB3175-082-P1-K1-A2
Method	BLASTX
NCBI GI	g2464850
BLAST score	632
E value	3.0e-66
Match length	136
% identity	90

NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	152658
Seq. ID	LIB3175-082-P1-K1-A3
Method	BLASTX
NCBI GI	g4432865
BLAST score	411
E value	7.0e-48
Match length	109
% identity	81
NCBI Description	(AC006300) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	152659
Seq. ID	LIB3175-082-P1-K1-A4
Method	BLASTX
NCBI GI	g4154281
BLAST score	498
E value	2.0e-50
Match length	122
% identity	75
NCBI Description	(AF082347) C13 endopeptidase NP1 precursor [Zea mays]

Seq. No.	152660
Seq. ID	LIB3175-082-P1-K1-A5
Method	BLASTX
NCBI GI	g1071912
BLAST score	593
E value	1.0e-61
Match length	127
% identity	94
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	152661
Seq. ID	LIB3175-082-P1-K1-A6
Method	BLASTX
NCBI GI	g3776005
BLAST score	685
E value	2.0e-72
Match length	138
% identity	98
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	152662
Seq. ID	LIB3175-082-P1-K1-A8
Method	BLASTX
NCBI GI	g131154
BLAST score	736
E value	2.0e-78
Match length	133
% identity	99
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_72673_pir__A2NTP7 photosystem I P700 apoprotein A2 - common tobacco chloroplast >gi_11829_emb_CAA77351_ (Z00044)

PSI P700 apoprotein A2 [Nicotiana tabacum]
>gi_225197_prf__1211235AB photosystem I P700 apoprotein A2
[Nicotiana tabacum]

Seq. No.	152663
Seq. ID	LIB3175-082-P1-K1-A9
Method	BLASTX
NCBI GI	g4589398
BLAST score	361
E value	2.0e-34
Match length	79
% identity	81
NCBI Description	(D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No.	152664
Seq. ID	LIB3175-082-P1-K1-B1
Method	BLASTX
NCBI GI	g1621539
BLAST score	650
E value	3.0e-68
Match length	128
% identity	42
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	152665
Seq. ID	LIB3175-082-P1-K1-B10
Method	BLASTX
NCBI GI	g3461820
BLAST score	439
E value	1.0e-43
Match length	115
% identity	75
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	152666
Seq. ID	LIB3175-082-P1-K1-B11
Method	BLASTN
NCBI GI	g4531433
BLAST score	25
E value	3.0e-04
Match length	113
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	152667
Seq. ID	LIB3175-082-P1-K1-B12
Method	BLASTX
NCBI GI	g122085
BLAST score	501
E value	8.0e-51
Match length	118
% identity	86
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136)

[Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	152668
Seq. ID	LIB3175-082-P1-K1-B2
Method	BLASTN
NCBI GI	g2264314
BLAST score	400
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	152669
Seq. ID	LIB3175-082-P1-K1-B3
Method	BLASTX
NCBI GI	g2129740
BLAST score	616
E value	2.0e-64
Match length	136
% identity	88
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	152670
Seq. ID	LIB3175-082-P1-K1-B4
Method	BLASTX
NCBI GI	g2894574
BLAST score	735
E value	3.0e-78
Match length	137
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	152671
Seq. ID	LIB3175-082-P1-K1-B6
Method	BLASTN
NCBI GI	g4584387
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	152672
Seq. ID	LIB3175-082-P1-K1-B7
Method	BLASTX
NCBI GI	g2623962
BLAST score	398
E value	1.0e-38
Match length	94
% identity	84
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	152673
Seq. ID	LIB3175-082-P1-K1-B8
Method	BLASTX
NCBI GI	g4263711
BLAST score	324
E value	4.0e-30
Match length	62
% identity	100
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	152674
Seq. ID	LIB3175-082-P1-K1-B9
Method	BLASTX
NCBI GI	g1168328
BLAST score	411
E value	3.0e-40
Match length	133
% identity	59
NCBI Description	ACTIN-LIKE PROTEIN 3 >gi_629878_pir__S48844 actin-like protein - slime mold (Dictyostelium discoideum) >gi_2130164_pir__S69002 actin-like protein - slime mold (Dictyostelium discoideum) >gi_563346_emb_CAA86553_ (Z46418) actin-like protein [Dictyostelium discoideum]

Seq. No.	152675
Seq. ID	LIB3175-082-P1-K1-C1
Method	BLASTN
NCBI GI	g2564051
BLAST score	381
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	152676
Seq. ID	LIB3175-082-P1-K1-C10
Method	BLASTX
NCBI GI	g2500082
BLAST score	624
E value	3.0e-65
Match length	118
% identity	100
NCBI Description	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi_984735_emb_CAA56907_ (X80932) photosystem II D1 protein [Vigna unguiculata]

Seq. No.	152677
Seq. ID	LIB3175-082-P1-K1-C11
Method	BLASTN
NCBI GI	g3292807
BLAST score	387
E value	0.0e+00
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	152678
Seq. ID	LIB3175-082-P1-K1-C12
Method	BLASTX
NCBI GI	g3928103
BLAST score	516
E value	1.0e-52
Match length	112
% identity	89
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	152679
Seq. ID	LIB3175-082-P1-K1-C2
Method	BLASTX
NCBI GI	g3413700
BLAST score	600
E value	2.0e-62
Match length	135
% identity	89
NCBI Description	(AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No.	152680
Seq. ID	LIB3175-082-P1-K1-C3
Method	BLASTX
NCBI GI	g4741940
BLAST score	533
E value	1.0e-54
Match length	97
% identity	65
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No. 152681

Seq. ID	LIB3175-082-P1-K1-C5
Method	BLASTX
NCBI GI	g3047125
BLAST score	668
E value	2.0e-70
Match length	128
% identity	98
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	152682
Seq. ID	LIB3175-082-P1-K1-C7
Method	BLASTN
NCBI GI	g1865678
BLAST score	266
E value	1.0e-148
Match length	360
% identity	100
NCBI Description	A.thaliana ATB2 gene

Seq. No.	152683
Seq. ID	LIB3175-082-P1-K1-C8
Method	BLASTN
NCBI GI	g4335744
BLAST score	73
E value	8.0e-33
Match length	197
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152684
Seq. ID	LIB3175-082-P1-K1-C9
Method	BLASTX
NCBI GI	g902586
BLAST score	588
E value	5.0e-61
Match length	118
% identity	22
NCBI Description	(U29162) ubiquitin [Zea mays]

Seq. No.	152685
Seq. ID	LIB3175-082-P1-K1-D1
Method	BLASTX
NCBI GI	g132074
BLAST score	647
E value	6.0e-68
Match length	119
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	152686
Seq. ID	LIB3175-082-P1-K1-D10
Method	BLASTN
NCBI GI	g3367567

BLAST score	119
E value	3.0e-60
Match length	349
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	152687
Seq. ID	LIB3175-082-P1-K1-D11
Method	BLASTX
NCBI GI	g3337356
BLAST score	442
E value	6.0e-44
Match length	93
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	152688
Seq. ID	LIB3175-082-P1-K1-D12
Method	BLASTX
NCBI GI	g3169173
BLAST score	673
E value	5.0e-71
Match length	131
% identity	95
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	152689
Seq. ID	LIB3175-082-P1-K1-D2
Method	BLASTX
NCBI GI	g1170503
BLAST score	89
E value	1.5e-02
Match length	127
% identity	81
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	152690
Seq. ID	LIB3175-082-P1-K1-D3
Method	BLASTN
NCBI GI	g2351064
BLAST score	412
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	152691
Seq. ID	LIB3175-082-P1-K1-D4

Method	BLASTX
NCBI GI	g4586265
BLAST score	510
E value	7.0e-52
Match length	136
% identity	74
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152692
Seq. ID	LIB3175-082-P1-K1-D5
Method	BLASTX
NCBI GI	g1931639
BLAST score	596
E value	6.0e-62
Match length	120
% identity	94
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	152693
Seq. ID	LIB3175-082-P1-K1-D6
Method	BLASTX
NCBI GI	g1170939
BLAST score	422
E value	2.0e-41
Match length	103
% identity	83
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	152694
Seq. ID	LIB3175-082-P1-K1-D7
Method	BLASTN
NCBI GI	g4376087
BLAST score	321
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	152695
Seq. ID	LIB3175-082-P1-K1-D9
Method	BLASTX
NCBI GI	g4415992
BLAST score	708
E value	4.0e-75
Match length	135
% identity	99
NCBI Description	(AF059288) beta-tubulin 2 [Eleusine indica]

Seq. No.	152696
Seq. ID	LIB3175-082-P1-K1-E12
Method	BLASTX

NCBI GI	g1705677
BLAST score	704
E value	1.0e-74
Match length	137
% identity	54
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	152697
Seq. ID	LIB3175-082-P1-K1-E2
Method	BLASTX
NCBI GI	g4158221
BLAST score	577
E value	9.0e-60
Match length	127
% identity	80
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	152698
Seq. ID	LIB3175-082-P1-K1-E3
Method	BLASTX
NCBI GI	g4538911
BLAST score	277
E value	1.0e-24
Match length	93
% identity	60
NCBI Description	(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152699
Seq. ID	LIB3175-082-P1-K1-E4
Method	BLASTX
NCBI GI	g3025189
BLAST score	405
E value	1.0e-39
Match length	133
% identity	59
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No.	152700
Seq. ID	LIB3175-082-P1-K1-E5
Method	BLASTX
NCBI GI	g4539335
BLAST score	287
E value	9.0e-26
Match length	135
% identity	44
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	152701
Seq. ID	LIB3175-082-P1-K1-E7
Method	BLASTX
NCBI GI	g4585980
BLAST score	643

E value	2.0e-67
Match length	135
% identity	90
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	152702
Seq. ID	LIB3175-082-P1-K1-E8
Method	BLASTX
NCBI GI	g1934730
BLAST score	498
E value	2.0e-50
Match length	101
% identity	97
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	152703
Seq. ID	LIB3175-082-P1-K1-E9
Method	BLASTX
NCBI GI	g1168256
BLAST score	651
E value	2.0e-68
Match length	126
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	152704
Seq. ID	LIB3175-082-P1-K1-F1
Method	BLASTN
NCBI GI	g2264310
BLAST score	353
E value	0.0e+00
Match length	396
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	152705
Seq. ID	LIB3175-082-P1-K1-F11
Method	BLASTX
NCBI GI	g131770
BLAST score	303
E value	1.0e-27
Match length	82
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	152706
Seq. ID	LIB3175-082-P1-K1-F2

Method	BLASTN
NCBI GI	g4199934
BLAST score	298
E value	1.0e-167
Match length	356
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	152707
Seq. ID	LIB3175-082-P1-K1-F3
Method	BLASTX
NCBI GI	g125606
BLAST score	225
E value	2.0e-18
Match length	67
% identity	67
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	152708
Seq. ID	LIB3175-082-P1-K1-F4
Method	BLASTN
NCBI GI	g4455262
BLAST score	387
E value	0.0e+00
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	152709
Seq. ID	LIB3175-082-P1-K1-F5
Method	BLASTN
NCBI GI	g3873174
BLAST score	262
E value	1.0e-145
Match length	338
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	152710
Seq. ID	LIB3175-082-P1-K1-F6
Method	BLASTN
NCBI GI	g4589443
BLAST score	182
E value	8.0e-98
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP7, complete sequence

Seq. No.	152711
Seq. ID	LIB3175-082-P1-K1-F7

Method	BLASTX
NCBI GI	g2529665
BLAST score	388
E value	1.0e-37
Match length	111
% identity	72
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	152712
Seq. ID	LIB3175-082-P1-K1-F8
Method	BLASTX
NCBI GI	g4006890
BLAST score	506
E value	2.0e-51
Match length	110
% identity	91
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	152713
Seq. ID	LIB3175-082-P1-K1-F9
Method	BLASTX
NCBI GI	g1169201
BLAST score	562
E value	5.0e-58
Match length	135
% identity	84
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	152714
Seq. ID	LIB3175-082-P1-K1-G1
Method	BLASTX
NCBI GI	g131770
BLAST score	429
E value	2.0e-42
Match length	115
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	152715
Seq. ID	LIB3175-082-P1-K1-G11
Method	BLASTX
NCBI GI	g1402908
BLAST score	590
E value	3.0e-61
Match length	131
% identity	88
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)

peroxidase [Arabidopsis thaliana]

Seq. No.	152716
Seq. ID	LIB3175-082-P1-K1-G12
Method	BLASTX
NCBI GI	g3668080
BLAST score	229
E value	3.0e-19
Match length	83
% identity	60
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	152717
Seq. ID	LIB3175-082-P1-K1-G2
Method	BLASTX
NCBI GI	g2342459
BLAST score	107
E value	1.0e-67
Match length	134
% identity	96
NCBI Description	(AB006068) acidic endochitinase [Arabidopsis thaliana]

Seq. No.	152718
Seq. ID	LIB3175-082-P1-K1-G3
Method	BLASTX
NCBI GI	g3193330
BLAST score	316
E value	4.0e-29
Match length	128
% identity	57
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	152719
Seq. ID	LIB3175-082-P1-K1-G4
Method	BLASTX
NCBI GI	g135449
BLAST score	644
E value	1.0e-67
Match length	137
% identity	90
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]

Seq. No.	152720
Seq. ID	LIB3175-082-P1-K1-G5
Method	BLASTX
NCBI GI	g3335371
BLAST score	668
E value	2.0e-70
Match length	136
% identity	99
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	152721

Seq. ID	LIB3175-082-P1-K1-G6
Method	BLASTN
NCBI GI	g4757394
BLAST score	251
E value	1.0e-139
Match length	281
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence

Seq. No.	152722
Seq. ID	LIB3175-082-P1-K1-G7
Method	BLASTX
NCBI GI	g1773330
BLAST score	568
E value	1.0e-58
Match length	133
% identity	83
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	152723
Seq. ID	LIB3175-082-P1-K1-G8
Method	BLASTX
NCBI GI	g4193388
BLAST score	385
E value	3.0e-37
Match length	107
% identity	71
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	152724
Seq. ID	LIB3175-082-P1-K1-G9
Method	BLASTN
NCBI GI	g2342717
BLAST score	389
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152725
Seq. ID	LIB3175-082-P1-K1-H10
Method	BLASTN
NCBI GI	g4733953
BLAST score	244
E value	1.0e-135
Match length	392
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	152726
Seq. ID	LIB3175-082-P1-K1-H12
Method	BLASTX
NCBI GI	g112681

BLAST score	559
E value	1.0e-57
Match length	114
% identity	93
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	152727
Seq. ID	LIB3175-082-P1-K1-H2
Method	BLASTN
NCBI GI	g2264310
BLAST score	356
E value	0.0e+00
Match length	395
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	152728
Seq. ID	LIB3175-082-P1-K1-H3
Method	BLASTX
NCBI GI	g1628583
BLAST score	615
E value	3.0e-64
Match length	120
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	152729
Seq. ID	LIB3175-082-P1-K1-H4
Method	BLASTN
NCBI GI	g4757414
BLAST score	385
E value	0.0e+00
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	152730
Seq. ID	LIB3175-082-P1-K1-H5
Method	BLASTX
NCBI GI	g3193323
BLAST score	638
E value	7.0e-67
Match length	126
% identity	100
NCBI Description	(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm, score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32 amino acids are different [Arabidopsis thaliana]

Seq. No.	152731
Seq. ID	LIB3175-082-P1-K1-H6
Method	BLASTX
NCBI GI	g2244879
BLAST score	57
E value	2.0e-67
Match length	134
% identity	96
NCBI Description	(Z97338) Nucleotide sequence of a cDNA clone encoding a beta-amylase from Arabidopsis thaliana

Seq. No.	152732
Seq. ID	LIB3175-082-P1-K1-H7
Method	BLASTN
NCBI GI	g3426033
BLAST score	246
E value	1.0e-136
Match length	349
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152733
Seq. ID	LIB3175-082-P1-K1-H8
Method	BLASTX
NCBI GI	g2853078
BLAST score	732
E value	6.0e-78
Match length	135
% identity	99
NCBI Description	(AL021768) TMV resistance protein N-like [Arabidopsis thaliana]

Seq. No.	152734
Seq. ID	LIB3176-001-Q1-K1-A1
Method	BLASTX
NCBI GI	g1546688
BLAST score	541
E value	1.0e-55
Match length	122
% identity	88
NCBI Description	(X98802) peroxidase ATP11a [Arabidopsis thaliana] >gi_2388572 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana] >gi_2388573 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]

Seq. No.	152735
Seq. ID	LIB3176-001-Q1-K1-A10
Method	BLASTX
NCBI GI	g4262242
BLAST score	571
E value	5.0e-59
Match length	111
% identity	99
NCBI Description	(AC006200) NADC homolog [Arabidopsis thaliana]

Seq. No.	152736
Seq. ID	LIB3176-001-Q1-K1-A11
Method	BLASTX
NCBI GI	g3150407
BLAST score	321
E value	5.0e-30
Match length	78
% identity	73
NCBI Description	(AC004165) hypothetical protein [Arabidopsis thaliana]

Seq. No.	152737
Seq. ID	LIB3176-001-Q1-K1-A12
Method	BLASTN
NCBI GI	g972918
BLAST score	227
E value	1.0e-125
Match length	235
% identity	99
NCBI Description	Arabidopsis thaliana IAA8 (IAA8) gene complete cds

Seq. No.	152738
Seq. ID	LIB3176-001-Q1-K1-A2
Method	BLASTX
NCBI GI	g1363488
BLAST score	514
E value	3.0e-52
Match length	100
% identity	100
NCBI Description	IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410) IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_ (AC006340) auxin-induced IAA8 protein [Arabidopsis thaliana]

Seq. No.	152739
Seq. ID	LIB3176-001-Q1-K1-A3
Method	BLASTX
NCBI GI	g2244910
BLAST score	231
E value	4.0e-19
Match length	111
% identity	48
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	152740
Seq. ID	LIB3176-001-Q1-K1-A4
Method	BLASTN
NCBI GI	g3413696
BLAST score	214
E value	1.0e-117
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152741
Seq. ID	LIB3176-001-Q1-K1-A5
Method	BLASTX

NCBI GI	g113032
BLAST score	225
E value	2.0e-24
Match length	81
% identity	76
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68210_pir__WZCSI isocitrate lyase (EC 4.1.3.1) - castor bean >gi_169707 (M17145) isocitrate lyase [Ricinus communis] >gi_225861_prf__1401247A isocitrate lyase [Ricinus communis]

Seq. No.	152742
Seq. ID	LIB3176-001-Q1-K1-A6
Method	BLASTX
NCBI GI	g4336752
BLAST score	446
E value	1.0e-44
Match length	88
% identity	94
NCBI Description	(AF104451) catalase [Brassica juncea]

Seq. No.	152743
Seq. ID	LIB3176-001-Q1-K1-A7
Method	BLASTX
NCBI GI	g4191778
BLAST score	562
E value	5.0e-58
Match length	128
% identity	88
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	152744
Seq. ID	LIB3176-001-Q1-K1-A9
Method	BLASTX
NCBI GI	g4240169
BLAST score	205
E value	4.0e-16
Match length	139
% identity	8
NCBI Description	(AB020647) KIAA0840 protein [Homo sapiens]

Seq. No.	152745
Seq. ID	LIB3176-001-Q1-K1-B1
Method	BLASTX
NCBI GI	g4049348
BLAST score	370
E value	2.0e-35
Match length	73
% identity	100
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	152746
Seq. ID	LIB3176-001-Q1-K1-B10
Method	BLASTX
NCBI GI	g3128180
BLAST score	387

E value	1.0e-37
Match length	84
% identity	96
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	152747
Seq. ID	LIB3176-001-Q1-K1-B11
Method	BLASTX
NCBI GI	g4678301
BLAST score	728
E value	2.0e-77
Match length	139
% identity	96
NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	152748
Seq. ID	LIB3176-001-Q1-K1-B12
Method	BLASTX
NCBI GI	g3212869
BLAST score	532
E value	2.0e-54
Match length	110
% identity	87
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	152749
Seq. ID	LIB3176-001-Q1-K1-B3
Method	BLASTX
NCBI GI	g1169476
BLAST score	685
E value	2.0e-72
Match length	131
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632) vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No.	152750
Seq. ID	LIB3176-001-Q1-K1-B4
Method	BLASTX
NCBI GI	g3123271
BLAST score	374
E value	3.0e-36
Match length	72
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	152751
Seq. ID	LIB3176-001-Q1-K1-B7
Method	BLASTX
NCBI GI	g119143
BLAST score	170
E value	1.0e-13
Match length	104
% identity	45

NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	152752
Seq. ID	LIB3176-001-Q1-K1-C1
Method	BLASTX
NCBI GI	g1673366
BLAST score	710
E value	2.0e-75
Match length	139
% identity	100
NCBI Description	(Z22673) cytosolic tRNA-Ala synthetase [Arabidopsis thaliana]

Seq. No.	152753
Seq. ID	LIB3176-001-Q1-K1-C10
Method	BLASTN
NCBI GI	g2702261
BLAST score	160
E value	1.0e-84
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152754
Seq. ID	LIB3176-001-Q1-K1-C11
Method	BLASTX
NCBI GI	g3668097
BLAST score	659
E value	2.0e-69
Match length	132
% identity	98
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	152755
Seq. ID	LIB3176-001-Q1-K1-C12
Method	BLASTN
NCBI GI	g4678291
BLAST score	41
E value	4.0e-14
Match length	129
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	152756
Seq. ID	LIB3176-001-Q1-K1-C2

Method	BLASTX
NCBI GI	g4584110
BLAST score	633
E value	3.0e-66
Match length	122
% identity	100
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	152757
Seq. ID	LIB3176-001-Q1-K1-C3
Method	BLASTX
NCBI GI	g1086833
BLAST score	267
E value	2.0e-23
Match length	115
% identity	40
NCBI Description	(U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No.	152758
Seq. ID	LIB3176-001-Q1-K1-C5
Method	BLASTX
NCBI GI	g2213583
BLAST score	308
E value	3.0e-28
Match length	120
% identity	49
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	152759
Seq. ID	LIB3176-001-Q1-K1-C6
Method	BLASTX
NCBI GI	g1076393
BLAST score	562
E value	5.0e-58
Match length	114
% identity	100
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	152760
Seq. ID	LIB3176-001-Q1-K1-C7
Method	BLASTX
NCBI GI	g4741962
BLAST score	88
E value	3.0e-42
Match length	128
% identity	52
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	152761
Seq. ID	LIB3176-001-Q1-K1-C8
Method	BLASTX
NCBI GI	g4741962
BLAST score	433

E value	8.0e-43
Match length	133
% identity	51
NCBI Description	(AF134131) PsbS protein [Arabidopsis thaliana]

Seq. No.	152762
Seq. ID	LIB3176-001-Q1-K1-C9
Method	BLASTX
NCBI GI	g480297
BLAST score	342
E value	3.0e-32
Match length	119
% identity	52
NCBI Description	glycoprotein EP1 - carrot >gi_349437 (L16983) N-glycosylation sites: (130..138), (244..252), (352..360), (734..742), (748..756), (865..873) [Daucus carota]

Seq. No.	152763
Seq. ID	LIB3176-001-Q1-K1-D10
Method	BLASTX
NCBI GI	g1173045
BLAST score	157
E value	2.0e-10
Match length	30
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L37A >gi_421866_pir__S34661 ribosomal protein L37a - turnip >gi_347062 (L21897) ribosomal protein [Brassica rapa] >gi_395077_emb_CAA80864_ (Z24739) ribosomal protein L37a [Brassica rapa]

Seq. No.	152764
Seq. ID	LIB3176-001-Q1-K1-D11
Method	BLASTX
NCBI GI	g2738248
BLAST score	719
E value	2.0e-76
Match length	141
% identity	98
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	152765
Seq. ID	LIB3176-001-Q1-K1-D12
Method	BLASTX
NCBI GI	g1706749
BLAST score	566
E value	2.0e-58
Match length	115
% identity	99
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177) 3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]

Seq. No.	152766
Seq. ID	LIB3176-001-Q1-K1-D2
Method	BLASTX

NCBI GI g2493045
BLAST score 545
E value 5.0e-56
Match length 127
% identity 83
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No. 152767
Seq. ID LIB3176-001-Q1-K1-D3
Method BLASTX
NCBI GI g1546690
BLAST score 699
E value 5.0e-74
Match length 138
% identity 100
NCBI Description (X98803) peroxidase ATP14a [Arabidopsis thaliana]

Seq. No. 152768
Seq. ID LIB3176-001-Q1-K1-D4
Method BLASTX
NCBI GI g4755189
BLAST score 371
E value 1.0e-35
Match length 130
% identity 57
NCBI Description (AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 152769
Seq. ID LIB3176-001-Q1-K1-D5
Method BLASTX
NCBI GI g115385
BLAST score 720
E value 2.0e-76
Match length 140
% identity 96
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 152770
Seq. ID LIB3176-001-Q1-K1-D6
Method BLASTX
NCBI GI g2924779
BLAST score 582
E value 2.0e-60
Match length 139
% identity 86
NCBI Description (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No. 152771
Seq. ID LIB3176-001-Q1-K1-D8

Method	BLASTN
NCBI GI	g2815519
BLAST score	58
E value	6.0e-24
Match length	246
% identity	94
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	152772
Seq. ID	LIB3176-001-Q1-K1-D9
Method	BLASTX
NCBI GI	g1363489
BLAST score	586
E value	7.0e-61
Match length	124
% identity	88
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152773
Seq. ID	LIB3176-001-Q1-K1-E10
Method	BLASTX
NCBI GI	g2341028
BLAST score	658
E value	3.0e-69
Match length	125
% identity	100
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	152774
Seq. ID	LIB3176-001-Q1-K1-E11
Method	BLASTX
NCBI GI	g3445200
BLAST score	389
E value	1.0e-37
Match length	90
% identity	86
NCBI Description	(AC004786) putative squalene epoxidase [Arabidopsis thaliana]

Seq. No.	152775
Seq. ID	LIB3176-001-Q1-K1-E12
Method	BLASTX
NCBI GI	g1854445
BLAST score	491
E value	1.0e-49
Match length	114
% identity	79
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	152776
Seq. ID	LIB3176-001-Q1-K1-E2
Method	BLASTX

NCBI GI	g3894178
BLAST score	327
E value	2.0e-30
Match length	70
% identity	87
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	152777
Seq. ID	LIB3176-001-Q1-K1-E3
Method	BLASTN
NCBI GI	g4512656
BLAST score	96
E value	1.0e-46
Match length	282
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	152778
Seq. ID	LIB3176-001-Q1-K1-E4
Method	BLASTX
NCBI GI	g3228279
BLAST score	135
E value	7.0e-12
Match length	120
% identity	37
NCBI Description	(AB005289) ABC transporter 7 protein [Homo sapiens]

Seq. No.	152779
Seq. ID	LIB3176-001-Q1-K1-E5
Method	BLASTX
NCBI GI	g2160166
BLAST score	712
E value	1.0e-75
Match length	139
% identity	100
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	152780
Seq. ID	LIB3176-001-Q1-K1-E6
Method	BLASTX
NCBI GI	g2924779
BLAST score	585
E value	1.0e-60
Match length	120
% identity	97
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	152781
Seq. ID	LIB3176-001-Q1-K1-E7
Method	BLASTX
NCBI GI	g119143

BLAST score	628
E value	8.0e-66
Match length	118
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	152782
Seq. ID	LIB3176-001-Q1-K1-E8
Method	BLASTX
NCBI GI	g2129777
BLAST score	169
E value	5.0e-15
Match length	50
% identity	78
NCBI Description	Y49 protein - Arabidopsis thaliana >gi_928969_emb_CAA62033_ (X90385) Y49 [Arabidopsis thaliana] >gi_1020157 (U26937) DNA-binding protein [Arabidopsis thaliana] >gi_4581115_gb_AAD24605.1_AC005825_12 (AC005825) MYB-like protein;very similar to GB:2129777 [Arabidopsis thaliana]

Seq. No.	152783
Seq. ID	LIB3176-001-Q1-K1-E9
Method	BLASTN
NCBI GI	g2564050
BLAST score	43
E value	6.0e-15
Match length	149
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	152784
Seq. ID	LIB3176-001-Q1-K1-F1
Method	BLASTN
NCBI GI	g3212846
BLAST score	154
E value	3.0e-81
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152785
Seq. ID	LIB3176-001-Q1-K1-F10
Method	BLASTX
NCBI GI	g4099090
BLAST score	216
E value	2.0e-17

Match length	123
% identity	46
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	152786
Seq. ID	LIB3176-001-Q1-K1-F11
Method	BLASTX
NCBI GI	g4099090
BLAST score	213
E value	5.0e-17
Match length	123
% identity	46
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	152787
Seq. ID	LIB3176-001-Q1-K1-F12
Method	BLASTN
NCBI GI	g2564050
BLAST score	34
E value	1.0e-09
Match length	46
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	152788
Seq. ID	LIB3176-001-Q1-K1-F2
Method	BLASTX
NCBI GI	g1175012
BLAST score	712
E value	1.0e-75
Match length	138
% identity	100
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	152789
Seq. ID	LIB3176-001-Q1-K1-F5
Method	BLASTX
NCBI GI	g1172872
BLAST score	586
E value	8.0e-61
Match length	111
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	152790
Seq. ID	LIB3176-001-Q1-K1-F6
Method	BLASTX
NCBI GI	g2129577
BLAST score	399

E value	7.0e-39
Match length	106
% identity	76
NCBI Description	DnaJ homolog protein - Arabidopsis thaliana >gi_727357 (U22340) DnaJ homolog [Arabidopsis thaliana]

Seq. No.	152791
Seq. ID	LIB3176-001-Q1-K1-F7
Method	BLASTX
NCBI GI	g232031
BLAST score	327
E value	2.0e-30
Match length	114
% identity	54
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	152792
Seq. ID	LIB3176-001-Q1-K1-F8
Method	BLASTX
NCBI GI	g113024
BLAST score	665
E value	4.0e-70
Match length	136
% identity	99
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	152793
Seq. ID	LIB3176-001-Q1-K1-F9
Method	BLASTN
NCBI GI	g4757678
BLAST score	362
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	152794
Seq. ID	LIB3176-001-Q1-K1-G1
Method	BLASTX
NCBI GI	g2506443
BLAST score	537
E value	4.0e-55
Match length	107
% identity	99
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No.	152795
Seq. ID	LIB3176-001-Q1-K1-G10
Method	BLASTX
NCBI GI	g3023500
BLAST score	189
E value	1.0e-14
Match length	63
% identity	60
NCBI Description	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2 (ENDOPEPTIDASE CLP 2) >gi_2351823 (U92039) ATP-dependent Clp protease, proteolytic subunit [Synechococcus PCC7942]

Seq. No.	152796
Seq. ID	LIB3176-001-Q1-K1-G11
Method	BLASTX
NCBI GI	g231586
BLAST score	211
E value	4.0e-17
Match length	91
% identity	55
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	152797
Seq. ID	LIB3176-001-Q1-K1-G2
Method	BLASTN
NCBI GI	g4585890
BLAST score	34
E value	2.0e-09
Match length	158
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	152798
Seq. ID	LIB3176-001-Q1-K1-G3
Method	BLASTX
NCBI GI	g135391
BLAST score	291
E value	8.0e-27
Match length	55
% identity	93
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_71583_pir__UBMUAM tubulin alpha-1 chain - Arabidopsis thaliana >gi_166896 (M21414) alpha-1-tubulin [Arabidopsis thaliana]

Seq. No.	152799
Seq. ID	LIB3176-001-Q1-K1-G4
Method	BLASTX
NCBI GI	g3402716
BLAST score	333
E value	4.0e-31

Match length	116
% identity	66
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	152800
Seq. ID	LIB3176-001-Q1-K1-G6
Method	BLASTX
NCBI GI	g4006883
BLAST score	321
E value	2.0e-30
Match length	71
% identity	85
NCBI Description	(Z99707) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	152801
Seq. ID	LIB3176-001-Q1-K1-G7
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	5.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	152802
Seq. ID	LIB3176-001-Q1-K1-G8
Method	BLASTX
NCBI GI	g3929649
BLAST score	364
E value	6.0e-35
Match length	76
% identity	100
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	152803
Seq. ID	LIB3176-001-Q1-K1-G9
Method	BLASTN
NCBI GI	g4589445
BLAST score	229
E value	1.0e-126
Match length	233
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	152804
Seq. ID	LIB3176-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g4337027
BLAST score	529
E value	4.0e-54
Match length	113
% identity	95
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	152805
Seq. ID	LIB3176-001-Q1-K1-H3
Method	BLASTX
NCBI GI	g480450
BLAST score	533
E value	1.0e-54
Match length	130
% identity	84
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	152806
Seq. ID	LIB3176-001-Q1-K1-H7
Method	BLASTN
NCBI GI	g4585890
BLAST score	168
E value	2.0e-89
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	152807
Seq. ID	LIB3176-001-Q1-K1-H8
Method	BLASTX
NCBI GI	g3915865
BLAST score	234
E value	4.0e-20
Match length	66
% identity	73
NCBI Description	40S RIBOSOMAL PROTEIN S4

Seq. No.	152808
Seq. ID	LIB3176-001-Q1-K1-H9
Method	BLASTX
NCBI GI	g730645
BLAST score	336
E value	1.0e-31
Match length	89
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	152809
Seq. ID	LIB3176-002-Q1-K1-A1
Method	BLASTX
NCBI GI	g1617013
BLAST score	148
E value	1.0e-09
Match length	30

% identity	97
NCBI Description	(Y07745) histone H2B like protein [Arabidopsis thaliana]

Seq. No.	152810
Seq. ID	LIB3176-002-Q1-K1-A10
Method	BLASTX
NCBI GI	g2062164
BLAST score	427
E value	2.0e-42
Match length	81
% identity	100
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	152811
Seq. ID	LIB3176-002-Q1-K1-A11
Method	BLASTX
NCBI GI	g3036806
BLAST score	422
E value	7.0e-42
Match length	83
% identity	100
NCBI Description	(AL022373) glycine-rich protein [Arabidopsis thaliana]

Seq. No.	152812
Seq. ID	LIB3176-002-Q1-K1-A12
Method	BLASTN
NCBI GI	g4519192
BLAST score	84
E value	1.0e-39
Match length	116
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	152813
Seq. ID	LIB3176-002-Q1-K1-A3
Method	BLASTX
NCBI GI	g3914386
BLAST score	229
E value	3.0e-19
Match length	95
% identity	46
NCBI Description	ALLERGEN MF1 >gi_3445490_dbj_BAA32435_ (AB011804) MF1 [Malassezia furfur]

Seq. No.	152814
Seq. ID	LIB3176-002-Q1-K1-A5
Method	BLASTX
NCBI GI	g120667
BLAST score	306
E value	3.0e-28
Match length	74
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	152815
Seq. ID	LIB3176-002-Q1-K1-A6
Method	BLASTN
NCBI GI	g3805839
BLAST score	128
E value	9.0e-66
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	152816
Seq. ID	LIB3176-002-Q1-K1-A8
Method	BLASTX
NCBI GI	g2642159
BLAST score	242
E value	5.0e-21
Match length	52
% identity	90
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	152817
Seq. ID	LIB3176-002-Q1-K1-A9
Method	BLASTX
NCBI GI	g137465
BLAST score	254
E value	4.0e-22
Match length	59
% identity	86
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	152818
Seq. ID	LIB3176-002-Q1-K1-B1
Method	BLASTX
NCBI GI	g1076366
BLAST score	291
E value	8.0e-27
Match length	62
% identity	87
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

09601-9LL0-0000

Seq. No.	152819
Seq. ID	LIB3176-002-Q1-K1-B10
Method	BLASTX
NCBI GI	g2253010
BLAST score	445
E value	1.0e-44
Match length	95
% identity	87
NCBI Description	(Y14199) MAP3K delta-1 protein kinase [Arabidopsis thaliana]

Seq. No.	152820
Seq. ID	LIB3176-002-Q1-K1-B11
Method	BLASTN
NCBI GI	g2264311
BLAST score	211
E value	1.0e-115
Match length	290
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	152821
Seq. ID	LIB3176-002-Q1-K1-B12
Method	BLASTX
NCBI GI	g2827699
BLAST score	232
E value	1.0e-19
Match length	92
% identity	59
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	152822
Seq. ID	LIB3176-002-Q1-K1-B2
Method	BLASTX
NCBI GI	g2497733
BLAST score	288
E value	4.0e-26
Match length	81
% identity	75
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	152823
Seq. ID	LIB3176-002-Q1-K1-B3
Method	BLASTX
NCBI GI	g114335
BLAST score	488
E value	1.0e-49
Match length	96
% identity	98
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629

(J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	152824
Seq. ID	LIB3176-002-Q1-K1-B4
Method	BLASTN
NCBI GI	g4454447
BLAST score	210
E value	1.0e-114
Match length	288
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152825
Seq. ID	LIB3176-002-Q1-K1-B6
Method	BLASTN
NCBI GI	g313837
BLAST score	203
E value	1.0e-110
Match length	251
% identity	96
NCBI Description	A.thaliana gene for hemC

Seq. No.	152826
Seq. ID	LIB3176-002-Q1-K1-B7
Method	BLASTX
NCBI GI	g2497733
BLAST score	409
E value	2.0e-40
Match length	78
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	152827
Seq. ID	LIB3176-002-Q1-K1-B8
Method	BLASTN
NCBI GI	g4006885
BLAST score	279
E value	1.0e-156
Match length	283
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	152828
Seq. ID	LIB3176-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g4454036
BLAST score	298
E value	1.0e-27
Match length	64
% identity	89
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	152829
Seq. ID	LIB3176-002-Q1-K1-C10
Method	BLASTN
NCBI GI	g2262135
BLAST score	108
E value	7.0e-54
Match length	277
% identity	96
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	152830
Seq. ID	LIB3176-002-Q1-K1-C11
Method	BLASTX
NCBI GI	g2829862
BLAST score	494
E value	3.0e-50
Match length	95
% identity	100
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	152831
Seq. ID	LIB3176-002-Q1-K1-C12
Method	BLASTX
NCBI GI	g4741948
BLAST score	429
E value	1.0e-42
Match length	80
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	152832
Seq. ID	LIB3176-002-Q1-K1-C2
Method	BLASTN
NCBI GI	g3659491
BLAST score	42
E value	1.0e-14
Match length	50
% identity	96
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	152833
Seq. ID	LIB3176-002-Q1-K1-C3
Method	BLASTX
NCBI GI	g1621268
BLAST score	261
E value	6.0e-23
Match length	82
% identity	60
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	152834
Seq. ID	LIB3176-002-Q1-K1-C4
Method	BLASTX

NCBI GI g132074
BLAST score 414
E value 6.0e-41
Match length 80
% identity 99
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No. 152835
Seq. ID LIB3176-002-Q1-K1-C5
Method BLASTX
NCBI GI g4582468
BLAST score 387
E value 1.0e-37
Match length 79
% identity 100
NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No. 152836
Seq. ID LIB3176-002-Q1-K1-C6
Method BLASTX
NCBI GI g3522929
BLAST score 350
E value 2.0e-33
Match length 68
% identity 100
NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 152837
Seq. ID LIB3176-002-Q1-K1-C7
Method BLASTN
NCBI GI g3212846
BLAST score 280
E value 1.0e-156
Match length 280
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 152838
Seq. ID LIB3176-002-Q1-K1-C8
Method BLASTN
NCBI GI g2924729
BLAST score 133
E value 9.0e-69
Match length 257
% identity 88
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No. 152839
Seq. ID LIB3176-002-Q1-K1-C9

Method	BLASTX
NCBI GI	g3688182
BLAST score	489
E value	1.0e-49
Match length	93
% identity	100
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No.	152840
Seq. ID	LIB3176-002-Q1-K1-D1
Method	BLASTX
NCBI GI	g166867
BLAST score	343
E value	1.0e-32
Match length	94
% identity	72
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	152841
Seq. ID	LIB3176-002-Q1-K1-D10
Method	BLASTN
NCBI GI	g3927822
BLAST score	286
E value	1.0e-160
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152842
Seq. ID	LIB3176-002-Q1-K1-D11
Method	BLASTN
NCBI GI	g3449326
BLAST score	47
E value	2.0e-17
Match length	135
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	152843
Seq. ID	LIB3176-002-Q1-K1-D2
Method	BLASTX
NCBI GI	g1669387
BLAST score	487
E value	2.0e-49
Match length	96
% identity	99
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	152844
Seq. ID	LIB3176-002-Q1-K1-D3
Method	BLASTX
NCBI GI	g231499
BLAST score	185
E value	5.0e-14

Match length	52
% identity	71
NCBI Description	ACTIN 2 >gi_282920_pir__S26435 actin - garden pea >gi_20635_emb_CAA48609_ (X68649) actin [Pisum sativum]

Seq. No.	152845
Seq. ID	LIB3176-002-Q1-K1-D4
Method	BLASTX
NCBI GI	g1170247
BLAST score	394
E value	1.0e-38
Match length	96
% identity	76
NCBI Description	HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880) pre-hevein-like protein [Arabidopsis thaliana]

Seq. No.	152846
Seq. ID	LIB3176-002-Q1-K1-D5
Method	BLASTX
NCBI GI	g1170028
BLAST score	486
E value	2.0e-49
Match length	95
% identity	100
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	152847
Seq. ID	LIB3176-002-Q1-K1-D6
Method	BLASTX
NCBI GI	g2809238
BLAST score	315
E value	3.0e-29
Match length	83
% identity	78
NCBI Description	(AC002560) F21B7.7 [Arabidopsis thaliana]

Seq. No.	152848
Seq. ID	LIB3176-002-Q1-K1-D7
Method	BLASTX
NCBI GI	g3123745
BLAST score	261
E value	6.0e-23
Match length	58
% identity	91
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	152849
Seq. ID	LIB3176-002-Q1-K1-D8
Method	BLASTN
NCBI GI	g4322420
BLAST score	102
E value	2.0e-50
Match length	203

% identity	91
NCBI Description	Arabidopsis thaliana cadmium resistance factor 1 (CRF1) mRNA, complete cds

Seq. No.	152850
Seq. ID	LIB3176-002-Q1-K1-D9
Method	BLASTX
NCBI GI	g3250674
BLAST score	148
E value	1.0e-09
Match length	92
% identity	37
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	152851
Seq. ID	LIB3176-002-Q1-K1-E1
Method	BLASTX
NCBI GI	g3004555
BLAST score	134
E value	4.0e-08
Match length	95
% identity	3
NCBI Description	(AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No.	152852
Seq. ID	LIB3176-002-Q1-K1-E11
Method	BLASTN
NCBI GI	g3869067
BLAST score	181
E value	2.0e-97
Match length	289
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	152853
Seq. ID	LIB3176-002-Q1-K1-E12
Method	BLASTN
NCBI GI	g4206762
BLAST score	251
E value	1.0e-139
Match length	282
% identity	96
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	152854
Seq. ID	LIB3176-002-Q1-K1-E2
Method	BLASTN
NCBI GI	g4587641
BLAST score	207
E value	1.0e-113
Match length	288
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	152855
Seq. ID	LIB3176-002-Q1-K1-E3
Method	BLASTN
NCBI GI	g2828180
BLAST score	243
E value	1.0e-134
Match length	290
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	152856
Seq. ID	LIB3176-002-Q1-K1-E5
Method	BLASTX
NCBI GI	g132110
BLAST score	380
E value	6.0e-37
Match length	78
% identity	96
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	152857
Seq. ID	LIB3176-002-Q1-K1-E6
Method	BLASTN
NCBI GI	g1946354
BLAST score	290
E value	1.0e-162
Match length	290
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	152858
Seq. ID	LIB3176-002-Q1-K1-E7
Method	BLASTX
NCBI GI	g3451075
BLAST score	214
E value	2.0e-17
Match length	95
% identity	39
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	152859
Seq. ID	LIB3176-002-Q1-K1-E9
Method	BLASTX
NCBI GI	g4337175
BLAST score	453
E value	2.0e-45
Match length	88
% identity	100
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,

gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	152860
Seq. ID	LIB3176-002-Q1-K1-F1
Method	BLASTX
NCBI GI	g1706130
BLAST score	444
E value	2.0e-44
Match length	96
% identity	89
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]

Seq. No.	152861
Seq. ID	LIB3176-002-Q1-K1-F10
Method	BLASTX
NCBI GI	g452470
BLAST score	517
E value	5.0e-53
Match length	95
% identity	100
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	152862
Seq. ID	LIB3176-002-Q1-K1-F11
Method	BLASTX
NCBI GI	g113024
BLAST score	440
E value	6.0e-44
Match length	95
% identity	86
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	152863
Seq. ID	LIB3176-002-Q1-K1-F12
Method	BLASTX
NCBI GI	g4220527
BLAST score	167
E value	6.0e-12
Match length	47
% identity	60
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	152864
Seq. ID	LIB3176-002-Q1-K1-F2
Method	BLASTN
NCBI GI	g3869074
BLAST score	287
E value	1.0e-160
Match length	291
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	152865
Seq. ID	LIB3176-002-Q1-K1-F3
Method	BLASTX
NCBI GI	g4587611
BLAST score	322
E value	4.0e-30
Match length	65
% identity	98
NCBI Description	(AC006951) putative 40S ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	152866
Seq. ID	LIB3176-002-Q1-K1-F4
Method	BLASTX
NCBI GI	g1071912
BLAST score	364
E value	5.0e-35
Match length	83
% identity	90
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	152867
Seq. ID	LIB3176-002-Q1-K1-F6
Method	BLASTN
NCBI GI	g3492855
BLAST score	148
E value	5.0e-78
Match length	152
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	152868
Seq. ID	LIB3176-002-Q1-K1-F9
Method	BLASTX
NCBI GI	g1710581
BLAST score	435
E value	2.0e-43
Match length	88
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	152869
Seq. ID	LIB3176-002-Q1-K1-G1
Method	BLASTX
NCBI GI	g4115377
BLAST score	391
E value	3.0e-38
Match length	95
% identity	80
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	152870
Seq. ID	LIB3176-002-Q1-K1-G10
Method	BLASTN
NCBI GI	g2351072
BLAST score	285
E value	1.0e-159
Match length	289
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYC6, complete sequence [Arabidopsis thaliana]

Seq. No.	152871
Seq. ID	LIB3176-002-Q1-K1-G11
Method	BLASTN
NCBI GI	g4662640
BLAST score	80
E value	4.0e-37
Match length	257
% identity	17
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	152872
Seq. ID	LIB3176-002-Q1-K1-G12
Method	BLASTX
NCBI GI	g4581146
BLAST score	396
E value	8.0e-39
Match length	80
% identity	100
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	152873
Seq. ID	LIB3176-002-Q1-K1-G2
Method	BLASTX
NCBI GI	g126766
BLAST score	509
E value	5.0e-52
Match length	96
% identity	98
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	152874
Seq. ID	LIB3176-002-Q1-K1-G3
Method	BLASTX
NCBI GI	g1363489
BLAST score	528
E value	3.0e-54
Match length	95
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	152875
Seq. ID	LIB3176-002-Q1-K1-G4
Method	BLASTX
NCBI GI	g99992
BLAST score	298
E value	3.0e-27
Match length	80
% identity	48
NCBI Description	protein disulfide-isomerase (EC 5.3.4.1) precursor - alfalfa (clone B2) >gi_166418 (M82973) putative endomembrane protein; putative [Medicago sativa]

Seq. No.	152876
Seq. ID	LIB3176-002-Q1-K1-G5
Method	BLASTN
NCBI GI	g4585890
BLAST score	168
E value	1.0e-89
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3G21 genomic sequence, complete sequence

Seq. No.	152877
Seq. ID	LIB3176-002-Q1-K1-G6
Method	BLASTX
NCBI GI	g544425
BLAST score	424
E value	4.0e-42
Match length	82
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	152878
Seq. ID	LIB3176-002-Q1-K1-G7
Method	BLASTN
NCBI GI	g4589434
BLAST score	166
E value	1.0e-88
Match length	166
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	152879
Seq. ID	LIB3176-002-Q1-K1-G8
Method	BLASTX
NCBI GI	g1362078
BLAST score	224
E value	1.0e-18
Match length	57

% identity	70
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	152880
Seq. ID	LIB3176-002-Q1-K1-G9
Method	BLASTX
NCBI GI	g4220446
BLAST score	302
E value	9.0e-28
Match length	76
% identity	80
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	152881
Seq. ID	LIB3176-002-Q1-K1-H1
Method	BLASTN
NCBI GI	g4220627
BLAST score	121
E value	1.0e-61
Match length	326
% identity	6
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	152882
Seq. ID	LIB3176-002-Q1-K1-H10
Method	BLASTX
NCBI GI	g3860247
BLAST score	501
E value	4.0e-51
Match length	95
% identity	98
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	152883
Seq. ID	LIB3176-002-Q1-K1-H11
Method	BLASTX
NCBI GI	g116392
BLAST score	438
E value	1.0e-43
Match length	84
% identity	100
NCBI Description	CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) >gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC 2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308) chalcone synthase [Arabidopsis thaliana]

Seq. No.	152884
Seq. ID	LIB3176-002-Q1-K1-H12
Method	BLASTX
NCBI GI	g461729

BLAST score	430
E value	1.0e-42
Match length	90
% identity	96
NCBI Description	10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi_2146744_pir__S65597 probable chaperonin, 10K - Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana]

Seq. No.	152885
Seq. ID	LIB3176-002-Q1-K1-H2
Method	BLASTN
NCBI GI	g3128143
BLAST score	94
E value	2.0e-45
Match length	232
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	152886
Seq. ID	LIB3176-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g2623881
BLAST score	507
E value	8.0e-52
Match length	95
% identity	96
NCBI Description	(AF031318) catalase [Raphanus sativus]

Seq. No.	152887
Seq. ID	LIB3176-002-Q1-K1-H7
Method	BLASTN
NCBI GI	g3128143
BLAST score	56
E value	9.0e-23
Match length	153
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	152888
Seq. ID	LIB3176-002-Q1-K1-H8
Method	BLASTX
NCBI GI	g3402676
BLAST score	91
E value	4.0e-03
Match length	31
% identity	21
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	152889
Seq. ID	LIB3176-002-Q1-K1-H9
Method	BLASTN
NCBI GI	g3046851
BLAST score	222

E value	1.0e-122
Match length	234
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	152890
Seq. ID	LIB3176-003-P1-K1-A1
Method	BLASTX
NCBI GI	g1906826
BLAST score	231
E value	1.0e-19
Match length	44
% identity	100
NCBI Description	(Y11827) heat shock protein [Arabidopsis thaliana]

Seq. No.	152891
Seq. ID	LIB3176-003-P1-K1-A10
Method	BLASTX
NCBI GI	g4454015
BLAST score	652
E value	1.0e-68
Match length	124
% identity	99
NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]

Seq. No.	152892
Seq. ID	LIB3176-003-P1-K1-A11
Method	BLASTN
NCBI GI	g3859658
BLAST score	107
E value	4.0e-53
Match length	349
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	152893
Seq. ID	LIB3176-003-P1-K1-A12
Method	BLASTX
NCBI GI	g2244750
BLAST score	320
E value	5.0e-30
Match length	63
% identity	100
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	152894
Seq. ID	LIB3176-003-P1-K1-A6
Method	BLASTX
NCBI GI	g137465
BLAST score	400
E value	2.0e-39
Match length	82
% identity	98

NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	152895
Seq. ID	LIB3176-003-P1-K1-A7
Method	BLASTX
NCBI GI	g2062157
BLAST score	622
E value	4.0e-65
Match length	122
% identity	29
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	152896
Seq. ID	LIB3176-003-P1-K1-A8
Method	BLASTX
NCBI GI	g99688
BLAST score	558
E value	1.0e-57
Match length	109
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	152897
Seq. ID	LIB3176-003-P1-K1-A9
Method	BLASTX
NCBI GI	g1854445
BLAST score	270
E value	4.0e-24
Match length	68
% identity	78
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	152898
Seq. ID	LIB3176-003-P1-K1-B1
Method	BLASTN
NCBI GI	g4454022
BLAST score	173
E value	9.0e-93
Match length	224
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	152899
Seq. ID	LIB3176-003-P1-K1-B2
Method	BLASTX
NCBI GI	g2911085
BLAST score	327
E value	5.0e-31
Match length	70

% identity	99
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	152900
Seq. ID	LIB3176-003-P1-K1-B5
Method	BLASTX
NCBI GI	g2143227
BLAST score	418
E value	2.0e-41
Match length	90
% identity	90
NCBI Description	(Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No.	152901
Seq. ID	LIB3176-003-P1-K1-B7
Method	BLASTN
NCBI GI	g4589440
BLAST score	152
E value	3.0e-80
Match length	187
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	152902
Seq. ID	LIB3176-003-P1-K1-B8
Method	BLASTN
NCBI GI	g2618599
BLAST score	125
E value	5.0e-64
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	152903
Seq. ID	LIB3176-003-P1-K1-C1
Method	BLASTN
NCBI GI	g4454022
BLAST score	222
E value	1.0e-122
Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	152904
Seq. ID	LIB3176-003-P1-K1-C10
Method	BLASTX
NCBI GI	g1362108
BLAST score	416
E value	5.0e-41
Match length	92
% identity	92

NCBI Description	histone H3 homolog - common tobacco

Seq. No.	152905
Seq. ID	LIB3176-003-P1-K1-C11
Method	BLASTN
NCBI GI	g3702735
BLAST score	319
E value	1.0e-179
Match length	327
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	152906
Seq. ID	LIB3176-003-P1-K1-C4
Method	BLASTN
NCBI GI	g3510340
BLAST score	270
E value	1.0e-150
Match length	282
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	152907
Seq. ID	LIB3176-003-P1-K1-D1
Method	BLASTN
NCBI GI	g4063737
BLAST score	191
E value	1.0e-103
Match length	195
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152908
Seq. ID	LIB3176-003-P1-K1-D10
Method	BLASTN
NCBI GI	g2264307
BLAST score	66
E value	5.0e-29
Match length	130
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	152909
Seq. ID	LIB3176-003-P1-K1-D3
Method	BLASTN
NCBI GI	g2584827
BLAST score	178
E value	8.0e-96
Match length	194
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152910
Seq. ID	LIB3176-003-P1-K1-D4
Method	BLASTN
NCBI GI	g166654
BLAST score	47
E value	1.0e-17
Match length	95
% identity	87
NCBI Description	Arabidopsis thaliana calmodulin-3 mRNA, 3' end

Seq. No.	152911
Seq. ID	LIB3176-003-P1-K1-D6
Method	BLASTN
NCBI GI	g2264311
BLAST score	206
E value	1.0e-112
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	152912
Seq. ID	LIB3176-003-P1-K1-D8
Method	BLASTX
NCBI GI	g4191778
BLAST score	117
E value	2.0e-06
Match length	60
% identity	70
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	152913
Seq. ID	LIB3176-003-P1-K1-D9
Method	BLASTX
NCBI GI	g3915824
BLAST score	328
E value	2.0e-30
Match length	64
% identity	100
NCBI Description	[Segment 2 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	152914
Seq. ID	LIB3176-003-P1-K1-E1
Method	BLASTN
NCBI GI	g4455321
BLAST score	176
E value	1.0e-94
Match length	176
% identity	50
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	152915
Seq. ID	LIB3176-003-P1-K1-E10
Method	BLASTN
NCBI GI	g4490734

BLAST score	251
E value	1.0e-139
Match length	357
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	152916
Seq. ID	LIB3176-003-P1-K1-E12
Method	BLASTX
NCBI GI	g3983125
BLAST score	146
E value	3.0e-09
Match length	47
% identity	70
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	152917
Seq. ID	LIB3176-003-P1-K1-E3
Method	BLASTX
NCBI GI	g132863
BLAST score	370
E value	7.0e-36
Match length	72
% identity	96
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	152918
Seq. ID	LIB3176-003-P1-K1-E4
Method	BLASTX
NCBI GI	g4741186
BLAST score	291
E value	2.0e-26
Match length	57
% identity	95
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	152919
Seq. ID	LIB3176-003-P1-K1-E6
Method	BLASTX
NCBI GI	g399013
BLAST score	267
E value	1.0e-23
Match length	68
% identity	82
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	152920

Seq. ID	LIB3176-003-P1-K1-E7
Method	BLASTX
NCBI GI	g1350720
BLAST score	543
E value	8.0e-56
Match length	111
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	152921
Seq. ID	LIB3176-003-P1-K1-E8
Method	BLASTX
NCBI GI	g132102
BLAST score	534
E value	8.0e-55
Match length	106
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	152922
Seq. ID	LIB3176-003-P1-K1-E9
Method	BLASTX
NCBI GI	g730645
BLAST score	428
E value	2.0e-42
Match length	100
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	152923
Seq. ID	LIB3176-003-P1-K1-F1
Method	BLASTN
NCBI GI	g2244901
BLAST score	192
E value	1.0e-104
Match length	213
% identity	53
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152924
Seq. ID	LIB3176-003-P1-K1-F10
Method	BLASTX
NCBI GI	g267069
BLAST score	484

E value	7.0e-49
Match length	90
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	152925
Seq. ID	LIB3176-003-P1-K1-F12
Method	BLASTN
NCBI GI	g2244829
BLAST score	399
E value	0.0e+00
Match length	475
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152926
Seq. ID	LIB3176-003-P1-K1-F2
Method	BLASTX
NCBI GI	g2506443
BLAST score	479
E value	2.0e-48
Match length	95
% identity	98
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	152927
Seq. ID	LIB3176-003-P1-K1-F4
Method	BLASTN
NCBI GI	g4589412
BLAST score	193
E value	1.0e-104
Match length	349
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	152928
Seq. ID	LIB3176-003-P1-K1-F6
Method	BLASTX
NCBI GI	g4581146
BLAST score	641
E value	3.0e-67
Match length	127
% identity	99
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase,

cytoplasmic [Arabidopsis thaliana]

Seq. No.	152929
Seq. ID	LIB3176-003-P1-K1-F7
Method	BLASTN
NCBI GI	g2245073
BLAST score	234
E value	1.0e-129
Match length	317
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	152930
Seq. ID	LIB3176-003-P1-K1-F8
Method	BLASTN
NCBI GI	g547390
BLAST score	426
E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana TRAP mRNA, partial cds

Seq. No.	152931
Seq. ID	LIB3176-003-P1-K1-F9
Method	BLASTX
NCBI GI	g113026
BLAST score	701
E value	3.0e-74
Match length	149
% identity	90
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	152932
Seq. ID	LIB3176-003-P1-K1-G1
Method	BLASTX
NCBI GI	g2149051
BLAST score	228
E value	2.0e-19
Match length	46
% identity	96
NCBI Description	(U73810) small Ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	152933
Seq. ID	LIB3176-003-P1-K1-G10
Method	BLASTX
NCBI GI	g399046
BLAST score	371
E value	2.0e-35
Match length	76

% identity	100
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	152934
Seq. ID	LIB3176-003-P1-K1-G11
Method	BLASTN
NCBI GI	g4757409
BLAST score	71
E value	1.0e-31
Match length	446
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	152935
Seq. ID	LIB3176-003-P1-K1-G12
Method	BLASTN
NCBI GI	g4757409
BLAST score	71
E value	1.0e-31
Match length	446
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	152936
Seq. ID	LIB3176-003-P1-K1-G2
Method	BLASTN
NCBI GI	g1906829
BLAST score	85
E value	1.0e-40
Match length	93
% identity	98
NCBI Description	A.thaliana hsp88.1 gene

Seq. No.	152937
Seq. ID	LIB3176-003-P1-K1-G3
Method	BLASTN
NCBI GI	g2264302
BLAST score	98
E value	4.0e-48
Match length	150
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	152938
Seq. ID	LIB3176-003-P1-K1-G4
Method	BLASTN
NCBI GI	g4468801
BLAST score	322

E value	0.0e+00
Match length	451
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	152939
Seq. ID	LIB3176-003-P1-K1-G6
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	7.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	152940
Seq. ID	LIB3176-003-P1-K1-G7
Method	BLASTN
NCBI GI	g3128135
BLAST score	166
E value	2.0e-88
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	152941
Seq. ID	LIB3176-003-P1-K1-G8
Method	BLASTN
NCBI GI	g3687221
BLAST score	118
E value	5.0e-60
Match length	190
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152942
Seq. ID	LIB3176-003-P1-K1-H1
Method	BLASTX
NCBI GI	g99752
BLAST score	437
E value	1.0e-43
Match length	81
% identity	100
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	152943
Seq. ID	LIB3176-003-P1-K1-H4
Method	BLASTX
NCBI GI	g4572678
BLAST score	684
E value	3.0e-72
Match length	144

% identity	92
NCBI Description	(AC006954) putative plasma membrane ATPase [Arabidopsis thaliana]

Seq. No.	152944
Seq. ID	LIB3176-003-P1-K1-H5
Method	BLASTN
NCBI GI	g870791
BLAST score	77
E value	1.0e-35
Match length	150
% identity	87
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete cds

Seq. No.	152945
Seq. ID	LIB3176-003-P1-K1-H7
Method	BLASTN
NCBI GI	g2351071
BLAST score	241
E value	1.0e-133
Match length	272
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	152946
Seq. ID	LIB3176-003-P1-K1-H8
Method	BLASTX
NCBI GI	g115783
BLAST score	303
E value	6.0e-28
Match length	65
% identity	91
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	152947
Seq. ID	LIB3176-003-P1-K1-H9
Method	BLASTX
NCBI GI	g730526
BLAST score	424
E value	4.0e-42
Match length	118
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	152948
Seq. ID	LIB3176-004-P1-K1-A1
Method	BLASTX
NCBI GI	g4678262
BLAST score	558

E value	1.0e-57
Match length	106
% identity	98
NCBI Description	(AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana]

Seq. No.	152949
Seq. ID	LIB3176-004-P1-K1-A10
Method	BLASTX
NCBI GI	g4586244
BLAST score	279
E value	1.0e-24
Match length	135
% identity	41
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	152950
Seq. ID	LIB3176-004-P1-K1-A11
Method	BLASTX
NCBI GI	g4240120
BLAST score	602
E value	1.0e-62
Match length	114
% identity	100
NCBI Description	(AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	152951
Seq. ID	LIB3176-004-P1-K1-A2
Method	BLASTX
NCBI GI	g2829893
BLAST score	510
E value	4.0e-52
Match length	99
% identity	98
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	152952
Seq. ID	LIB3176-004-P1-K1-A3
Method	BLASTX
NCBI GI	g120675
BLAST score	438
E value	1.0e-43
Match length	102
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	152953
Seq. ID	LIB3176-004-P1-K1-A5
Method	BLASTX
NCBI GI	g2407802
BLAST score	309
E value	2.0e-28
Match length	64

% identity	98
NCBI Description	(Y12576) histone H2B [Arabidopsis thaliana]

Seq. No.	152954
Seq. ID	LIB3176-004-P1-K1-A7
Method	BLASTX
NCBI GI	g445612
BLAST score	375
E value	3.0e-36
Match length	80
% identity	90
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	152955
Seq. ID	LIB3176-004-P1-K1-A8
Method	BLASTN
NCBI GI	g1402935
BLAST score	102
E value	4.0e-50
Match length	173
% identity	87
NCBI Description	A.thaliana genomic DNA fragment (ecotype MARBURG-0)

Seq. No.	152956
Seq. ID	LIB3176-004-P1-K1-B1
Method	BLASTX
NCBI GI	g4309738
BLAST score	246
E value	5.0e-21
Match length	94
% identity	52
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	152957
Seq. ID	LIB3176-004-P1-K1-B10
Method	BLASTN
NCBI GI	g1871173
BLAST score	481
E value	0.0e+00
Match length	497
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	152958
Seq. ID	LIB3176-004-P1-K1-B12
Method	BLASTN
NCBI GI	g2494106
BLAST score	101
E value	1.0e-49
Match length	290
% identity	92
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152959
Seq. ID	LIB3176-004-P1-K1-B4

Method	BLASTX
NCBI GI	g4490732
BLAST score	614
E value	5.0e-65
Match length	128
% identity	99
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	152960
Seq. ID	LIB3176-004-P1-K1-B5
Method	BLASTX
NCBI GI	g4704613
BLAST score	508
E value	7.0e-52
Match length	100
% identity	94
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	152961
Seq. ID	LIB3176-004-P1-K1-B7
Method	BLASTX
NCBI GI	g1702986
BLAST score	484
E value	6.0e-49
Match length	98
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	152962
Seq. ID	LIB3176-004-P1-K1-B8
Method	BLASTN
NCBI GI	g2656030
BLAST score	21
E value	7.1e-02
Match length	335
% identity	65
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8

Seq. No.	152963
Seq. ID	LIB3176-004-P1-K1-B9
Method	BLASTN
NCBI GI	g4835223
BLAST score	278
E value	1.0e-155
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	152964
Seq. ID	LIB3176-004-P1-K1-C1
Method	BLASTX
NCBI GI	g4455256

BLAST score	653
E value	1.0e-68
Match length	122
% identity	100
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	152965
Seq. ID	LIB3176-004-P1-K1-C10
Method	BLASTN
NCBI GI	g3869067
BLAST score	204
E value	1.0e-111
Match length	252
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	152966
Seq. ID	LIB3176-004-P1-K1-C11
Method	BLASTX
NCBI GI	g1931640
BLAST score	287
E value	8.0e-26
Match length	107
% identity	54
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	152967
Seq. ID	LIB3176-004-P1-K1-C12
Method	BLASTX
NCBI GI	g4587572
BLAST score	701
E value	3.0e-74
Match length	135
% identity	99
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

Seq. No.	152968
Seq. ID	LIB3176-004-P1-K1-C2
Method	BLASTX
NCBI GI	g4455364
BLAST score	320
E value	1.0e-29
Match length	128
% identity	47
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	152969
Seq. ID	LIB3176-004-P1-K1-C3
Method	BLASTX
NCBI GI	g2832661

BLAST score	601
E value	1.0e-62
Match length	137
% identity	91
NCBI Description	(AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No.	152970
Seq. ID	LIB3176-004-P1-K1-C4
Method	BLASTX
NCBI GI	g4454464
BLAST score	539
E value	3.0e-55
Match length	127
% identity	83
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	152971
Seq. ID	LIB3176-004-P1-K1-C5
Method	BLASTX
NCBI GI	g2062161
BLAST score	559
E value	1.0e-57
Match length	108
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	152972
Seq. ID	LIB3176-004-P1-K1-C6
Method	BLASTN
NCBI GI	g2088638
BLAST score	152
E value	6.0e-80
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	152973
Seq. ID	LIB3176-004-P1-K1-C7
Method	BLASTX
NCBI GI	g3256066
BLAST score	456
E value	6.0e-46
Match length	92
% identity	99
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No.	152974
Seq. ID	LIB3176-004-P1-K1-C8
Method	BLASTX
NCBI GI	g3367568
BLAST score	410
E value	3.0e-40
Match length	115
% identity	64

NCBI Description	(AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	152975
Seq. ID	LIB3176-004-P1-K1-C9
Method	BLASTN
NCBI GI	g4559344
BLAST score	326
E value	0.0e+00
Match length	351
% identity	9
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	152976
Seq. ID	LIB3176-004-P1-K1-D1
Method	BLASTN
NCBI GI	g2264321
BLAST score	246
E value	1.0e-136
Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	152977
Seq. ID	LIB3176-004-P1-K1-D10
Method	BLASTX
NCBI GI	g3149952
BLAST score	244
E value	1.0e-20
Match length	43
% identity	98
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	152978
Seq. ID	LIB3176-004-P1-K1-D11
Method	BLASTX
NCBI GI	g3599491
BLAST score	191
E value	2.0e-14
Match length	45
% identity	82
NCBI Description	(AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.	152979
Seq. ID	LIB3176-004-P1-K1-D12
Method	BLASTN
NCBI GI	g1946354
BLAST score	366
E value	0.0e+00
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	152980

Seq. ID	LIB3176-004-P1-K1-D2
Method	BLASTX
NCBI GI	g464707
BLAST score	373
E value	8.0e-36
Match length	85
% identity	85
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	152981
Seq. ID	LIB3176-004-P1-K1-D5
Method	BLASTX
NCBI GI	g1168258
BLAST score	454
E value	2.0e-45
Match length	110
% identity	82
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	152982
Seq. ID	LIB3176-004-P1-K1-D6
Method	BLASTN
NCBI GI	g1946354
BLAST score	228
E value	1.0e-125
Match length	293
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	152983
Seq. ID	LIB3176-004-P1-K1-D7
Method	BLASTX
NCBI GI	g3492806
BLAST score	230
E value	5.0e-19
Match length	97
% identity	47
NCBI Description	(AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No.	152984
Seq. ID	LIB3176-004-P1-K1-D8
Method	BLASTN
NCBI GI	g2924729
BLAST score	224
E value	1.0e-123
Match length	367
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	152985
Seq. ID	LIB3176-004-P1-K1-E1
Method	BLASTX
NCBI GI	g4454036
BLAST score	761
E value	3.0e-81
Match length	139
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	152986
Seq. ID	LIB3176-004-P1-K1-E10
Method	BLASTX
NCBI GI	g4204285
BLAST score	741
E value	2.0e-78
Match length	146
% identity	95
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	152987
Seq. ID	LIB3176-004-P1-K1-E12
Method	BLASTX
NCBI GI	g2501056
BLAST score	735
E value	3.0e-78
Match length	140
% identity	99
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	152988
Seq. ID	LIB3176-004-P1-K1-E2
Method	BLASTX
NCBI GI	g2506276
BLAST score	567
E value	2.0e-58
Match length	113
% identity	100
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain -

Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No.	152989
Seq. ID	LIB3176-004-P1-K1-E3
Method	BLASTX
NCBI GI	g3319350
BLAST score	601
E value	1.0e-62
Match length	118
% identity	100
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	152990
Seq. ID	LIB3176-004-P1-K1-E4
Method	BLASTN
NCBI GI	g2264304
BLAST score	168
E value	1.0e-89
Match length	225
% identity	54
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	152991
Seq. ID	LIB3176-004-P1-K1-E6
Method	BLASTN
NCBI GI	g4741928
BLAST score	252
E value	1.0e-140
Match length	264
% identity	99
NCBI Description	Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds

Seq. No.	152992
Seq. ID	LIB3176-004-P1-K1-E7
Method	BLASTX
NCBI GI	g3850580
BLAST score	504
E value	3.0e-51
Match length	97
% identity	96
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_84105 and gb_AI100071 come from this gene. [Arabidopsis thaliana]

Seq. No.	152993
Seq. ID	LIB3176-004-P1-K1-E8
Method	BLASTX
NCBI GI	g1702988
BLAST score	421
E value	2.0e-41
Match length	109

% identity	81
NCBI Description	14-3-3-LIKE PROTEIN GF14 UPSILON >gi_1508785 (L09109) GF14 upsilon chain [Arabidopsis thaliana] >gi_2232148_gb_AAB62225_ (AF001415) 14-3-3-like protein GF14 upsilon [Arabidopsis thaliana]
Seq. No.	152994
Seq. ID	LIB3176-004-P1-K1-E9
Method	BLASTX
NCBI GI	g3355468
BLAST score	371
E value	1.0e-35
Match length	112
% identity	74
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]
Seq. No.	152995
Seq. ID	LIB3176-004-P1-K1-F1
Method	BLASTN
NCBI GI	g4159699
BLAST score	113
E value	7.0e-57
Match length	251
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence
Seq. No.	152996
Seq. ID	LIB3176-004-P1-K1-F10
Method	BLASTN
NCBI GI	g402551
BLAST score	170
E value	5.0e-91
Match length	182
% identity	98
NCBI Description	A.thaliana gene for acetohydroxy acid isomeroreductase
Seq. No.	152997
Seq. ID	LIB3176-004-P1-K1-F11
Method	BLASTX
NCBI GI	g4138912
BLAST score	516
E value	2.0e-52
Match length	106
% identity	83
NCBI Description	(AF059487) expansin precursor [Lycopersicon esculentum]
Seq. No.	152998
Seq. ID	LIB3176-004-P1-K1-F12
Method	BLASTX
NCBI GI	g2738248
BLAST score	145
E value	1.0e-09
Match length	37
% identity	81
NCBI Description	(U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

Seq. No.	152999
Seq. ID	LIB3176-004-P1-K1-F2
Method	BLASTX
NCBI GI	g400515
BLAST score	238
E value	6.0e-20
Match length	84
% identity	54
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8) (CI-B8) >gi_346540_pir__S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine >gi_246_emb_CAA44904_ (X63219) NADH dehydrogenase [Bos taurus]

Seq. No.	153000
Seq. ID	LIB3176-004-P1-K1-F3
Method	BLASTX
NCBI GI	g2245131
BLAST score	242
E value	2.0e-20
Match length	83
% identity	64
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153001
Seq. ID	LIB3176-004-P1-K1-F4
Method	BLASTX
NCBI GI	g1486472
BLAST score	577
E value	9.0e-60
Match length	130
% identity	87
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	153002
Seq. ID	LIB3176-004-P1-K1-F5
Method	BLASTX
NCBI GI	g2118220
BLAST score	248
E value	2.0e-21
Match length	67
% identity	76
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	153003
Seq. ID	LIB3176-004-P1-K1-F6
Method	BLASTX
NCBI GI	g2677614
BLAST score	439
E value	1.0e-43
Match length	86
% identity	100
NCBI Description	(Y07625) NLM1 protein (NodLikeMip1) [Arabidopsis thaliana]

Seq. No.	153004
Seq. ID	LIB3176-004-P1-K1-F7
Method	BLASTX
NCBI GI	g1906826
BLAST score	365
E value	6.0e-35
Match length	122
% identity	62
NCBI Description	(Y11827) heat shock protein [Arabidopsis thaliana]

Seq. No.	153005
Seq. ID	LIB3176-004-P1-K1-F8
Method	BLASTX
NCBI GI	g119150
BLAST score	645
E value	1.0e-67
Match length	126
% identity	98
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir__S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]

Seq. No.	153006
Seq. ID	LIB3176-004-P1-K1-F9
Method	BLASTX
NCBI GI	g113024
BLAST score	594
E value	1.0e-61
Match length	134
% identity	85
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	153007
Seq. ID	LIB3176-004-P1-K1-G1
Method	BLASTN
NCBI GI	g3335331
BLAST score	286
E value	1.0e-160
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153008
Seq. ID	LIB3176-004-P1-K1-G10
Method	BLASTN
NCBI GI	g4539331
BLAST score	365
E value	0.0e+00
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	153009
Seq. ID	LIB3176-004-P1-K1-G11
Method	BLASTN
NCBI GI	g2252639
BLAST score	219
E value	1.0e-120
Match length	331
% identity	96
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	153010
Seq. ID	LIB3176-004-P1-K1-G2
Method	BLASTN
NCBI GI	g16473
BLAST score	254
E value	1.0e-141
Match length	302
% identity	96
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	153011
Seq. ID	LIB3176-004-P1-K1-G3
Method	BLASTX
NCBI GI	g730688
BLAST score	401
E value	3.0e-39
Match length	76
% identity	100
NCBI Description	MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S19 PRECURSOR >gi_2129722_pir__S71114 ribosomal protein S19 precursor, mitochondrial - Arabidopsis thaliana >gi_457760_emb_CAA54951_ (X77989) ribosomal protein S19 [Arabidopsis thaliana] >gi_459422_emb_CAA54965_ (X78035) mitochondrial ribosomal protein S19, nuclear encoded [Arabidopsis thaliana]

Seq. No.	153012
Seq. ID	LIB3176-004-P1-K1-G4
Method	BLASTX
NCBI GI	g1710780
BLAST score	361
E value	2.0e-34
Match length	99
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_

(X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	153013
Seq. ID	LIB3176-004-P1-K1-G5
Method	BLASTX
NCBI GI	g1172995
BLAST score	189
E value	2.0e-14
Match length	82
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus]

Seq. No.	153014
Seq. ID	LIB3176-004-P1-K1-G6
Method	BLASTX
NCBI GI	g2829883
BLAST score	624
E value	3.0e-65
Match length	138
% identity	88
NCBI Description	(AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No.	153015
Seq. ID	LIB3176-004-P1-K1-G7
Method	BLASTX
NCBI GI	g2760349
BLAST score	447
E value	1.0e-44
Match length	90
% identity	21
NCBI Description	(U84969) ubiquitin [Arabidopsis thaliana]

Seq. No.	153016
Seq. ID	LIB3176-004-P1-K1-G8
Method	BLASTX
NCBI GI	g2781354
BLAST score	430
E value	1.0e-42
Match length	84
% identity	100
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	153017
Seq. ID	LIB3176-004-P1-K1-G9
Method	BLASTX
NCBI GI	g114171
BLAST score	456
E value	9.0e-46
Match length	104
% identity	85
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP

SYNTHASE) >gi_99781_pir__S12744 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape >gi_17815_emb_CAA35839_ (X51475) 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]

Seq. No.	153018
Seq. ID	LIB3176-004-P1-K1-H1
Method	BLASTN
NCBI GI	g2645198
BLAST score	45
E value	4.0e-16
Match length	162
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153019
Seq. ID	LIB3176-004-P1-K1-H10
Method	BLASTX
NCBI GI	g3421096
BLAST score	397
E value	9.0e-39
Match length	78
% identity	100
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	153020
Seq. ID	LIB3176-004-P1-K1-H11
Method	BLASTX
NCBI GI	g3785983
BLAST score	377
E value	2.0e-36
Match length	97
% identity	69
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153021
Seq. ID	LIB3176-004-P1-K1-H12
Method	BLASTN
NCBI GI	g3746808
BLAST score	233
E value	1.0e-128
Match length	257
% identity	98
NCBI Description	Arabidopsis thaliana adenylate kinase (ADK1) mRNA, complete cds

Seq. No.	153022
Seq. ID	LIB3176-004-P1-K1-H3
Method	BLASTN
NCBI GI	g4586024
BLAST score	198
E value	1.0e-107
Match length	409

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic sequence, complete sequence

Seq. No.	153023
Seq. ID	LIB3176-004-P1-K1-H4
Method	BLASTX
NCBI GI	g2507455
BLAST score	362
E value	1.0e-34
Match length	87
% identity	78
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	153024
Seq. ID	LIB3176-004-P1-K1-H5
Method	BLASTX
NCBI GI	g2781394
BLAST score	247
E value	4.0e-21
Match length	98
% identity	69
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	153025
Seq. ID	LIB3176-004-P1-K1-H6
Method	BLASTX
NCBI GI	g2058282
BLAST score	229
E value	5.0e-19
Match length	43
% identity	93
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	153026
Seq. ID	LIB3176-004-P1-K1-H7
Method	BLASTX
NCBI GI	g2119927
BLAST score	384
E value	3.0e-37
Match length	82
% identity	91
NCBI Description	translation elongation factor G, chloroplast - soybean

Seq. No.	153027
Seq. ID	LIB3176-004-P1-K1-H9
Method	BLASTX
NCBI GI	g4324597
BLAST score	289
E value	2.0e-26
Match length	76
% identity	80
NCBI Description	(AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]

Seq. No.	153028
Seq. ID	LIB3176-005-P1-K1-A1
Method	BLASTX
NCBI GI	g2459415
BLAST score	70
E value	1.0e-24
Match length	91
% identity	73
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153029
Seq. ID	LIB3176-005-P1-K1-A10
Method	BLASTX
NCBI GI	g4539292
BLAST score	204
E value	4.0e-33
Match length	86
% identity	82
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153030
Seq. ID	LIB3176-005-P1-K1-A12
Method	BLASTX
NCBI GI	g283966
BLAST score	234
E value	3.0e-30
Match length	120
% identity	62
NCBI Description	activator 1 37K chain - human

Seq. No.	153031
Seq. ID	LIB3176-005-P1-K1-A2
Method	BLASTX
NCBI GI	g543841
BLAST score	164
E value	5.0e-15
Match length	54
% identity	86
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	153032
Seq. ID	LIB3176-005-P1-K1-A4
Method	BLASTX
NCBI GI	g1350956
BLAST score	377
E value	2.0e-36
Match length	100
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No.	153033
Seq. ID	LIB3176-005-P1-K1-A6
Method	BLASTN
NCBI GI	g4589436
BLAST score	119
E value	3.0e-60
Match length	263
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	153034
Seq. ID	LIB3176-005-P1-K1-A7
Method	BLASTX
NCBI GI	g2062161
BLAST score	289
E value	3.0e-60
Match length	124
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153035
Seq. ID	LIB3176-005-P1-K1-A8
Method	BLASTX
NCBI GI	g4581146
BLAST score	322
E value	2.0e-40
Match length	98
% identity	87
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	153036
Seq. ID	LIB3176-005-P1-K1-B1
Method	BLASTX
NCBI GI	g3914541
BLAST score	292
E value	1.0e-62
Match length	123
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_1928872 (U91966) ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Arabidopsis thaliana]

Seq. No.	153037
Seq. ID	LIB3176-005-P1-K1-B11
Method	BLASTX
NCBI GI	g2244885
BLAST score	141
E value	4.0e-13
Match length	77
% identity	57
NCBI Description	(Z97338) strong similarity to UTP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	153038
Seq. ID	LIB3176-005-P1-K1-B12
Method	BLASTN
NCBI GI	g4733953
BLAST score	372
E value	0.0e+00
Match length	413
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	153039
Seq. ID	LIB3176-005-P1-K1-B3
Method	BLASTX
NCBI GI	g132939
BLAST score	297
E value	6.0e-42
Match length	99
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	153040
Seq. ID	LIB3176-005-P1-K1-B4
Method	BLASTX
NCBI GI	g119143
BLAST score	253
E value	1.0e-45
Match length	103
% identity	91
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	153041
Seq. ID	LIB3176-005-P1-K1-B5
Method	BLASTX
NCBI GI	g3831487
BLAST score	292
E value	1.0e-37
Match length	129
% identity	61
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_1353642 (U39807) isocitrate lyase [Pinus taeda]

Seq. No.	153042
Seq. ID	LIB3176-005-P1-K1-B6
Method	BLASTN

NCBI GI	g3482964
BLAST score	203
E value	1.0e-110
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4 (ESSAII project)

Seq. No.	153043
Seq. ID	LIB3176-005-P1-K1-C1
Method	BLASTN
NCBI GI	g2570223
BLAST score	326
E value	0.0e+00
Match length	340
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153044
Seq. ID	LIB3176-005-P1-K1-C10
Method	BLASTX
NCBI GI	g2529229
BLAST score	219
E value	5.0e-47
Match length	119
% identity	86
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	153045
Seq. ID	LIB3176-005-P1-K1-C12
Method	BLASTX
NCBI GI	g2245107
BLAST score	250
E value	7.0e-41
Match length	130
% identity	40
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	153046
Seq. ID	LIB3176-005-P1-K1-C2
Method	BLASTX
NCBI GI	g543841
BLAST score	192
E value	4.0e-25
Match length	71
% identity	90
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	153047
Seq. ID	LIB3176-005-P1-K1-C3
Method	BLASTX

NCBI GI	g400923
BLAST score	153
E value	4.0e-23
Match length	61
% identity	98
NCBI Description	RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600_ (X65650) RAS-related GTP-binding protein [Pisum sativum]

Seq. No.	153048
Seq. ID	LIB3176-005-P1-K1-C4
Method	BLASTX
NCBI GI	g4587519
BLAST score	199
E value	1.0e-15
Match length	40
% identity	100
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	153049
Seq. ID	LIB3176-005-P1-K1-C5
Method	BLASTX
NCBI GI	g1363489
BLAST score	227
E value	2.0e-53
Match length	111
% identity	95
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153050
Seq. ID	LIB3176-005-P1-K1-C6
Method	BLASTX
NCBI GI	g1723347
BLAST score	216
E value	8.0e-36
Match length	126
% identity	68
NCBI Description	HYPOTHETICAL 64.2 KD PROTEIN YCF45 (ORF565) >gi_2147571_pir__S73202 hypothetical protein 565 - Porphyra purpurea chloroplast >gi_1276747 (U38804) trnS [Porphyra purpurea]

Seq. No.	153051
Seq. ID	LIB3176-005-P1-K1-C7
Method	BLASTX
NCBI GI	g2369766
BLAST score	263
E value	3.0e-25
Match length	66
% identity	89
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	153052
Seq. ID	LIB3176-005-P1-K1-C8
Method	BLASTX
NCBI GI	g115783
BLAST score	218
E value	3.0e-35
Match length	84
% identity	84
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	153053
Seq. ID	LIB3176-005-P1-K1-C9
Method	BLASTX
NCBI GI	g1742961
BLAST score	217
E value	7.0e-27
Match length	78
% identity	96
NCBI Description	(X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	153054
Seq. ID	LIB3176-005-P1-K1-D1
Method	BLASTN
NCBI GI	g4757407
BLAST score	218
E value	1.0e-119
Match length	344
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	153055
Seq. ID	LIB3176-005-P1-K1-D11
Method	BLASTX
NCBI GI	g4008441
BLAST score	117
E value	1.0e-22
Match length	101
% identity	63
NCBI Description	(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	153056
Seq. ID	LIB3176-005-P1-K1-D12
Method	BLASTX
NCBI GI	g1724100
BLAST score	197
E value	8.0e-24
Match length	121
% identity	49
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	153057
Seq. ID	LIB3176-005-P1-K1-D2
Method	BLASTX
NCBI GI	g4490705
BLAST score	266
E value	2.0e-40
Match length	146
% identity	72
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	153058
Seq. ID	LIB3176-005-P1-K1-D3
Method	BLASTN
NCBI GI	g608672
BLAST score	231
E value	1.0e-127
Match length	299
% identity	95
NCBI Description	Arabadopsis thaliana Landsberg AAP5 mRNA

Seq. No.	153059
Seq. ID	LIB3176-005-P1-K1-D4
Method	BLASTX
NCBI GI	g2980641
BLAST score	342
E value	4.0e-72
Match length	150
% identity	100
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	153060
Seq. ID	LIB3176-005-P1-K1-D5
Method	BLASTX
NCBI GI	g3924612
BLAST score	179
E value	2.0e-34
Match length	99
% identity	89
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	153061
Seq. ID	LIB3176-005-P1-K1-D7
Method	BLASTN
NCBI GI	g3327867
BLAST score	360
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana CIP7 mRNA for COP1-Interacting Protein 7, complete cds

Seq. No.	153062
Seq. ID	LIB3176-005-P1-K1-D8

Method	BLASTX
NCBI GI	g267077
BLAST score	190
E value	1.0e-17
Match length	69
% identity	80
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	153063
Seq. ID	LIB3176-005-P1-K1-E1
Method	BLASTN
NCBI GI	g3928074
BLAST score	162
E value	6.0e-86
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153064
Seq. ID	LIB3176-005-P1-K1-E10
Method	BLASTX
NCBI GI	g1076305
BLAST score	208
E value	1.0e-16
Match length	112
% identity	51
NCBI Description	RNA-binding protein cp31 precursor - Arabidopsis thaliana >gi_681906_dbj_BAA06520_ (D31712) cp31 [Arabidopsis thaliana]

Seq. No.	153065
Seq. ID	LIB3176-005-P1-K1-E11
Method	BLASTN
NCBI GI	g2618683
BLAST score	43
E value	3.0e-15
Match length	107
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153066
Seq. ID	LIB3176-005-P1-K1-E2
Method	BLASTX
NCBI GI	g1175013
BLAST score	262
E value	3.0e-35
Match length	95
% identity	93
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	153067
Seq. ID	LIB3176-005-P1-K1-E3
Method	BLASTX
NCBI GI	g2388943
BLAST score	89
E value	6.0e-22
Match length	88
% identity	61
NCBI Description	(Z98978) SPAC27E2.03c, putative gtp-binding protein, len:392a a, similar eg. to YBR025C, YBN5_YEAST, P38219, hypothetica l 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also sim

Seq. No.	153068
Seq. ID	LIB3176-005-P1-K1-E4
Method	BLASTX
NCBI GI	g419757
BLAST score	288
E value	1.0e-28
Match length	78
% identity	81
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana

Seq. No.	153069
Seq. ID	LIB3176-005-P1-K1-E5
Method	BLASTX
NCBI GI	g132110
BLAST score	221
E value	2.0e-46
Match length	118
% identity	91
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	153070
Seq. ID	LIB3176-005-P1-K1-E6
Method	BLASTX
NCBI GI	g2245095
BLAST score	394
E value	2.0e-38
Match length	124
% identity	69
NCBI Description	(Z97343) formyltransferase purU homolog [Arabidopsis thaliana]

Seq. No.	153071
Seq. ID	LIB3176-005-P1-K1-E7
Method	BLASTN
NCBI GI	g4220644
BLAST score	49
E value	1.0e-18

Match length	178
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	153072
Seq. ID	LIB3176-005-P1-K1-E8
Method	BLASTN
NCBI GI	g1429206
BLAST score	75
E value	2.0e-34
Match length	149
% identity	89
NCBI Description	A.thaliana mRNA for annexin

Seq. No.	153073
Seq. ID	LIB3176-005-P1-K1-E9
Method	BLASTN
NCBI GI	g4490717
BLAST score	262
E value	1.0e-145
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	153074
Seq. ID	LIB3176-005-P1-K1-F1
Method	BLASTX
NCBI GI	g2924779
BLAST score	242
E value	9.0e-42
Match length	102
% identity	99
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	153075
Seq. ID	LIB3176-005-P1-K1-F10
Method	BLASTX
NCBI GI	g4539405
BLAST score	253
E value	4.0e-54
Match length	123
% identity	88
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	153076
Seq. ID	LIB3176-005-P1-K1-F11
Method	BLASTX
NCBI GI	g2281099
BLAST score	327
E value	2.0e-41

Match length	100
% identity	96
NCBI Description	(AC002333) stearoyl-ACP desaturase [Arabidopsis thaliana]

Seq. No.	153077
Seq. ID	LIB3176-005-P1-K1-F2
Method	BLASTN
NCBI GI	g4454447
BLAST score	79
E value	2.0e-36
Match length	448
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153078
Seq. ID	LIB3176-005-P1-K1-F3
Method	BLASTX
NCBI GI	g2062164
BLAST score	263
E value	8.0e-37
Match length	121
% identity	55
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153079
Seq. ID	LIB3176-005-P1-K1-F4
Method	BLASTX
NCBI GI	g267069
BLAST score	368
E value	1.0e-60
Match length	127
% identity	88
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	153080
Seq. ID	LIB3176-005-P1-K1-F6
Method	BLASTN
NCBI GI	g4220644
BLAST score	350
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	153081
Seq. ID	LIB3176-005-P1-K1-F7
Method	BLASTX
NCBI GI	g2500497
BLAST score	186
E value	8.0e-20
Match length	70

% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225.1_ (X98656) ribosomal protein S21 [Zea mays]

Seq. No.	153082
Seq. ID	LIB3176-005-P1-K1-F8
Method	BLASTX
NCBI GI	g2262167
BLAST score	328
E value	8.0e-59
Match length	124
% identity	98
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	153083
Seq. ID	LIB3176-005-P1-K1-F9
Method	BLASTX
NCBI GI	g417103
BLAST score	173
E value	3.0e-42
Match length	104
% identity	98
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	153084
Seq. ID	LIB3176-005-P1-K1-G1
Method	BLASTX
NCBI GI	g4633131
BLAST score	342
E value	7.0e-57
Match length	122
% identity	99
NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	153085
Seq. ID	LIB3176-005-P1-K1-G11

Method	BLASTX
NCBI GI	g2443886
BLAST score	53
E value	2.0e-35
Match length	82
% identity	96
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	153086
Seq. ID	LIB3176-005-P1-K1-G12
Method	BLASTX
NCBI GI	g4314378
BLAST score	163
E value	3.0e-36
Match length	133
% identity	65
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	153087
Seq. ID	LIB3176-005-P1-K1-G2
Method	BLASTX
NCBI GI	g2347098
BLAST score	325
E value	3.0e-30
Match length	64
% identity	95
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	153088
Seq. ID	LIB3176-005-P1-K1-G3
Method	BLASTN
NCBI GI	g2760171
BLAST score	59
E value	2.0e-24
Match length	267
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]

Seq. No.	153089
Seq. ID	LIB3176-005-P1-K1-G5
Method	BLASTX
NCBI GI	g115783
BLAST score	186
E value	2.0e-42
Match length	102
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	153090
Seq. ID	LIB3176-005-P1-K1-G6
Method	BLASTX

NCBI GI	g464621
BLAST score	228
E value	3.0e-44
Match length	113
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	153091
Seq. ID	LIB3176-005-P1-K1-G8
Method	BLASTX
NCBI GI	g1769905
BLAST score	114
E value	2.0e-30
Match length	98
% identity	70
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	153092
Seq. ID	LIB3176-005-P1-K1-H1
Method	BLASTN
NCBI GI	g4584841
BLAST score	36
E value	8.0e-11
Match length	346
% identity	70
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	153093
Seq. ID	LIB3176-005-P1-K1-H10
Method	BLASTX
NCBI GI	g2924779
BLAST score	346
E value	2.0e-60
Match length	134
% identity	96
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	153094
Seq. ID	LIB3176-005-P1-K1-H11
Method	BLASTX
NCBI GI	g4678308
BLAST score	198
E value	3.0e-36
Match length	135
% identity	29
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	153095

Seq. ID	LIB3176-005-P1-K1-H12
Method	BLASTX
NCBI GI	g3129952
BLAST score	176
E value	5.0e-13
Match length	82
% identity	45
NCBI Description	(AJ006052) copper amine oxidase [Cicer arietinum]

Seq. No.	153096
Seq. ID	LIB3176-005-P1-K1-H2
Method	BLASTX
NCBI GI	g1710557
BLAST score	231
E value	3.0e-32
Match length	119
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_1181129_emb_CAA93269_ (Z69337) ribosomal protein L3 [Caenorhabditis elegans] >gi_1181131_emb_CAA93268_ (Z69336) ribosomal protein L3 [Caenorhabditis elegans] >gi_3874745_emb_CAA91277_ (Z66495) similar to 60S ribosomal protein L3; cDNA EST EMBL:M75754 comes from this gene; cDNA EST EMBL:M88798 comes from this gene; cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene; cDNA EST ... >gi_3875827_emb_CAA90183_ (Z49936) similar to 60S ribosomal protein L3; cDNA EST EMBL:M75754 comes from this gene; cDNA EST EMBL:M88798 comes from this gene; cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene; cDNA EST

Seq. No.	153097
Seq. ID	LIB3176-005-P1-K1-H4
Method	BLASTX
NCBI GI	g1402902
BLAST score	406
E value	1.0e-39
Match length	116
% identity	76
NCBI Description	(X98323) peroxidase [Arabidopsis thaliana] >gi_1419386_emb_CAA67428_ (X98928) peroxidase ATP10a [Arabidopsis thaliana]

Seq. No.	153098
Seq. ID	LIB3176-005-P1-K1-H5
Method	BLASTX
NCBI GI	g132677
BLAST score	284
E value	2.0e-36
Match length	93
% identity	89
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	153099
Seq. ID	LIB3176-005-P1-K1-H6
Method	BLASTN
NCBI GI	g2739359
BLAST score	349
E value	0.0e+00
Match length	412
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153100
Seq. ID	LIB3176-005-P1-K1-H7
Method	BLASTX
NCBI GI	g4097547
BLAST score	216
E value	2.0e-17
Match length	40
% identity	50
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	153101
Seq. ID	LIB3176-005-P1-K1-H8
Method	BLASTX
NCBI GI	g1351840
BLAST score	176
E value	1.0e-39
Match length	109
% identity	78
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_1084319_pir__S53505 isocitrate lyase - cucumber >gi_1052578_emb_CAA84632_ (Z35499) isocitrate lyase [Cucumis sativus]

Seq. No.	153102
Seq. ID	LIB3176-005-P1-K1-H9
Method	BLASTX
NCBI GI	g3128205
BLAST score	226
E value	4.0e-43
Match length	112
% identity	87
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]

Seq. No.	153103
Seq. ID	LIB3176-006-P1-K1-A1
Method	BLASTX
NCBI GI	g3914740
BLAST score	509
E value	1.0e-51
Match length	144
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No. 153104

Seq. ID	LIB3176-006-P1-K1-A11
Method	BLASTX
NCBI GI	g544134
BLAST score	335
E value	3.0e-31
Match length	150
% identity	22
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	153105
Seq. ID	LIB3176-006-P1-K1-A2
Method	BLASTX
NCBI GI	g3377797
BLAST score	579
E value	6.0e-60
Match length	137
% identity	82
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	153106
Seq. ID	LIB3176-006-P1-K1-A3
Method	BLASTX
NCBI GI	g133028
BLAST score	329
E value	9.0e-31
Match length	76
% identity	86
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_ (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	153107
Seq. ID	LIB3176-006-P1-K1-A4
Method	BLASTX
NCBI GI	g2388578
BLAST score	706
E value	7.0e-75
Match length	141
% identity	100
NCBI Description	(AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs gb_T75785,gb_R30580,gb_T04698 come from this gene. [Arabidopsis thaliana]

Seq. No.	153108
Seq. ID	LIB3176-006-P1-K1-A5
Method	BLASTX
NCBI GI	g1429211

BLAST score	479
E value	4.0e-48
Match length	127
% identity	76
NCBI Description	(X99116) HMG-I/Y protein [Arabidopsis thaliana] >gi_2809402 (AF041253) high mobility group protein a [Arabidopsis thaliana]

Seq. No.	153109
Seq. ID	LIB3176-006-P1-K1-A6
Method	BLASTN
NCBI GI	g2245073
BLAST score	141
E value	2.0e-73
Match length	213
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	153110
Seq. ID	LIB3176-006-P1-K1-A7
Method	BLASTX
NCBI GI	g2245030
BLAST score	291
E value	1.0e-26
Match length	68
% identity	87
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	153111
Seq. ID	LIB3176-006-P1-K1-A9
Method	BLASTX
NCBI GI	g1363489
BLAST score	648
E value	5.0e-68
Match length	124
% identity	94
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153112
Seq. ID	LIB3176-006-P1-K1-B1
Method	BLASTX
NCBI GI	g3603353
BLAST score	481
E value	2.0e-48
Match length	100
% identity	94
NCBI Description	(AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana]

Seq. No.	153113
Seq. ID	LIB3176-006-P1-K1-B11
Method	BLASTX
NCBI GI	g1345132

BLAST score	213
E value	5.0e-17
Match length	141
% identity	6
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	153114
Seq. ID	LIB3176-006-P1-K1-B2
Method	BLASTX
NCBI GI	g587564
BLAST score	48
E value	1.0e-48
Match length	132
% identity	77
NCBI Description	(X80235) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	153115
Seq. ID	LIB3176-006-P1-K1-B3
Method	BLASTX
NCBI GI	g1769905
BLAST score	569
E value	1.0e-58
Match length	149
% identity	74
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	153116
Seq. ID	LIB3176-006-P1-K1-B4
Method	BLASTN
NCBI GI	g4585891
BLAST score	387
E value	0.0e+00
Match length	451
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	153117
Seq. ID	LIB3176-006-P1-K1-B7
Method	BLASTX
NCBI GI	g99752
BLAST score	582
E value	2.0e-60
Match length	119
% identity	99
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	153118
Seq. ID	LIB3176-006-P1-K1-B8
Method	BLASTX
NCBI GI	g132074

BLAST score	835
E value	6.0e-90
Match length	157
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	153119
Seq. ID	LIB3176-006-P1-K1-C1
Method	BLASTX
NCBI GI	g3150415
BLAST score	698
E value	8.0e-74
Match length	128
% identity	39
NCBI Description	(AC004165) sec13-related protein [Arabidopsis thaliana] >gi_3420046 (AC004680) sec13-related protein [Arabidopsis thaliana]

Seq. No.	153120
Seq. ID	LIB3176-006-P1-K1-C11
Method	BLASTX
NCBI GI	g139780
BLAST score	179
E value	5.0e-13
Match length	67
% identity	51
NCBI Description	WOUND-INDUCED PROTEIN 1 >gi_82293_pir__JQ0398 wun1 protein - potato

Seq. No.	153121
Seq. ID	LIB3176-006-P1-K1-C12
Method	BLASTN
NCBI GI	g511080
BLAST score	285
E value	1.0e-159
Match length	289
% identity	100
NCBI Description	A.thaliana HEM15 mRNA for ferrochelatase

Seq. No.	153122
Seq. ID	LIB3176-006-P1-K1-C2
Method	BLASTX
NCBI GI	g120667
BLAST score	652
E value	2.0e-68
Match length	144
% identity	88
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	153123
Seq. ID	LIB3176-006-P1-K1-C3
Method	BLASTX
NCBI GI	g1899025
BLAST score	108
E value	2.0e-78
Match length	157
% identity	96
NCBI Description	(U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232 (AC005169) hexokinase [Arabidopsis thaliana]

Seq. No.	153124
Seq. ID	LIB3176-006-P1-K1-C6
Method	BLASTX
NCBI GI	g2781354
BLAST score	653
E value	1.0e-68
Match length	128
% identity	97
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	153125
Seq. ID	LIB3176-006-P1-K1-C7
Method	BLASTX
NCBI GI	g4454016
BLAST score	615
E value	4.0e-64
Match length	122
% identity	100
NCBI Description	(AL035396) UMP/CMP kinase like protein [Arabidopsis thaliana]

Seq. No.	153126
Seq. ID	LIB3176-006-P1-K1-C8
Method	BLASTX
NCBI GI	g119194
BLAST score	561
E value	8.0e-58
Match length	112
% identity	97
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	153127
Seq. ID	LIB3176-006-P1-K1-C9
Method	BLASTN
NCBI GI	g3869069
BLAST score	268
E value	1.0e-149
Match length	481
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	153128
Seq. ID	LIB3176-006-P1-K1-D1
Method	BLASTN
NCBI GI	g3883121
BLAST score	468
E value	0.0e+00
Match length	491
% identity	99
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP2) mRNA, complete cds

Seq. No.	153129
Seq. ID	LIB3176-006-P1-K1-D10
Method	BLASTX
NCBI GI	g4586264
BLAST score	443
E value	6.0e-44
Match length	93
% identity	87
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	153130
Seq. ID	LIB3176-006-P1-K1-D11
Method	BLASTX
NCBI GI	g2388583
BLAST score	624
E value	4.0e-65
Match length	159
% identity	80
NCBI Description	(AC000098) Similar to Synechocystis hypothetical protein (gb_D90908). [Arabidopsis thaliana]

Seq. No.	153131
Seq. ID	LIB3176-006-P1-K1-D12
Method	BLASTX
NCBI GI	g3261659
BLAST score	182
E value	2.0e-13
Match length	90
% identity	43
NCBI Description	(Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]

Seq. No.	153132
Seq. ID	LIB3176-006-P1-K1-D2
Method	BLASTX
NCBI GI	g2062161
BLAST score	766
E value	8.0e-82
Match length	146
% identity	51
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153133
Seq. ID	LIB3176-006-P1-K1-D3
Method	BLASTX
NCBI GI	g3063472
BLAST score	681
E value	6.0e-72
Match length	129
% identity	98
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	153134
Seq. ID	LIB3176-006-P1-K1-D4
Method	BLASTX
NCBI GI	g3869088
BLAST score	719
E value	3.0e-76
Match length	141
% identity	98
NCBI Description	(AB019427) elongation factor-1 alpha [Nicotiana paniculata]

Seq. No.	153135
Seq. ID	LIB3176-006-P1-K1-D7
Method	BLASTX
NCBI GI	g1370186
BLAST score	346
E value	1.0e-32
Match length	85
% identity	80
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	153136
Seq. ID	LIB3176-006-P1-K1-D8
Method	BLASTN
NCBI GI	g2749918
BLAST score	78
E value	1.0e-35
Match length	295
% identity	84
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153137
Seq. ID	LIB3176-006-P1-K1-D9
Method	BLASTX
NCBI GI	g3212849
BLAST score	611
E value	1.0e-63
Match length	145
% identity	83
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	153138
Seq. ID	LIB3176-006-P1-K1-E1
Method	BLASTN
NCBI GI	g4584351
BLAST score	211
E value	1.0e-115

Match length	330
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	153139
Seq. ID	LIB3176-006-P1-K1-E10
Method	BLASTN
NCBI GI	g517330
BLAST score	448
E value	0.0e+00
Match length	459
% identity	99
NCBI Description	A.thaliana mRNA for ribosomal protein S10

Seq. No.	153140
Seq. ID	LIB3176-006-P1-K1-E11
Method	BLASTX
NCBI GI	g2062158
BLAST score	609
E value	2.0e-63
Match length	125
% identity	48
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153141
Seq. ID	LIB3176-006-P1-K1-E12
Method	BLASTX
NCBI GI	g4220512
BLAST score	190
E value	3.0e-14
Match length	93
% identity	42
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	153142
Seq. ID	LIB3176-006-P1-K1-E2
Method	BLASTX
NCBI GI	g4539444
BLAST score	228
E value	1.0e-18
Match length	139
% identity	41
NCBI Description	(AL049523) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153143
Seq. ID	LIB3176-006-P1-K1-E3
Method	BLASTN
NCBI GI	g3928074
BLAST score	137
E value	6.0e-71
Match length	485
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153144
Seq. ID	LIB3176-006-P1-K1-E4
Method	BLASTX
NCBI GI	g2829862
BLAST score	212
E value	8.0e-17
Match length	139
% identity	43
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	153145
Seq. ID	LIB3176-006-P1-K1-E6
Method	BLASTX
NCBI GI	g3983125
BLAST score	644
E value	2.0e-67
Match length	152
% identity	83
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	153146
Seq. ID	LIB3176-006-P1-K1-E8
Method	BLASTN
NCBI GI	g3641835
BLAST score	235
E value	1.0e-129
Match length	366
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	153147
Seq. ID	LIB3176-006-P1-K1-F1
Method	BLASTX
NCBI GI	g113026
BLAST score	818
E value	7.0e-88
Match length	160
% identity	96
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	153148
Seq. ID	LIB3176-006-P1-K1-F10
Method	BLASTX
NCBI GI	g2853219
BLAST score	411
E value	3.0e-40
Match length	104
% identity	67

NCBI Description	(AJ000923) glutathione transferase [Carica papaya]

Seq. No.	153149
Seq. ID	LIB3176-006-P1-K1-F11
Method	BLASTX
NCBI GI	g4056469
BLAST score	196
E value	3.0e-15
Match length	35
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t

Seq. No.	153150
Seq. ID	LIB3176-006-P1-K1-F12
Method	BLASTX
NCBI GI	g3335365
BLAST score	686
E value	2.0e-72
Match length	159
% identity	89
NCBI Description	(AC003028) high affinity calcium antiporter [Arabidopsis thaliana]

Seq. No.	153151
Seq. ID	LIB3176-006-P1-K1-F2
Method	BLASTX
NCBI GI	g3776571
BLAST score	514
E value	3.0e-52
Match length	114
% identity	89
NCBI Description	(AC005388) T22H22.18 [Arabidopsis thaliana]

Seq. No.	153152
Seq. ID	LIB3176-006-P1-K1-F3
Method	BLASTX
NCBI GI	g349379
BLAST score	159
E value	1.0e-10
Match length	97
% identity	48
NCBI Description	(L22847) HAHB-1 [Helianthus annuus]

Seq. No.	153153
Seq. ID	LIB3176-006-P1-K1-F4
Method	BLASTX
NCBI GI	g132110
BLAST score	815
E value	1.0e-87
Match length	156
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	153154
Seq. ID	LIB3176-006-P1-K1-F5
Method	BLASTX
NCBI GI	g4454051
BLAST score	848
E value	2.0e-91
Match length	159
% identity	97
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	153155
Seq. ID	LIB3176-006-P1-K1-F6
Method	BLASTN
NCBI GI	g4220643
BLAST score	205
E value	1.0e-112
Match length	270
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	153156
Seq. ID	LIB3176-006-P1-K1-F7
Method	BLASTN
NCBI GI	g2337888
BLAST score	422
E value	0.0e+00
Match length	456
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	153157
Seq. ID	LIB3176-006-P1-K1-F8
Method	BLASTX
NCBI GI	g1170503
BLAST score	610
E value	2.0e-63
Match length	118
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	153158
Seq. ID	LIB3176-006-P1-K1-F9
Method	BLASTX
NCBI GI	g3421087
BLAST score	448

E value	5.0e-47
Match length	105
% identity	93
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	153159
Seq. ID	LIB3176-006-P1-K1-G10
Method	BLASTX
NCBI GI	g886116
BLAST score	721
E value	1.0e-76
Match length	133
% identity	98
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	153160
Seq. ID	LIB3176-006-P1-K1-G11
Method	BLASTX
NCBI GI	g4263711
BLAST score	335
E value	3.0e-31
Match length	71
% identity	87
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	153161
Seq. ID	LIB3176-006-P1-K1-G12
Method	BLASTN
NCBI GI	g4519193
BLAST score	466
E value	0.0e+00
Match length	470
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	153162
Seq. ID	LIB3176-006-P1-K1-G2
Method	BLASTX
NCBI GI	g1419388
BLAST score	389
E value	1.0e-37
Match length	85
% identity	86
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	153163
Seq. ID	LIB3176-006-P1-K1-G3
Method	BLASTN
NCBI GI	g2262097
BLAST score	312
E value	1.0e-175

Match length	481
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	153164
Seq. ID	LIB3176-006-P1-K1-G4
Method	BLASTX
NCBI GI	g3024022
BLAST score	487
E value	3.0e-49
Match length	103
% identity	88
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	153165
Seq. ID	LIB3176-006-P1-K1-G5
Method	BLASTN
NCBI GI	g4662640
BLAST score	285
E value	1.0e-159
Match length	352
% identity	33
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	153166
Seq. ID	LIB3176-006-P1-K1-G6
Method	BLASTN
NCBI GI	g2842474
BLAST score	146
E value	2.0e-76
Match length	411
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	153167
Seq. ID	LIB3176-006-P1-K1-G7
Method	BLASTX
NCBI GI	g544425
BLAST score	189
E value	3.0e-14
Match length	40
% identity	88
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	153168
Seq. ID	LIB3176-006-P1-K1-G9
Method	BLASTX

NCBI GI	g1168748
BLAST score	638
E value	6.0e-67
Match length	125
% identity	62
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	153169
Seq. ID	LIB3176-006-P1-K1-H1
Method	BLASTN
NCBI GI	g4519183
BLAST score	92
E value	4.0e-44
Match length	390
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	153170
Seq. ID	LIB3176-006-P1-K1-H10
Method	BLASTX
NCBI GI	g3123264
BLAST score	547
E value	3.0e-56
Match length	115
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153171
Seq. ID	LIB3176-006-P1-K1-H11
Method	BLASTX
NCBI GI	g1732570
BLAST score	816
E value	1.0e-87
Match length	154
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	153172
Seq. ID	LIB3176-006-P1-K1-H12
Method	BLASTX
NCBI GI	g3540186
BLAST score	641
E value	4.0e-67
Match length	119
% identity	99
NCBI Description	(AC004122) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	153173
Seq. ID	LIB3176-006-P1-K1-H4
Method	BLASTX
NCBI GI	g2677828
BLAST score	491
E value	1.0e-49

Match length 128
% identity 71
NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 153174
Seq. ID LIB3176-006-P1-K1-H5
Method BLASTX
NCBI GI g3297813
BLAST score 426
E value 3.0e-42
Match length 94
% identity 89
NCBI Description (AL031032) hypothetical protein [Arabidopsis thaliana]

Seq. No. 153175
Seq. ID LIB3176-006-P1-K1-H6
Method BLASTX
NCBI GI g2564112
BLAST score 200
E value 1.0e-15
Match length 77
% identity 62
NCBI Description (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No. 153176
Seq. ID LIB3176-006-P1-K1-H7
Method BLASTX
NCBI GI g1702986
BLAST score 352
E value 1.0e-33
Match length 75
% identity 96
NCBI Description 14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No. 153177
Seq. ID LIB3176-006-P1-K1-H9
Method BLASTX
NCBI GI g3822036
BLAST score 261
E value 1.0e-22
Match length 146
% identity 40
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 153178
Seq. ID LIB3176-007-P1-K1-A1
Method BLASTX
NCBI GI g282865
BLAST score 722
E value 9.0e-77
Match length 135
% identity 76
NCBI Description chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding

protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	153179
Seq. ID	LIB3176-007-P1-K1-A12
Method	BLASTX
NCBI GI	g1170170
BLAST score	366
E value	5.0e-35
Match length	117
% identity	65
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT3 (HD-ZIP PROTEIN 3) >gi_549889 (U09338) homeobox protein [Arabidopsis thaliana] >gi_549890 (U09339) homeobox protein [Arabidopsis thaliana]

Seq. No.	153180
Seq. ID	LIB3176-007-P1-K1-A2
Method	BLASTX
NCBI GI	g3738257
BLAST score	432
E value	6.0e-43
Match length	97
% identity	88
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	153181
Seq. ID	LIB3176-007-P1-K1-A3
Method	BLASTX
NCBI GI	g3738257
BLAST score	509
E value	8.0e-52
Match length	118
% identity	86
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	153182
Seq. ID	LIB3176-007-P1-K1-A4
Method	BLASTX
NCBI GI	g1669387
BLAST score	533
E value	1.0e-65
Match length	136
% identity	96
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	153183
Seq. ID	LIB3176-007-P1-K1-A5
Method	BLASTX
NCBI GI	g1709846
BLAST score	148
E value	5.0e-10
Match length	71
% identity	38

NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]
Seq. No.	153184
Seq. ID	LIB3176-007-P1-K1-A6
Method	BLASTX
NCBI GI	g132074
BLAST score	634
E value	2.0e-66
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	153185
Seq. ID	LIB3176-007-P1-K1-A7
Method	BLASTX
NCBI GI	g4587552
BLAST score	421
E value	1.0e-41
Match length	82
% identity	99
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb
Seq. No.	153186
Seq. ID	LIB3176-007-P1-K1-A8
Method	BLASTX
NCBI GI	g2335192
BLAST score	597
E value	4.0e-62
Match length	123
% identity	94
NCBI Description	(AF013465) bHLH protein [Arabidopsis thaliana]
Seq. No.	153187
Seq. ID	LIB3176-007-P1-K1-A9
Method	BLASTN
NCBI GI	g4587641
BLAST score	184
E value	3.0e-99
Match length	224
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence
Seq. No.	153188
Seq. ID	LIB3176-007-P1-K1-B1
Method	BLASTX
NCBI GI	g2827039
BLAST score	542
E value	9.0e-56

Match length	118
% identity	91
NCBI Description	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]

Seq. No.	153189
Seq. ID	LIB3176-007-P1-K1-B11
Method	BLASTX
NCBI GI	g3510259
BLAST score	56
E value	3.0e-13
Match length	46
% identity	83
NCBI Description	(AC005310) putative inorganic pyrophosphatase [Arabidopsis thaliana] >gi_3522960 (AC004411) putative inorganic pyrophosphatase [Arabidopsis thaliana]

Seq. No.	153190
Seq. ID	LIB3176-007-P1-K1-B12
Method	BLASTN
NCBI GI	g3299824
BLAST score	211
E value	1.0e-115
Match length	319
% identity	97
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	153191
Seq. ID	LIB3176-007-P1-K1-B2
Method	BLASTX
NCBI GI	g1076316
BLAST score	540
E value	2.0e-55
Match length	114
% identity	98
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	153192
Seq. ID	LIB3176-007-P1-K1-B3
Method	BLASTX
NCBI GI	g3286693
BLAST score	645
E value	1.0e-67
Match length	129
% identity	100
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	153193
Seq. ID	LIB3176-007-P1-K1-B4
Method	BLASTN
NCBI GI	g4582444
BLAST score	387
E value	0.0e+00

Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	153194
Seq. ID	LIB3176-007-P1-K1-B5
Method	BLASTX
NCBI GI	g2832625
BLAST score	465
E value	1.0e-46
Match length	104
% identity	84
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	153195
Seq. ID	LIB3176-007-P1-K1-B8
Method	BLASTX
NCBI GI	g2160158
BLAST score	482
E value	1.0e-48
Match length	113
% identity	82
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	153196
Seq. ID	LIB3176-007-P1-K1-B9
Method	BLASTX
NCBI GI	g1170939
BLAST score	557
E value	2.0e-57
Match length	114
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	153197
Seq. ID	LIB3176-007-P1-K1-C1
Method	BLASTN
NCBI GI	g3242970
BLAST score	238
E value	1.0e-131
Match length	250
% identity	99
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	153198
Seq. ID	LIB3176-007-P1-K1-C10
Method	BLASTX
NCBI GI	g431164

BLAST score	620
E value	8.0e-65
Match length	136
% identity	88
NCBI Description	(D21823) ORF [Lilium longiflorum]

Seq. No.	153199
Seq. ID	LIB3176-007-P1-K1-C12
Method	BLASTN
NCBI GI	g3241917
BLAST score	148
E value	1.0e-77
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	153200
Seq. ID	LIB3176-007-P1-K1-C3
Method	BLASTX
NCBI GI	g1946362
BLAST score	420
E value	2.0e-41
Match length	123
% identity	68
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	153201
Seq. ID	LIB3176-007-P1-K1-C4
Method	BLASTX
NCBI GI	g1669389
BLAST score	487
E value	3.0e-49
Match length	90
% identity	99
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	153202
Seq. ID	LIB3176-007-P1-K1-C7
Method	BLASTX
NCBI GI	g1616787
BLAST score	582
E value	2.0e-60
Match length	113
% identity	97
NCBI Description	(U71122) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No.	153203
Seq. ID	LIB3176-007-P1-K1-C8
Method	BLASTX
NCBI GI	g2764941
BLAST score	544
E value	5.0e-56
Match length	98
% identity	98
NCBI Description	(X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	153204
Seq. ID	LIB3176-007-P1-K1-C9
Method	BLASTN
NCBI GI	g3510339
BLAST score	137
E value	2.0e-71
Match length	165
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	153205
Seq. ID	LIB3176-007-P1-K1-D1
Method	BLASTN
NCBI GI	g2924733
BLAST score	57
E value	5.0e-24
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	153206
Seq. ID	LIB3176-007-P1-K1-D10
Method	BLASTX
NCBI GI	g3377797
BLAST score	575
E value	2.0e-59
Match length	136
% identity	82
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	153207
Seq. ID	LIB3176-007-P1-K1-D11
Method	BLASTX
NCBI GI	g4704766
BLAST score	484
E value	8.0e-49
Match length	127
% identity	43
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	153208
Seq. ID	LIB3176-007-P1-K1-D2
Method	BLASTX
NCBI GI	g2384956
BLAST score	236
E value	9.0e-20
Match length	113

% identity	41
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	153209
Seq. ID	LIB3176-007-P1-K1-D3
Method	BLASTX
NCBI GI	g113024
BLAST score	585
E value	1.0e-60
Match length	133
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	153210
Seq. ID	LIB3176-007-P1-K1-D4
Method	BLASTX
NCBI GI	g2497733
BLAST score	615
E value	3.0e-64
Match length	118
% identity	100
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) >gi_1177796 (M80567) non-specific lipid transfer protein [Arabidopsis thaliana] >gi_3786018 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	153211
Seq. ID	LIB3176-007-P1-K1-D5
Method	BLASTX
NCBI GI	g3776003
BLAST score	498
E value	4.0e-53
Match length	115
% identity	98
NCBI Description	(AJ010465) RNA helicase [Arabidopsis thaliana]

Seq. No.	153212
Seq. ID	LIB3176-007-P1-K1-D6
Method	BLASTX
NCBI GI	g267077
BLAST score	636
E value	1.0e-66
Match length	119
% identity	99
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	153213
Seq. ID	LIB3176-007-P1-K1-D7
Method	BLASTX
NCBI GI	g4689366
BLAST score	264
E value	5.0e-23
Match length	110

% identity	51
NCBI Description	(AF134155) RING finger protein [Arabidopsis thaliana]

Seq. No.	153214
Seq. ID	LIB3176-007-P1-K1-D8
Method	BLASTX
NCBI GI	g2435604
BLAST score	248
E value	4.0e-21
Match length	119
% identity	39
NCBI Description	(AF026213) strong similarity to Saccharomyces cerevisiae endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]

Seq. No.	153215
Seq. ID	LIB3176-007-P1-K1-D9
Method	BLASTX
NCBI GI	g132110
BLAST score	619
E value	1.0e-64
Match length	114
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	153216
Seq. ID	LIB3176-007-P1-K1-E1
Method	BLASTX
NCBI GI	g2119846
BLAST score	690
E value	6.0e-73
Match length	130
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	153217
Seq. ID	LIB3176-007-P1-K1-E10
Method	BLASTN
NCBI GI	g3172156
BLAST score	246
E value	1.0e-136
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153218

Seq. ID	LIB3176-007-P1-K1-E12
Method	BLASTX
NCBI GI	g1076393
BLAST score	515
E value	2.0e-52
Match length	106
% identity	99
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	153219
Seq. ID	LIB3176-007-P1-K1-E2
Method	BLASTX
NCBI GI	g1518540
BLAST score	648
E value	5.0e-68
Match length	138
% identity	89
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	153220
Seq. ID	LIB3176-007-P1-K1-E3
Method	BLASTX
NCBI GI	g4432855
BLAST score	413
E value	2.0e-40
Match length	86
% identity	99
NCBI Description	(AC006300) unknown protein [Arabidopsis thaliana]

Seq. No.	153221
Seq. ID	LIB3176-007-P1-K1-E4
Method	BLASTN
NCBI GI	g4432847
BLAST score	33
E value	6.0e-09
Match length	185
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153222
Seq. ID	LIB3176-007-P1-K1-E5
Method	BLASTX
NCBI GI	g2911055
BLAST score	505
E value	2.0e-51
Match length	124
% identity	82
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	153223
Seq. ID	LIB3176-007-P1-K1-E6
Method	BLASTX
NCBI GI	g1175011
BLAST score	479

E value	2.0e-50
Match length	107
% identity	95
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	153224
Seq. ID	LIB3176-007-P1-K1-E7
Method	BLASTX
NCBI GI	g3962377
BLAST score	531
E value	2.0e-54
Match length	122
% identity	88
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	153225
Seq. ID	LIB3176-007-P1-K1-F1
Method	BLASTX
NCBI GI	g2388582
BLAST score	324
E value	1.0e-30
Match length	73
% identity	86
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	153226
Seq. ID	LIB3176-007-P1-K1-F10
Method	BLASTX
NCBI GI	g507808
BLAST score	689
E value	7.0e-73
Match length	138
% identity	96
NCBI Description	(D13987) phosphoenolpyruvate carboxylase [Brassica napus] >gi_743641_prf__2013218A phosphoenolpyruvate carboxylase [Brassica napus]

Seq. No.	153227
Seq. ID	LIB3176-007-P1-K1-F12
Method	BLASTN
NCBI GI	g3985949
BLAST score	58
E value	2.0e-24
Match length	98
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	153228
Seq. ID	LIB3176-007-P1-K1-F2
Method	BLASTX
NCBI GI	g3819699
BLAST score	517

E value	1.0e-52
Match length	133
% identity	73
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	153229
Seq. ID	LIB3176-007-P1-K1-F4
Method	BLASTN
NCBI GI	g3785968
BLAST score	124
E value	3.0e-63
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153230
Seq. ID	LIB3176-007-P1-K1-F5
Method	BLASTX
NCBI GI	g2281649
BLAST score	291
E value	2.0e-26
Match length	69
% identity	86
NCBI Description	(AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]

Seq. No.	153231
Seq. ID	LIB3176-007-P1-K1-F6
Method	BLASTX
NCBI GI	g1168256
BLAST score	460
E value	4.0e-46
Match length	94
% identity	95
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	153232
Seq. ID	LIB3176-007-P1-K1-F8
Method	BLASTN
NCBI GI	g1871173
BLAST score	301
E value	1.0e-169
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	153233
Seq. ID	LIB3176-007-P1-K1-F9
Method	BLASTX
NCBI GI	g2495179
BLAST score	507

E value	1.0e-51
Match length	103
% identity	100
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	153234
Seq. ID	LIB3176-007-P1-K1-G1
Method	BLASTN
NCBI GI	g3810584
BLAST score	188
E value	1.0e-101
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153235
Seq. ID	LIB3176-007-P1-K1-G10
Method	BLASTX
NCBI GI	g832876
BLAST score	481
E value	2.0e-48
Match length	113
% identity	82
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	153236
Seq. ID	LIB3176-007-P1-K1-G11
Method	BLASTN
NCBI GI	g11919
BLAST score	49
E value	1.0e-18
Match length	162
% identity	87
NCBI Description	Oenothera elata subsp. hookeri plastid gene for pre-apocytochrome f (Euoenothera plastome I)

Seq. No.	153237
Seq. ID	LIB3176-007-P1-K1-G2
Method	BLASTX
NCBI GI	g2244762
BLAST score	468
E value	6.0e-47
Match length	119
% identity	72
NCBI Description	(Z97335) major latex protein [Arabidopsis thaliana]

Seq. No.	153238

Seq. ID	LIB3176-007-P1-K1-G4
Method	BLASTX
NCBI GI	g2495179
BLAST score	545
E value	6.0e-56
Match length	111
% identity	99
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_1084340_pir__S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi_313150_emb_CAA51941_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi_313838_emb_CAA52061_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

Seq. No.	153239
Seq. ID	LIB3176-007-P1-K1-G5
Method	BLASTX
NCBI GI	g3421096
BLAST score	536
E value	5.0e-55
Match length	108
% identity	99
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	153240
Seq. ID	LIB3176-007-P1-K1-G7
Method	BLASTX
NCBI GI	g2924779
BLAST score	375
E value	5.0e-36
Match length	111
% identity	69
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	153241
Seq. ID	LIB3176-007-P1-K1-G8
Method	BLASTN
NCBI GI	g4519195
BLAST score	233
E value	1.0e-128
Match length	397
% identity	59
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	153242
Seq. ID	LIB3176-007-P1-K1-H1
Method	BLASTN
NCBI GI	g4587641

BLAST score	208
E value	1.0e-113
Match length	354
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	153243
Seq. ID	LIB3176-007-P1-K1-H2
Method	BLASTN
NCBI GI	g2182287
BLAST score	269
E value	1.0e-150
Match length	403
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	153244
Seq. ID	LIB3176-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2924779
BLAST score	262
E value	6.0e-23
Match length	53
% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	153245
Seq. ID	LIB3176-007-P1-K1-H4
Method	BLASTN
NCBI GI	g4558586
BLAST score	369
E value	0.0e+00
Match length	433
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	153246
Seq. ID	LIB3176-007-P1-K1-H6
Method	BLASTX
NCBI GI	g2809246
BLAST score	178
E value	4.0e-13
Match length	101
% identity	31
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	153247
Seq. ID	LIB3176-007-P1-K1-H8
Method	BLASTX
NCBI GI	g1709633

BLAST score 230
E value 4.0e-19
Match length 76
% identity 57
NCBI Description XAA-PRO DIPEPTIDASE (X-PRO DIPEPTIDASE) (PROLINE DIPEPTIDASE) (PROLIDASE) (IMIDODIPEPTIDASE) (PEPTIDASE 4) >gi_1236706 (U51014) prolidase [Mus musculus]

Seq. No. 153248
Seq. ID LIB3176-008-P1-K1-A10
Method BLASTX
NCBI GI g4678226
BLAST score 552
E value 8.0e-57
Match length 118
% identity 94
NCBI Description (AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No. 153249
Seq. ID LIB3176-008-P1-K1-A11
Method BLASTX
NCBI GI g1905876
BLAST score 535
E value 9.0e-55
Match length 108
% identity 99
NCBI Description (U90879) biotin carboxylase subunit [Arabidopsis thaliana] >gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]

Seq. No. 153250
Seq. ID LIB3176-008-P1-K1-A12
Method BLASTX
NCBI GI g3023848
BLAST score 692
E value 3.0e-73
Match length 143
% identity 35
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 153251
Seq. ID LIB3176-008-P1-K1-A3
Method BLASTX
NCBI GI g1363489
BLAST score 637
E value 9.0e-67
Match length 135
% identity 89
NCBI Description thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153252
Seq. ID	LIB3176-008-P1-K1-A4
Method	BLASTX
NCBI GI	g1724100
BLAST score	403
E value	3.0e-39
Match length	140
% identity	54
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	153253
Seq. ID	LIB3176-008-P1-K1-A5
Method	BLASTX
NCBI GI	g4164473
BLAST score	171
E value	4.0e-12
Match length	51
% identity	69
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	153254
Seq. ID	LIB3176-008-P1-K1-A6
Method	BLASTX
NCBI GI	g2443357
BLAST score	490
E value	2.0e-49
Match length	138
% identity	72
NCBI Description	(AB004293) SigB [Arabidopsis thaliana] >gi_2597831_emb_CAA75584_ (Y15362) sigma factor [Arabidopsis thaliana] >gi_2879922_dbj_BAA24825_ (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] >gi_3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]

Seq. No.	153255
Seq. ID	LIB3176-008-P1-K1-A7
Method	BLASTX
NCBI GI	g2243120
BLAST score	262
E value	6.0e-23
Match length	90
% identity	76
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153256
Seq. ID	LIB3176-008-P1-K1-A8
Method	BLASTX
NCBI GI	g3337361
BLAST score	554
E value	4.0e-57
Match length	125
% identity	80
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 153257

Seq. ID	LIB3176-008-P1-K1-A9
Method	BLASTX
NCBI GI	g3176676
BLAST score	508
E value	1.0e-51
Match length	106
% identity	96
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	153258
Seq. ID	LIB3176-008-P1-K1-B1
Method	BLASTX
NCBI GI	g2119848
BLAST score	603
E value	9.0e-63
Match length	113
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	153259
Seq. ID	LIB3176-008-P1-K1-B11
Method	BLASTX
NCBI GI	g2129769
BLAST score	536
E value	9.0e-57
Match length	118
% identity	97
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	153260
Seq. ID	LIB3176-008-P1-K1-B12
Method	BLASTX
NCBI GI	g4583153
BLAST score	151
E value	7.0e-10
Match length	62
% identity	45
NCBI Description	(AF108211) cytosolic inorganic pyrophosphatase [Homo sapiens]

Seq. No.	153261
Seq. ID	LIB3176-008-P1-K1-B4
Method	BLASTX
NCBI GI	g3023742
BLAST score	450
E value	7.0e-45

Match length	117
% identity	81
NCBI Description	FERREDOXIN 2 PRECURSOR >gi_1931646 (U95973) ferredoxin precusor isolog [Arabidopsis thaliana]

Seq. No.	153262
Seq. ID	LIB3176-008-P1-K1-B6
Method	BLASTX
NCBI GI	g3122572
BLAST score	456
E value	2.0e-45
Match length	139
% identity	66
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	153263
Seq. ID	LIB3176-008-P1-K1-B7
Method	BLASTX
NCBI GI	g3337361
BLAST score	582
E value	2.0e-60
Match length	139
% identity	76
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153264
Seq. ID	LIB3176-008-P1-K1-B8
Method	BLASTX
NCBI GI	g1175013
BLAST score	495
E value	3.0e-50
Match length	97
% identity	99
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	153265
Seq. ID	LIB3176-008-P1-K1-C1
Method	BLASTX
NCBI GI	g542157
BLAST score	546
E value	4.0e-56
Match length	127
% identity	82
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	153266
Seq. ID	LIB3176-008-P1-K1-C10
Method	BLASTX
NCBI GI	g4539292

BLAST score	486
E value	4.0e-49
Match length	96
% identity	96
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153267
Seq. ID	LIB3176-008-P1-K1-C11
Method	BLASTX
NCBI GI	g132677
BLAST score	484
E value	7.0e-49
Match length	124
% identity	78
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	153268
Seq. ID	LIB3176-008-P1-K1-C12
Method	BLASTX
NCBI GI	g3914740
BLAST score	516
E value	1.0e-52
Match length	128
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	153269
Seq. ID	LIB3176-008-P1-K1-C2
Method	BLASTX
NCBI GI	g2245000
BLAST score	577
E value	9.0e-60
Match length	122
% identity	96
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153270
Seq. ID	LIB3176-008-P1-K1-C3
Method	BLASTX
NCBI GI	g3892056
BLAST score	629
E value	8.0e-66
Match length	128
% identity	99
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	153271
Seq. ID	LIB3176-008-P1-K1-C4
Method	BLASTX
NCBI GI	g2129639
BLAST score	277

E value	9.0e-60
Match length	128
% identity	95
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	153272
Seq. ID	LIB3176-008-P1-K1-C6
Method	BLASTX
NCBI GI	g2342728
BLAST score	368
E value	3.0e-35
Match length	120
% identity	61
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	153273
Seq. ID	LIB3176-008-P1-K1-C7
Method	BLASTX
NCBI GI	g1143427
BLAST score	286
E value	3.0e-26
Match length	66
% identity	86
NCBI Description	(X73961) heat shock protein 70 [Cucumis sativus]

Seq. No.	153274
Seq. ID	LIB3176-008-P1-K1-D1
Method	BLASTX
NCBI GI	g113026
BLAST score	322
E value	8.0e-30
Match length	67
% identity	93
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	153275
Seq. ID	LIB3176-008-P1-K1-D10
Method	BLASTX
NCBI GI	g114335
BLAST score	140
E value	4.0e-09
Match length	28
% identity	100
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	153276
Seq. ID	LIB3176-008-P1-K1-D11
Method	BLASTX
NCBI GI	g117238
BLAST score	472
E value	2.0e-47
Match length	133
% identity	77
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	153277
Seq. ID	LIB3176-008-P1-K1-D12
Method	BLASTN
NCBI GI	g4581084
BLAST score	327
E value	0.0e+00
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	153278
Seq. ID	LIB3176-008-P1-K1-D2
Method	BLASTX
NCBI GI	g1718097
BLAST score	458
E value	1.0e-45
Match length	126
% identity	63
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	153279
Seq. ID	LIB3176-008-P1-K1-D3
Method	BLASTN
NCBI GI	g3046851
BLAST score	398
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	153280
Seq. ID	LIB3176-008-P1-K1-D4

Method	BLASTX
NCBI GI	g4559354
BLAST score	218
E value	6.0e-22
Match length	69
% identity	17
NCBI Description	(AC006585) unknown protein [Arabidopsis thaliana]

Seq. No.	153281
Seq. ID	LIB3176-008-P1-K1-D5
Method	BLASTX
NCBI GI	g115767
BLAST score	730
E value	1.0e-77
Match length	141
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	153282
Seq. ID	LIB3176-008-P1-K1-D6
Method	BLASTX
NCBI GI	g4309731
BLAST score	216
E value	2.0e-17
Match length	113
% identity	40
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153283
Seq. ID	LIB3176-008-P1-K1-D7
Method	BLASTX
NCBI GI	g2224911
BLAST score	459
E value	6.0e-46
Match length	136
% identity	71
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	153284
Seq. ID	LIB3176-008-P1-K1-D8
Method	BLASTN
NCBI GI	g3128134
BLAST score	348
E value	0.0e+00
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	153285

Seq. ID	LIB3176-008-P1-K1-D9
Method	BLASTX
NCBI GI	g166765
BLAST score	561
E value	7.0e-58
Match length	109
% identity	98
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	153286
Seq. ID	LIB3176-008-P1-K1-E1
Method	BLASTX
NCBI GI	g2497857
BLAST score	382
E value	6.0e-53
Match length	129
% identity	85
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_2117463_pir__S57958 malate dehydrogenase (EC 1.1.1.37) - rape >gi_899226_emb_CAA61621_ (X89451) malate dehydrogenase [Brassica napus]

Seq. No.	153287
Seq. ID	LIB3176-008-P1-K1-E10
Method	BLASTX
NCBI GI	g3769300
BLAST score	555
E value	4.0e-57
Match length	130
% identity	85
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	153288
Seq. ID	LIB3176-008-P1-K1-E11
Method	BLASTX
NCBI GI	g497325
BLAST score	141
E value	1.0e-08
Match length	40
% identity	70
NCBI Description	(U09867) unknown [Chlorobium vibrioforme] >gi_1098330_prf__2115394E ORF Z [Chlorobium vibrioforme]

Seq. No.	153289
Seq. ID	LIB3176-008-P1-K1-E12
Method	BLASTX
NCBI GI	g1172873
BLAST score	242
E value	2.0e-20
Match length	112
% identity	47
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	153290

Seq. ID	LIB3176-008-P1-K1-E2
Method	BLASTX
NCBI GI	g4454036
BLAST score	748
E value	1.0e-79
Match length	138
% identity	99
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	153291
Seq. ID	LIB3176-008-P1-K1-E3
Method	BLASTX
NCBI GI	g2062157
BLAST score	408
E value	3.0e-72
Match length	202
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153292
Seq. ID	LIB3176-008-P1-K1-E4
Method	BLASTX
NCBI GI	g4469007
BLAST score	99
E value	2.0e-25
Match length	62
% identity	85
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	153293
Seq. ID	LIB3176-008-P1-K1-E5
Method	BLASTX
NCBI GI	g1762584
BLAST score	626
E value	2.0e-65
Match length	128
% identity	56
NCBI Description	(U63373) polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]

Seq. No.	153294
Seq. ID	LIB3176-008-P1-K1-E6
Method	BLASTX
NCBI GI	g280386
BLAST score	657
E value	4.0e-69
Match length	127
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	153295
Seq. ID	LIB3176-008-P1-K1-E7
Method	BLASTX
NCBI GI	g3128180
BLAST score	757
E value	8.0e-81
Match length	145
% identity	99
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	153296
Seq. ID	LIB3176-008-P1-K1-E9
Method	BLASTX
NCBI GI	g3688799
BLAST score	483
E value	9.0e-49
Match length	104
% identity	93
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	153297
Seq. ID	LIB3176-008-P1-K1-F1
Method	BLASTN
NCBI GI	g2618605
BLAST score	201
E value	1.0e-109
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	153298
Seq. ID	LIB3176-008-P1-K1-F10
Method	BLASTX
NCBI GI	g2244759
BLAST score	603
E value	9.0e-63
Match length	137
% identity	76
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	153299
Seq. ID	LIB3176-008-P1-K1-F11
Method	BLASTX
NCBI GI	g113026
BLAST score	689
E value	8.0e-73
Match length	132
% identity	98
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A

isocitrate lyase [Brassica napus]

Seq. No.	153300
Seq. ID	LIB3176-008-P1-K1-F12
Method	BLASTN
NCBI GI	g4539290
BLAST score	38
E value	2.0e-12
Match length	102
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	153301
Seq. ID	LIB3176-008-P1-K1-F2
Method	BLASTX
NCBI GI	g132939
BLAST score	611
E value	1.0e-63
Match length	132
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	153302
Seq. ID	LIB3176-008-P1-K1-F3
Method	BLASTX
NCBI GI	g1170503
BLAST score	470
E value	3.0e-53
Match length	110
% identity	94
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	153303
Seq. ID	LIB3176-008-P1-K1-F5
Method	BLASTX
NCBI GI	g2959734
BLAST score	213
E value	5.0e-17
Match length	43
% identity	100
NCBI Description	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	153304
Seq. ID	LIB3176-008-P1-K1-F6
Method	BLASTX
NCBI GI	g3915847
BLAST score	290
E value	3.0e-26
Match length	71

% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	153305
Seq. ID	LIB3176-008-P1-K1-F7
Method	BLASTX
NCBI GI	g2245144
BLAST score	445
E value	3.0e-44
Match length	115
% identity	79
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153306
Seq. ID	LIB3176-008-P1-K1-F8
Method	BLASTX
NCBI GI	g2583128
BLAST score	298
E value	5.0e-27
Match length	131
% identity	43
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153307
Seq. ID	LIB3176-008-P1-K1-F9
Method	BLASTX
NCBI GI	g2736155
BLAST score	778
E value	3.0e-83
Match length	149
% identity	98
NCBI Description	(AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No.	153308
Seq. ID	LIB3176-008-P1-K1-G1
Method	BLASTX
NCBI GI	g267073
BLAST score	644
E value	1.0e-67
Match length	118
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	153309
Seq. ID	LIB3176-008-P1-K1-G10
Method	BLASTX
NCBI GI	g2062161
BLAST score	604
E value	7.0e-63
Match length	114
% identity	50

NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153310
Seq. ID	LIB3176-008-P1-K1-G11
Method	BLASTX
NCBI GI	g4587519
BLAST score	673
E value	5.0e-71
Match length	136
% identity	97
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	153311
Seq. ID	LIB3176-008-P1-K1-G12
Method	BLASTX
NCBI GI	g3080371
BLAST score	544
E value	6.0e-56
Match length	120
% identity	84
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	153312
Seq. ID	LIB3176-008-P1-K1-G2
Method	BLASTX
NCBI GI	g3540219
BLAST score	431
E value	1.0e-42
Match length	139
% identity	57
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	153313
Seq. ID	LIB3176-008-P1-K1-G3
Method	BLASTX
NCBI GI	g629602
BLAST score	314
E value	7.0e-29
Match length	103
% identity	53
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	153314
Seq. ID	LIB3176-008-P1-K1-G4
Method	BLASTX
NCBI GI	g2306917
BLAST score	693
E value	3.0e-73
Match length	136
% identity	99

NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	153315
Seq. ID	LIB3176-008-P1-K1-G5
Method	BLASTN
NCBI GI	g4220627
BLAST score	39
E value	1.0e-12
Match length	201
% identity	4
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	153316
Seq. ID	LIB3176-008-P1-K1-G6
Method	BLASTX
NCBI GI	g4193388
BLAST score	418
E value	4.0e-41
Match length	112
% identity	73
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	153317
Seq. ID	LIB3176-008-P1-K1-G7
Method	BLASTX
NCBI GI	g132074
BLAST score	649
E value	3.0e-68
Match length	121
% identity	98
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	153318
Seq. ID	LIB3176-008-P1-K1-G9
Method	BLASTX
NCBI GI	g629541
BLAST score	581
E value	3.0e-60
Match length	124
% identity	92
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	153319
Seq. ID	LIB3176-008-P1-K1-H1
Method	BLASTN
NCBI GI	g4582444
BLAST score	447
E value	0.0e+00
Match length	454

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	153320
Seq. ID	LIB3176-008-P1-K1-H11
Method	BLASTN
NCBI GI	g4455168
BLAST score	126
E value	2.0e-64
Match length	359
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	153321
Seq. ID	LIB3176-008-P1-K1-H12
Method	BLASTX
NCBI GI	g2961346
BLAST score	492
E value	9.0e-50
Match length	108
% identity	84
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	153322
Seq. ID	LIB3176-008-P1-K1-H2
Method	BLASTX
NCBI GI	g4262180
BLAST score	421
E value	2.0e-56
Match length	116
% identity	84
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	153323
Seq. ID	LIB3176-008-P1-K1-H3
Method	BLASTX
NCBI GI	g1151244
BLAST score	583
E value	2.0e-60
Match length	118
% identity	100
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	153324
Seq. ID	LIB3176-008-P1-K1-H4
Method	BLASTN
NCBI GI	g3688169
BLAST score	208
E value	1.0e-113
Match length	347
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	153325
Seq. ID	LIB3176-008-P1-K1-H5
Method	BLASTN
NCBI GI	g2618599
BLAST score	113
E value	6.0e-57
Match length	156
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	153326
Seq. ID	LIB3176-008-P1-K1-H8
Method	BLASTX
NCBI GI	g2062161
BLAST score	674
E value	4.0e-71
Match length	127
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153327
Seq. ID	LIB3176-008-P1-K1-H9
Method	BLASTX
NCBI GI	g2369766
BLAST score	416
E value	7.0e-41
Match length	143
% identity	58
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	153328
Seq. ID	LIB3176-008-P1-K2-A1
Method	BLASTX
NCBI GI	g1169199
BLAST score	511
E value	7.0e-56
Match length	118
% identity	97
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102 >gi_479739_pir__S35271 hypothetical protein - Arabidopsis thaliana >gi_166928 (L11368) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	153329
Seq. ID	LIB3176-008-P1-K2-A10
Method	BLASTX
NCBI GI	g4678226
BLAST score	549
E value	2.0e-56
Match length	119
% identity	92
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	153330
Seq. ID	LIB3176-008-P1-K2-A11
Method	BLASTX
NCBI GI	g1865671
BLAST score	724
E value	8.0e-77
Match length	149
% identity	98
NCBI Description	(Y09061) acetyl-CoA carboxylase, biotin carboxylase subunit [Arabidopsis thaliana]

Seq. No.	153331
Seq. ID	LIB3176-008-P1-K2-A12
Method	BLASTX
NCBI GI	g3023848
BLAST score	874
E value	2.0e-94
Match length	182
% identity	48
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	153332
Seq. ID	LIB3176-008-P1-K2-A2
Method	BLASTX
NCBI GI	g2864609
BLAST score	249
E value	4.0e-21
Match length	93
% identity	51
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	153333
Seq. ID	LIB3176-008-P1-K2-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	668
E value	3.0e-70
Match length	137
% identity	91
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153334
Seq. ID	LIB3176-008-P1-K2-A4
Method	BLASTX
NCBI GI	g1724100
BLAST score	456
E value	2.0e-45
Match length	181
% identity	48
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	153335
Seq. ID	LIB3176-008-P1-K2-A5
Method	BLASTX
NCBI GI	g4164473
BLAST score	225
E value	3.0e-18
Match length	104
% identity	50
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	153336
Seq. ID	LIB3176-008-P1-K2-A6
Method	BLASTX
NCBI GI	g2353173
BLAST score	134
E value	2.0e-50
Match length	164
% identity	69
NCBI Description	(AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No.	153337
Seq. ID	LIB3176-008-P1-K2-A7
Method	BLASTX
NCBI GI	g2243120
BLAST score	262
E value	1.0e-22
Match length	97
% identity	78
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153338
Seq. ID	LIB3176-008-P1-K2-A8
Method	BLASTX
NCBI GI	g3337361
BLAST score	720
E value	2.0e-76
Match length	177
% identity	72
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153339
Seq. ID	LIB3176-008-P1-K2-A9
Method	BLASTX
NCBI GI	g3176676
BLAST score	648
E value	5.0e-68
Match length	131
% identity	98
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	153340
Seq. ID	LIB3176-008-P1-K2-B1
Method	BLASTX

NCBI GI	g2119848
BLAST score	626
E value	2.0e-65
Match length	119
% identity	97
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	153341
Seq. ID	LIB3176-008-P1-K2-B10
Method	BLASTN
NCBI GI	g2182289
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153342
Seq. ID	LIB3176-008-P1-K2-B11
Method	BLASTX
NCBI GI	g126985
BLAST score	453
E value	2.0e-45
Match length	100
% identity	88
NCBI Description	MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis thaliana]

Seq. No.	153343
Seq. ID	LIB3176-008-P1-K2-B12
Method	BLASTX
NCBI GI	g4583153
BLAST score	325
E value	5.0e-30
Match length	112
% identity	56
NCBI Description	(AF108211) cytosolic inorganic pyrophosphatase [Homo sapiens]

Seq. No.	153344
Seq. ID	LIB3176-008-P1-K2-B2
Method	BLASTX
NCBI GI	g3582340
BLAST score	164
E value	5.0e-11
Match length	125
% identity	43
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	153345
Seq. ID	LIB3176-008-P1-K2-B3
Method	BLASTN
NCBI GI	g2924733
BLAST score	63
E value	3.0e-27
Match length	146
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	153346
Seq. ID	LIB3176-008-P1-K2-B4
Method	BLASTX
NCBI GI	g3023742
BLAST score	503
E value	7.0e-51
Match length	139
% identity	77
NCBI Description	FERREDOXIN 2 PRECURSOR >gi_1931646 (U95973) ferredoxin precusor isolog [Arabidopsis thaliana]

Seq. No.	153347
Seq. ID	LIB3176-008-P1-K2-B5
Method	BLASTN
NCBI GI	g4220637
BLAST score	34
E value	2.0e-09
Match length	147
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	153348
Seq. ID	LIB3176-008-P1-K2-B6
Method	BLASTN
NCBI GI	g4589436
BLAST score	242
E value	1.0e-134
Match length	262
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	153349
Seq. ID	LIB3176-008-P1-K2-B8
Method	BLASTX
NCBI GI	g1175013
BLAST score	97
E value	6.0e-26
Match length	70
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	153350
Seq. ID	LIB3176-008-P1-K2-C1
Method	BLASTX
NCBI GI	g3915826
BLAST score	841
E value	2.0e-90
Match length	205
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	153351
Seq. ID	LIB3176-008-P1-K2-C10
Method	BLASTX
NCBI GI	g4539292
BLAST score	523
E value	2.0e-53
Match length	132
% identity	78
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153352
Seq. ID	LIB3176-008-P1-K2-C11
Method	BLASTX
NCBI GI	g132677
BLAST score	127
E value	7.0e-07
Match length	145
% identity	60
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	153353
Seq. ID	LIB3176-008-P1-K2-C2
Method	BLASTX
NCBI GI	g2245000
BLAST score	449
E value	6.0e-45
Match length	95
% identity	99
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153354
Seq. ID	LIB3176-008-P1-K2-C3
Method	BLASTX
NCBI GI	g3892056
BLAST score	50
E value	7.0e-17
Match length	123
% identity	56
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	153355
Seq. ID	LIB3176-008-P1-K2-C4

Method	BLASTX
NCBI GI	g2129639
BLAST score	563
E value	3.0e-58
Match length	118
% identity	97
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	153356
Seq. ID	LIB3176-008-P1-K2-C5
Method	BLASTN
NCBI GI	g3790547
BLAST score	32
E value	1.0e-08
Match length	40
% identity	95
NCBI Description	Arabidopsis thaliana cultivar Columbia flavanone 3-hydroxylase (F3H) gene, complete cds

Seq. No.	153357
Seq. ID	LIB3176-008-P1-K2-C6
Method	BLASTX
NCBI GI	g2342728
BLAST score	363
E value	2.0e-34
Match length	114
% identity	62
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	153358
Seq. ID	LIB3176-008-P1-K2-C7
Method	BLASTX
NCBI GI	g1928991
BLAST score	162
E value	1.0e-11
Match length	54
% identity	63
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]

Seq. No.	153359
Seq. ID	LIB3176-008-P1-K2-C9
Method	BLASTX
NCBI GI	g2252866
BLAST score	303
E value	2.0e-27
Match length	78
% identity	79
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	153360
Seq. ID	LIB3176-008-P1-K2-D1
Method	BLASTX

NCBI GI	g1695645
BLAST score	207
E value	2.0e-16
Match length	43
% identity	88
NCBI Description	(D78256) Isocitrate Lyase [Cucurbita sp.]

Seq. No.	153361
Seq. ID	LIB3176-008-P1-K2-D10
Method	BLASTX
NCBI GI	g114335
BLAST score	152
E value	2.0e-10
Match length	32
% identity	97
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	153362
Seq. ID	LIB3176-008-P1-K2-D11
Method	BLASTX
NCBI GI	g117238
BLAST score	501
E value	9.0e-51
Match length	132
% identity	80
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	153363
Seq. ID	LIB3176-008-P1-K2-D12
Method	BLASTN
NCBI GI	g4581084
BLAST score	363
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	153364
Seq. ID	LIB3176-008-P1-K2-D2
Method	BLASTX
NCBI GI	g1718097
BLAST score	317
E value	2.0e-29
Match length	93

% identity	60
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	153365
Seq. ID	LIB3176-008-P1-K2-D3
Method	BLASTN
NCBI GI	g3046851
BLAST score	446
E value	0.0e+00
Match length	473
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	153366
Seq. ID	LIB3176-008-P1-K2-D5
Method	BLASTX
NCBI GI	g2196772
BLAST score	146
E value	1.0e-09
Match length	71
% identity	48
NCBI Description	(AF003128) chlorophyll a/b-binding protein [Mesembryanthemum crystallinum]

Seq. No.	153367
Seq. ID	LIB3176-008-P1-K2-D6
Method	BLASTX
NCBI GI	g4455332
BLAST score	182
E value	2.0e-13
Match length	81
% identity	48
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	153368
Seq. ID	LIB3176-008-P1-K2-D7
Method	BLASTX
NCBI GI	g2224911
BLAST score	380
E value	5.0e-37
Match length	84
% identity	88
NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	153369
Seq. ID	LIB3176-008-P1-K2-D8
Method	BLASTN
NCBI GI	g3046851
BLAST score	60
E value	2.0e-25
Match length	104

% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	153370
Seq. ID	LIB3176-008-P1-K2-D9
Method	BLASTX
NCBI GI	g166765
BLAST score	476
E value	6.0e-48
Match length	103
% identity	91
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	153371
Seq. ID	LIB3176-008-P1-K2-E1
Method	BLASTX
NCBI GI	g3929649
BLAST score	849
E value	2.0e-91
Match length	194
% identity	87
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	153372
Seq. ID	LIB3176-008-P1-K2-E10
Method	BLASTX
NCBI GI	g3769300
BLAST score	510
E value	7.0e-52
Match length	129
% identity	78
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	153373
Seq. ID	LIB3176-008-P1-K2-E12
Method	BLASTX
NCBI GI	g2511693
BLAST score	284
E value	3.0e-25
Match length	142
% identity	44
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	153374
Seq. ID	LIB3176-008-P1-K2-E2
Method	BLASTN
NCBI GI	g4454022
BLAST score	51
E value	4.0e-20
Match length	88
% identity	61
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	153375

Seq. ID	LIB3176-008-P1-K2-E3
Method	BLASTX
NCBI GI	g2062157
BLAST score	484
E value	8.0e-58
Match length	131
% identity	37
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153376
Seq. ID	LIB3176-008-P1-K2-E4
Method	BLASTX
NCBI GI	g4469007
BLAST score	822
E value	2.0e-88
Match length	162
% identity	98
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	153377
Seq. ID	LIB3176-008-P1-K2-E6
Method	BLASTX
NCBI GI	g280386
BLAST score	627
E value	1.0e-65
Match length	126
% identity	97
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	153378
Seq. ID	LIB3176-008-P1-K2-E7
Method	BLASTX
NCBI GI	g4454036
BLAST score	511
E value	4.0e-52
Match length	103
% identity	92
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	153379
Seq. ID	LIB3176-008-P1-K2-E9
Method	BLASTX
NCBI GI	g2062157
BLAST score	225
E value	4.0e-19
Match length	72
% identity	62
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153380
Seq. ID	LIB3176-008-P1-K2-F1
Method	BLASTX
NCBI GI	g3688799
BLAST score	435
E value	3.0e-43
Match length	89
% identity	98
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	153381
Seq. ID	LIB3176-008-P1-K2-F10
Method	BLASTX
NCBI GI	g2244759
BLAST score	635
E value	2.0e-66
Match length	141
% identity	78
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	153382
Seq. ID	LIB3176-008-P1-K2-F11
Method	BLASTX
NCBI GI	g113026
BLAST score	376
E value	2.0e-36
Match length	94
% identity	81
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	153383
Seq. ID	LIB3176-008-P1-K2-F12
Method	BLASTX
NCBI GI	g4539292
BLAST score	286
E value	3.0e-26
Match length	58
% identity	95
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153384
Seq. ID	LIB3176-008-P1-K2-F2
Method	BLASTX
NCBI GI	g2245144
BLAST score	321
E value	9.0e-30
Match length	78
% identity	82

NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153385
Seq. ID	LIB3176-008-P1-K2-F3
Method	BLASTX
NCBI GI	g1170503
BLAST score	639
E value	7.0e-67
Match length	127
% identity	99
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	153386
Seq. ID	LIB3176-008-P1-K2-F5
Method	BLASTX
NCBI GI	g2959734
BLAST score	289
E value	7.0e-26
Match length	61
% identity	93
NCBI Description	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	153387
Seq. ID	LIB3176-008-P1-K2-F7
Method	BLASTN
NCBI GI	g2618605
BLAST score	169
E value	4.0e-90
Match length	394
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	153388
Seq. ID	LIB3176-008-P1-K2-F9
Method	BLASTX
NCBI GI	g2736155
BLAST score	733
E value	6.0e-78
Match length	152
% identity	92
NCBI Description	(AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No.	153389
Seq. ID	LIB3176-008-P1-K2-G1
Method	BLASTX
NCBI GI	g267073
BLAST score	723
E value	1.0e-76
Match length	139

% identity	96
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	153390
Seq. ID	LIB3176-008-P1-K2-G10
Method	BLASTX
NCBI GI	g2062161
BLAST score	621
E value	9.0e-65
Match length	157
% identity	44
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153391
Seq. ID	LIB3176-008-P1-K2-G11
Method	BLASTX
NCBI GI	g4587519
BLAST score	738
E value	2.0e-78
Match length	162
% identity	90
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	153392
Seq. ID	LIB3176-008-P1-K2-G12
Method	BLASTX
NCBI GI	g3080371
BLAST score	620
E value	1.0e-64
Match length	145
% identity	78
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	153393
Seq. ID	LIB3176-008-P1-K2-G2
Method	BLASTX
NCBI GI	g3540219
BLAST score	197
E value	1.0e-15
Match length	63
% identity	56
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	153394
Seq. ID	LIB3176-008-P1-K2-G3
Method	BLASTX
NCBI GI	g629602
BLAST score	510
E value	1.0e-51

Match length	197
% identity	49
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	153395
Seq. ID	LIB3176-008-P1-K2-G4
Method	BLASTX
NCBI GI	g2306917
BLAST score	389
E value	5.0e-38
Match length	87
% identity	91
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	153396
Seq. ID	LIB3176-008-P1-K2-G5
Method	BLASTN
NCBI GI	g4584531
BLAST score	34
E value	1.0e-09
Match length	162
% identity	14
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	153397
Seq. ID	LIB3176-008-P1-K2-G6
Method	BLASTX
NCBI GI	g401169
BLAST score	246
E value	2.0e-21
Match length	50
% identity	96
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	153398
Seq. ID	LIB3176-008-P1-K2-G9
Method	BLASTX
NCBI GI	g1175012
BLAST score	529
E value	4.0e-54
Match length	115
% identity	90
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	153399
Seq. ID	LIB3176-008-P1-K2-H1
Method	BLASTN
NCBI GI	g4582444
BLAST score	551
E value	0.0e+00
Match length	567

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	153400
Seq. ID	LIB3176-008-P1-K2-H11
Method	BLASTN
NCBI GI	g4455168
BLAST score	100
E value	5.0e-49
Match length	315
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	153401
Seq. ID	LIB3176-008-P1-K2-H12
Method	BLASTN
NCBI GI	g2961335
BLAST score	147
E value	3.0e-77
Match length	191
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	153402
Seq. ID	LIB3176-008-P1-K2-H2
Method	BLASTX
NCBI GI	g1172806
BLAST score	567
E value	1.0e-58
Match length	124
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	153403
Seq. ID	LIB3176-008-P1-K2-H3
Method	BLASTX
NCBI GI	g1151244
BLAST score	242
E value	1.0e-20
Match length	69
% identity	75
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	153404
Seq. ID	LIB3176-008-P1-K2-H4
Method	BLASTN
NCBI GI	g3688169
BLAST score	200
E value	1.0e-108
Match length	336

% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	153405
Seq. ID	LIB3176-008-P1-K2-H5
Method	BLASTN
NCBI GI	g2618599
BLAST score	69
E value	1.0e-30
Match length	270
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	153406
Seq. ID	LIB3176-008-P1-K2-H8
Method	BLASTX
NCBI GI	g2062161
BLAST score	818
E value	8.0e-88
Match length	174
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153407
Seq. ID	LIB3176-008-P1-K2-H9
Method	BLASTN
NCBI GI	g4757405
BLAST score	249
E value	1.0e-138
Match length	357
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	153408
Seq. ID	LIB3176-008-P1-K3-A1
Method	BLASTN
NCBI GI	g166927
BLAST score	81
E value	9.0e-38
Match length	116
% identity	95
NCBI Description	Arabidopsis thaliana unidentified mRNA sequence, complete cds

Seq. No.	153409
Seq. ID	LIB3176-008-P1-K3-A11
Method	BLASTX
NCBI GI	g1905876
BLAST score	288
E value	4.0e-26
Match length	61
% identity	95
NCBI Description	(U90879) biotin carboxylase subunit [Arabidopsis thaliana]

>gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]

Seq. No.	153410
Seq. ID	LIB3176-008-P1-K3-A12
Method	BLASTX
NCBI GI	g3023848
BLAST score	636
E value	1.0e-66
Match length	134
% identity	49
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	153411
Seq. ID	LIB3176-008-P1-K3-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	328
E value	8.0e-31
Match length	70
% identity	90
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153412
Seq. ID	LIB3176-008-P1-K3-A4
Method	BLASTN
NCBI GI	g3128137
BLAST score	50
E value	2.0e-19
Match length	121
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	153413
Seq. ID	LIB3176-008-P1-K3-A5
Method	BLASTX
NCBI GI	g4164473
BLAST score	152
E value	4.0e-10
Match length	35
% identity	80
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	153414
Seq. ID	LIB3176-008-P1-K3-A6
Method	BLASTX
NCBI GI	g2353173
BLAST score	385

E value	1.0e-37
Match length	79
% identity	97
NCBI Description	(AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No.	153415
Seq. ID	LIB3176-008-P1-K3-A7
Method	BLASTX
NCBI GI	g2243120
BLAST score	262
E value	8.0e-23
Match length	97
% identity	77
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153416
Seq. ID	LIB3176-008-P1-K3-A8
Method	BLASTX
NCBI GI	g3337361
BLAST score	373
E value	2.0e-36
Match length	77
% identity	87
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153417
Seq. ID	LIB3176-008-P1-K3-A9
Method	BLASTX
NCBI GI	g3176676
BLAST score	358
E value	3.0e-34
Match length	91
% identity	82
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	153418
Seq. ID	LIB3176-008-P1-K3-B1
Method	BLASTX
NCBI GI	g2119848
BLAST score	304
E value	6.0e-28
Match length	73
% identity	79
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	153419
Seq. ID	LIB3176-008-P1-K3-B10
Method	BLASTN

NCBI GI	g2182289
BLAST score	248
E value	1.0e-137
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	153420
Seq. ID	LIB3176-008-P1-K3-B11
Method	BLASTX
NCBI GI	g2129769
BLAST score	302
E value	7.0e-28
Match length	75
% identity	80
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	153421
Seq. ID	LIB3176-008-P1-K3-B12
Method	BLASTN
NCBI GI	g3985955
BLAST score	252
E value	1.0e-140
Match length	252
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	153422
Seq. ID	LIB3176-008-P1-K3-B2
Method	BLASTX
NCBI GI	g3582340
BLAST score	161
E value	9.0e-11
Match length	133
% identity	42
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	153423
Seq. ID	LIB3176-008-P1-K3-B4
Method	BLASTX
NCBI GI	g3023742
BLAST score	164
E value	7.0e-12
Match length	38
% identity	92
NCBI Description	FERREDOXIN 2 PRECURSOR >gi_1931646 (U95973) ferredoxin precusor isolog [Arabidopsis thaliana]

Seq. No.	153424
Seq. ID	LIB3176-008-P1-K3-B6
Method	BLASTN
NCBI GI	g4589436
BLAST score	201

E value	1.0e-109
Match length	261
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	153425
Seq. ID	LIB3176-008-P1-K3-B7
Method	BLASTX
NCBI GI	g3337361
BLAST score	283
E value	7.0e-26
Match length	68
% identity	79
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153426
Seq. ID	LIB3176-008-P1-K3-B8
Method	BLASTX
NCBI GI	g1175013
BLAST score	171
E value	1.0e-12
Match length	61
% identity	61
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	153427
Seq. ID	LIB3176-008-P1-K3-C1
Method	BLASTX
NCBI GI	g3915826
BLAST score	729
E value	1.0e-83
Match length	195
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	153428
Seq. ID	LIB3176-008-P1-K3-C10
Method	BLASTX
NCBI GI	g4539292
BLAST score	414
E value	7.0e-41
Match length	81
% identity	95
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153429
Seq. ID	LIB3176-008-P1-K3-C11
Method	BLASTX
NCBI GI	g132677
BLAST score	379
E value	1.0e-36
Match length	90

% identity	83
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	153430
Seq. ID	LIB3176-008-P1-K3-C2
Method	BLASTX
NCBI GI	g2245000
BLAST score	452
E value	3.0e-45
Match length	102
% identity	94
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153431
Seq. ID	LIB3176-008-P1-K3-C3
Method	BLASTX
NCBI GI	g3892056
BLAST score	607
E value	3.0e-63
Match length	127
% identity	98
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	153432
Seq. ID	LIB3176-008-P1-K3-C5
Method	BLASTX
NCBI GI	g3790548
BLAST score	280
E value	2.0e-25
Match length	53
% identity	98
NCBI Description	(AF064064) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	153433
Seq. ID	LIB3176-008-P1-K3-C6
Method	BLASTX
NCBI GI	g2342728
BLAST score	171
E value	2.0e-12
Match length	68
% identity	54
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	153434
Seq. ID	LIB3176-008-P1-K3-C7
Method	BLASTX
NCBI GI	g1928991
BLAST score	164
E value	7.0e-12
Match length	37
% identity	86
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus

lanatus]

Seq. No.	153435
Seq. ID	LIB3176-008-P1-K3-C9
Method	BLASTN
NCBI GI	g2252848
BLAST score	153
E value	8.0e-81
Match length	193
% identity	95
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	153436
Seq. ID	LIB3176-008-P1-K3-D1
Method	BLASTN
NCBI GI	g4589440
BLAST score	92
E value	1.0e-44
Match length	92
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	153437
Seq. ID	LIB3176-008-P1-K3-D10
Method	BLASTN
NCBI GI	g166628
BLAST score	93
E value	2.0e-45
Match length	93
% identity	100
NCBI Description	A.thaliana plasma membrane H+-ATPase gene, complete cds

Seq. No.	153438
Seq. ID	LIB3176-008-P1-K3-D11
Method	BLASTX
NCBI GI	g117238
BLAST score	416
E value	7.0e-41
Match length	126
% identity	73
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	153439
Seq. ID	LIB3176-008-P1-K3-D12
Method	BLASTN
NCBI GI	g4581084
BLAST score	313

E value	1.0e-176
Match length	341
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	153440
Seq. ID	LIB3176-008-P1-K3-D3
Method	BLASTN
NCBI GI	g3046851
BLAST score	372
E value	0.0e+00
Match length	416
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	153441
Seq. ID	LIB3176-008-P1-K3-D5
Method	BLASTX
NCBI GI	g115767
BLAST score	402
E value	1.0e-39
Match length	79
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	153442
Seq. ID	LIB3176-008-P1-K3-D6
Method	BLASTX
NCBI GI	g4455332
BLAST score	183
E value	1.0e-13
Match length	81
% identity	48
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	153443
Seq. ID	LIB3176-008-P1-K3-D8
Method	BLASTN
NCBI GI	g3128134
BLAST score	52
E value	3.0e-21
Match length	60
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	153444
Seq. ID	LIB3176-008-P1-K3-D9
Method	BLASTX

NCBI GI	g166765
BLAST score	400
E value	3.0e-39
Match length	78
% identity	97
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	153445
Seq. ID	LIB3176-008-P1-K3-E1
Method	BLASTX
NCBI GI	g2497857
BLAST score	375
E value	3.0e-36
Match length	89
% identity	84
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_2117463_pir__S57958 malate dehydrogenase (EC 1.1.1.37) - rape >gi_899226_emb_CAA61621_ (X89451) malate dehydrogenase [Brassica napus]

Seq. No.	153446
Seq. ID	LIB3176-008-P1-K3-E10
Method	BLASTX
NCBI GI	g2642434
BLAST score	444
E value	3.0e-44
Match length	107
% identity	82
NCBI Description	(AC002391) putative Rer1 protein [Arabidopsis thaliana]

Seq. No.	153447
Seq. ID	LIB3176-008-P1-K3-E12
Method	BLASTX
NCBI GI	g1172873
BLAST score	226
E value	1.0e-18
Match length	107
% identity	47
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	153448
Seq. ID	LIB3176-008-P1-K3-E2
Method	BLASTX
NCBI GI	g4454036
BLAST score	766
E value	9.0e-82
Match length	151
% identity	95
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	153449
Seq. ID	LIB3176-008-P1-K3-E3
Method	BLASTX

NCBI GI	g2062157
BLAST score	157
E value	2.0e-21
Match length	57
% identity	95
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153450
Seq. ID	LIB3176-008-P1-K3-E4
Method	BLASTX
NCBI GI	g4469007
BLAST score	462
E value	2.0e-46
Match length	92
% identity	97
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	153451
Seq. ID	LIB3176-008-P1-K3-E6
Method	BLASTX
NCBI GI	g280386
BLAST score	417
E value	2.0e-41
Match length	85
% identity	99
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	153452
Seq. ID	LIB3176-008-P1-K3-E7
Method	BLASTX
NCBI GI	g3128180
BLAST score	410
E value	1.0e-40
Match length	79
% identity	100
NCBI Description	(AC004521) citrate synthetase [Arabidopsis thaliana]

Seq. No.	153453
Seq. ID	LIB3176-008-P1-K3-E9
Method	BLASTX
NCBI GI	g3688799
BLAST score	291
E value	1.0e-26
Match length	66
% identity	89
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	153454
Seq. ID	LIB3176-008-P1-K3-F1

Method	BLASTN
NCBI GI	g2618605
BLAST score	182
E value	4.0e-98
Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	153455
Seq. ID	LIB3176-008-P1-K3-F10
Method	BLASTX
NCBI GI	g2244759
BLAST score	305
E value	2.0e-28
Match length	70
% identity	77
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	153456
Seq. ID	LIB3176-008-P1-K3-F11
Method	BLASTX
NCBI GI	g113026
BLAST score	405
E value	9.0e-40
Match length	93
% identity	86
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	153457
Seq. ID	LIB3176-008-P1-K3-F12
Method	BLASTX
NCBI GI	g4539292
BLAST score	320
E value	3.0e-30
Match length	65
% identity	94
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153458
Seq. ID	LIB3176-008-P1-K3-F2
Method	BLASTX
NCBI GI	g132939
BLAST score	287
E value	2.0e-26
Match length	55
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	153459
Seq. ID	LIB3176-008-P1-K3-F3
Method	BLASTX
NCBI GI	g1170503
BLAST score	503
E value	4.0e-51
Match length	99
% identity	98
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	153460
Seq. ID	LIB3176-008-P1-K3-F5
Method	BLASTN
NCBI GI	g3641835
BLAST score	188
E value	1.0e-101
Match length	204
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	153461
Seq. ID	LIB3176-008-P1-K3-F7
Method	BLASTX
NCBI GI	g2245144
BLAST score	197
E value	1.0e-15
Match length	50
% identity	76
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153462
Seq. ID	LIB3176-008-P1-K3-F8
Method	BLASTN
NCBI GI	g3449326
BLAST score	154
E value	2.0e-81
Match length	158
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	153463
Seq. ID	LIB3176-008-P1-K3-G10
Method	BLASTX
NCBI GI	g2062161
BLAST score	340
E value	2.0e-32
Match length	66
% identity	56
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153464
Seq. ID	LIB3176-008-P1-K3-G11
Method	BLASTX
NCBI GI	g4587519
BLAST score	628
E value	8.0e-66
Match length	120
% identity	100
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	153465
Seq. ID	LIB3176-008-P1-K3-G12
Method	BLASTX
NCBI GI	g3080371
BLAST score	681
E value	8.0e-72
Match length	161
% identity	78
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	153466
Seq. ID	LIB3176-008-P1-K3-G2
Method	BLASTX
NCBI GI	g3183207
BLAST score	221
E value	2.0e-18
Match length	67
% identity	61
NCBI Description	HYPOTHETICAL PROTEIN KIAA0017 >gi_285999_dbj_BAA02805_ (D13642) KIAA0017 [Homo sapiens]

Seq. No.	153467
Seq. ID	LIB3176-008-P1-K3-G4
Method	BLASTX
NCBI GI	g2306917
BLAST score	202
E value	2.0e-16
Match length	59
% identity	73
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	153468
Seq. ID	LIB3176-008-P1-K3-G5
Method	BLASTN
NCBI GI	g4220627
BLAST score	51
E value	9.0e-20
Match length	193
% identity	4
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	153469
Seq. ID	LIB3176-008-P1-K3-G6
Method	BLASTX
NCBI GI	g401169
BLAST score	232
E value	7.0e-20
Match length	49
% identity	94
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	153470
Seq. ID	LIB3176-008-P1-K3-G7
Method	BLASTX
NCBI GI	g132074
BLAST score	370
E value	5.0e-36
Match length	77
% identity	95
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana

Seq. No.	153471
Seq. ID	LIB3176-008-P1-K3-G9
Method	BLASTX
NCBI GI	g629541
BLAST score	233
E value	7.0e-20
Match length	67
% identity	72
NCBI Description	plasma membrane intrinsic protein 1c - Arabidopsis thaliana >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]

Seq. No.	153472
Seq. ID	LIB3176-008-P1-K3-H1
Method	BLASTN
NCBI GI	g4582444
BLAST score	219
E value	1.0e-120
Match length	245
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	153473
Seq. ID	LIB3176-008-P1-K3-H11
Method	BLASTN
NCBI GI	g4455168
BLAST score	151
E value	2.0e-79
Match length	315
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	153474
Seq. ID	LIB3176-008-P1-K3-H2
Method	BLASTX
NCBI GI	g4262180
BLAST score	236
E value	2.0e-20
Match length	42
% identity	100
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	153475
Seq. ID	LIB3176-008-P1-K3-H3
Method	BLASTX
NCBI GI	g1151244
BLAST score	282
E value	2.0e-25
Match length	57
% identity	100
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	153476
Seq. ID	LIB3176-008-P1-K3-H4
Method	BLASTN
NCBI GI	g3688169
BLAST score	208
E value	1.0e-113
Match length	347
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	153477
Seq. ID	LIB3176-008-P1-K3-H5
Method	BLASTN
NCBI GI	g2618599
BLAST score	114
E value	2.0e-57
Match length	248
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	153478
Seq. ID	LIB3176-008-P1-K3-H8
Method	BLASTX
NCBI GI	g2062161
BLAST score	782
E value	1.0e-83
Match length	165
% identity	50
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	153479
Seq. ID	LIB3176-008-P1-K3-H9
Method	BLASTN

NCBI GI	g4757405
BLAST score	267
E value	1.0e-149
Match length	271
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	153480
Seq. ID	LIB3176-008-P1-K4-A1
Method	BLASTX
NCBI GI	g1169199
BLAST score	433
E value	1.0e-46
Match length	108
% identity	94
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102 >gi_479739_pir__S35271 hypothetical protein - Arabidopsis thaliana >gi_166928 (L11368) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	153481
Seq. ID	LIB3176-008-P1-K4-A10
Method	BLASTX
NCBI GI	g4678226
BLAST score	208
E value	5.0e-17
Match length	44
% identity	93
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	153482
Seq. ID	LIB3176-008-P1-K4-A11
Method	BLASTX
NCBI GI	g1865671
BLAST score	791
E value	1.0e-84
Match length	157
% identity	99
NCBI Description	(Y09061) acetyl-CoA carboxylase, biotin carboxylase subunit [Arabidopsis thaliana]

Seq. No.	153483
Seq. ID	LIB3176-008-P1-K4-A12
Method	BLASTX
NCBI GI	g3023848
BLAST score	965
E value	1.0e-105
Match length	204
% identity	49
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	153484
Seq. ID	LIB3176-008-P1-K4-A2
Method	BLASTX
NCBI GI	g2864609
BLAST score	188
E value	5.0e-14
Match length	75
% identity	48
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana] >gi_4049337_emb_CAA22562_ (AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	153485
Seq. ID	LIB3176-008-P1-K4-A3
Method	BLASTX
NCBI GI	g1363489
BLAST score	515
E value	1.0e-52
Match length	95
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	153486
Seq. ID	LIB3176-008-P1-K4-A4
Method	BLASTX
NCBI GI	g1724100
BLAST score	477
E value	9.0e-48
Match length	189
% identity	49
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	153487
Seq. ID	LIB3176-008-P1-K4-A5
Method	BLASTX
NCBI GI	g4164473
BLAST score	174
E value	3.0e-12
Match length	104
% identity	43
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	153488
Seq. ID	LIB3176-008-P1-K4-A6
Method	BLASTX
NCBI GI	g2353173
BLAST score	619
E value	2.0e-64
Match length	168
% identity	76
NCBI Description	(AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No.	153489
Seq. ID	LIB3176-008-P1-K4-A7

Method	BLASTX
NCBI GI	g2243120
BLAST score	262
E value	8.0e-23
Match length	93
% identity	77
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	153490
Seq. ID	LIB3176-008-P1-K4-A8
Method	BLASTX
NCBI GI	g3337361
BLAST score	675
E value	4.0e-71
Match length	165
% identity	73
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153491
Seq. ID	LIB3176-008-P1-K4-A9
Method	BLASTX
NCBI GI	g3176676
BLAST score	659
E value	3.0e-69
Match length	131
% identity	99
NCBI Description	(AC003671) Similar to carbonic anhydrase gb_L19255 from Nicotiana tabacum. ESTs gb_AA597643, gb_T45390, gb_T43963 and gb_AA597734 come from this gene. [Arabidopsis thaliana]

Seq. No.	153492
Seq. ID	LIB3176-008-P1-K4-B1
Method	BLASTX
NCBI GI	g2119848
BLAST score	907
E value	3.0e-98
Match length	174
% identity	98
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	153493
Seq. ID	LIB3176-008-P1-K4-B11
Method	BLASTX
NCBI GI	g126985
BLAST score	608
E value	2.0e-63
Match length	118
% identity	99
NCBI Description	MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis thaliana]

Seq. No.	153494
Seq. ID	LIB3176-008-P1-K4-B12
Method	BLASTX
NCBI GI	g4583153
BLAST score	375
E value	8.0e-36
Match length	138
% identity	54
NCBI Description	(AF108211) cytosolic inorganic pyrophosphatase [Homo sapiens]

Seq. No.	153495
Seq. ID	LIB3176-008-P1-K4-B2
Method	BLASTX
NCBI GI	g3582340
BLAST score	164
E value	4.0e-11
Match length	125
% identity	43
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	153496
Seq. ID	LIB3176-008-P1-K4-B3
Method	BLASTN
NCBI GI	g16263
BLAST score	55
E value	2.0e-22
Match length	177
% identity	93
NCBI Description	Arabidopsis thaliana EF-1 alpha-A4 (NAEEFTU 4) gene for elongation factor 1-alpha

Seq. No.	153497
Seq. ID	LIB3176-008-P1-K4-B4
Method	BLASTX
NCBI GI	g3023742
BLAST score	563
E value	7.0e-58
Match length	139
% identity	84
NCBI Description	FERREDOXIN 2 PRECURSOR >gi_1931646 (U95973) ferredoxin precusor isolog [Arabidopsis thaliana]

Seq. No.	153498
Seq. ID	LIB3176-008-P1-K4-B5
Method	BLASTN
NCBI GI	g4220637
BLAST score	69
E value	3.0e-30
Match length	303
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	153499
Seq. ID	LIB3176-008-P1-K4-B6

Method	BLASTX
NCBI GI	g3122572
BLAST score	391
E value	6.0e-38
Match length	125
% identity	63
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	153500
Seq. ID	LIB3176-008-P1-K4-B7
Method	BLASTX
NCBI GI	g3337361
BLAST score	280
E value	5.0e-25
Match length	62
% identity	81
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	153501
Seq. ID	LIB3176-008-P1-K4-B8
Method	BLASTX
NCBI GI	g1175013
BLAST score	374
E value	3.0e-36
Match length	94
% identity	79
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	153502
Seq. ID	LIB3176-008-P1-K4-C1
Method	BLASTX
NCBI GI	g3915826
BLAST score	791
E value	1.0e-84
Match length	195
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	153503
Seq. ID	LIB3176-008-P1-K4-C10
Method	BLASTX
NCBI GI	g4539292
BLAST score	494
E value	5.0e-50
Match length	96
% identity	97
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	153504
Seq. ID	LIB3176-008-P1-K4-C11
Method	BLASTX
NCBI GI	g132677
BLAST score	666
E value	5.0e-70
Match length	163
% identity	80
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	153505
Seq. ID	LIB3176-008-P1-K4-C12
Method	BLASTX
NCBI GI	g3914740
BLAST score	557
E value	3.0e-57
Match length	142
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	153506
Seq. ID	LIB3176-008-P1-K4-C2
Method	BLASTX
NCBI GI	g2245000
BLAST score	517
E value	9.0e-53
Match length	113
% identity	95
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153507
Seq. ID	LIB3176-008-P1-K4-C3
Method	BLASTX
NCBI GI	g3892056
BLAST score	623
E value	6.0e-65
Match length	128
% identity	98
NCBI Description	(AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	153508
Seq. ID	LIB3176-008-P1-K4-C4
Method	BLASTX
NCBI GI	g2129639
BLAST score	642
E value	2.0e-67
Match length	128
% identity	100
NCBI Description	luminal binding protein (BiP) - Arabidopsis thaliana >gi_1303695_dbj_BAA12348_ (D84414) luminal binding protein (BiP) [Arabidopsis thaliana]

Seq. No.	153509
Seq. ID	LIB3176-008-P1-K4-C5
Method	BLASTX
NCBI GI	g1002803
BLAST score	489
E value	2.0e-49
Match length	105
% identity	91
NCBI Description	(U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	153510
Seq. ID	LIB3176-008-P1-K4-C6
Method	BLASTX
NCBI GI	g2342728
BLAST score	357
E value	6.0e-34
Match length	120
% identity	57
NCBI Description	(AC002341) Cysteine proteinase isolog [Arabidopsis thaliana]

Seq. No.	153511
Seq. ID	LIB3176-008-P1-K4-C7
Method	BLASTX
NCBI GI	g1928991
BLAST score	138
E value	8.0e-09
Match length	30
% identity	90
NCBI Description	(U92815) heat shock protein 70 precursor [Citrullus lanatus]

Seq. No.	153512
Seq. ID	LIB3176-008-P1-K4-C9
Method	BLASTN
NCBI GI	g2252848
BLAST score	161
E value	2.0e-85
Match length	233
% identity	93
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	153513
Seq. ID	LIB3176-008-P1-K4-D1
Method	BLASTX
NCBI GI	g113026
BLAST score	341
E value	5.0e-32
Match length	67
% identity	97
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	153514
Seq. ID	LIB3176-008-P1-K4-D10
Method	BLASTX
NCBI GI	g114335
BLAST score	238
E value	3.0e-20
Match length	50
% identity	96
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	153515
Seq. ID	LIB3176-008-P1-K4-D11
Method	BLASTX
NCBI GI	g117238
BLAST score	503
E value	5.0e-51
Match length	142
% identity	75
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	153516
Seq. ID	LIB3176-008-P1-K4-D12
Method	BLASTN
NCBI GI	g4581084
BLAST score	376
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	153517
Seq. ID	LIB3176-008-P1-K4-D2
Method	BLASTX
NCBI GI	g1718097
BLAST score	589
E value	6.0e-61
Match length	165
% identity	62
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	153518
Seq. ID	LIB3176-008-P1-K4-D3
Method	BLASTN
NCBI GI	g3046851
BLAST score	446
E value	0.0e+00
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	153519
Seq. ID	LIB3176-008-P1-K4-D4
Method	BLASTN
NCBI GI	g4559344
BLAST score	50
E value	4.0e-19
Match length	384
% identity	13
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	153520
Seq. ID	LIB3176-008-P1-K4-D5
Method	BLASTX
NCBI GI	g115767
BLAST score	612
E value	6.0e-64
Match length	118
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	153521
Seq. ID	LIB3176-008-P1-K4-D6
Method	BLASTX
NCBI GI	g4309731
BLAST score	219
E value	1.0e-17
Match length	110
% identity	41
NCBI Description	(AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No.	153522
Seq. ID	LIB3176-008-P1-K4-D7
Method	BLASTX
NCBI GI	g2224911
BLAST score	90
E value	4.0e-36
Match length	98
% identity	77

NCBI Description	(U93048) somatic embryogenesis receptor-like kinase [Daucus carota]

Seq. No.	153523
Seq. ID	LIB3176-008-P1-K4-D9
Method	BLASTX
NCBI GI	g1170373
BLAST score	705
E value	1.0e-74
Match length	147
% identity	93
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	153524
Seq. ID	LIB3176-008-P1-K4-E1
Method	BLASTX
NCBI GI	g2497857
BLAST score	777
E value	5.0e-83
Match length	178
% identity	88
NCBI Description	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi_2117463_pir__S57958 malate dehydrogenase (EC 1.1.1.37) - rape >gi_899226_emb_CAA61621_ (X89451) malate dehydrogenase [Brassica napus]

Seq. No.	153525
Seq. ID	LIB3176-008-P1-K4-E10
Method	BLASTX
NCBI GI	g3769300
BLAST score	664
E value	5.0e-73
Match length	164
% identity	86
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	153526
Seq. ID	LIB3176-008-P1-K4-E11
Method	BLASTX
NCBI GI	g2905657
BLAST score	154
E value	5.0e-10
Match length	71
% identity	48
NCBI Description	(AF047469) arsenite translocating ATPase [Homo sapiens]

Seq. No.	153527
Seq. ID	LIB3176-008-P1-K4-E12
Method	BLASTX
NCBI GI	g1172873
BLAST score	282
E value	4.0e-25
Match length	149
% identity	45

NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.	153528
Seq. ID	LIB3176-008-P1-K4-E2
Method	BLASTX
NCBI GI	g4454036
BLAST score	822
E value	3.0e-88
Match length	151
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]
Seq. No.	153529
Seq. ID	LIB3176-008-P1-K4-E3
Method	BLASTX
NCBI GI	g2062157
BLAST score	411
E value	1.0e-40
Match length	83
% identity	37
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
Seq. No.	153530
Seq. ID	LIB3176-008-P1-K4-E4
Method	BLASTX
NCBI GI	g4469007
BLAST score	691
E value	4.0e-73
Match length	134
% identity	99
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]
Seq. No.	153531
Seq. ID	LIB3176-008-P1-K4-E5
Method	BLASTX
NCBI GI	g1762584
BLAST score	373
E value	5.0e-36
Match length	95
% identity	79
NCBI Description	(U63373) polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]
Seq. No.	153532
Seq. ID	LIB3176-008-P1-K4-E6
Method	BLASTX
NCBI GI	g280386
BLAST score	652
E value	2.0e-68
Match length	127
% identity	99